

```

Oy 1 ANGFLXXLRNGSLAKRCXXLTSEFXAEXIFRNXXXTXRTQFW 41
    | | | | | : | | | | | : | | | | |
Db 1 ANSFLEELRHSSLERECIEICDFEAKKEIFQVDDTLAFW 41

```

```

RESULT 7
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US2003002354A1
; GENERAL INFORMATION:
; APPLICANT: Grilutz, Bryce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grimmel, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-182-263-2

```

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 47.1%          | Score 90          | DB 9     | Length 461 |
| Best Local Similarity | 46.3%          | Pred. No. 1.2e-07 |          |            |
| Matches 19            | Conservative 3 | Mismatches 19     | Indels 0 | Gaps 0     |

```

Oy      1  ANGFLXXLRNGSLRXCRXXLCSFXXAAXIFRXXXXRTQFM 41
         |||||:|||||:|||||:|||||:|||||:|||||:
Db      43  ANSFLEELRHSSLRRECIETICPEEAEKIFQVDDTLAFW 83

```

```

RESULT 8
US-09-978-917A-2
: Sequence 2, Application US/09978917A
: Publication No. US20030027299A1
: GENERAL INFORMATION:
: APPLICANT: Maxygen Aps; Maxygen Holdings
: TITLE OF INVENTION: Protein C or activated protein C-like molecules
: FILE REFERENCE: 0219u8310 - protein C
: CURRENT APPLICATION NUMBER: US/09/978, 917A
: CURRENT FILING DATE: 2001-10-17
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 461
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: (1)...(42)
: FEATURE:
: NAME/KEY: CHAIN
: LOCATION: (43)...(461)
US-09-978-917A-2

```

|                          |       |                    |           |             |
|--------------------------|-------|--------------------|-----------|-------------|
| Query Match              | 47.1% | Score 90;          | DB 9;     | Length 461; |
| Best Local Similarity    | 46.3% | Pred. No. 1.2e-07; |           |             |
| Matches 19; Conservative | 3;    | Mismatches 19;     | Indels 0; | Gaps 0      |

Qy 1 ANGFLXXLRNGSLRXCRXXLCGFXFAFXIFRNXXRTQFW 41  
|||:||||:|||||  
Db 43 ANGFLEELRHSSLERECIEICDEBEAKEIFQVNDTLTAFW 83

## RESULT 9

```

US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          46.6%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.6e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

```

```

Qy      1 ANGFLXXLRNGSLRXCRXXLCGFXXAAXFI PRNXRRTOFW 411
         ||| ||| ||| : ||| ||| : |||
Db      1 ANSFLEELRQGSLERECIETCOPEEAEIIFEDVDTLAFW 411

```

```

RESULT 10
US-09-118-748-2
: Sequence 2, Application US/09118748A
: Patent No. US20020031799A1
: GENERAL INFORMATION:
: APPLICANT: Stafford, Darrel W.
: APPLICANT: Chang, JinLi
: TITLE OF INVENTION: Factor Ix Antihemophilic Factor with Increased Clotting
: TITLE OF INVENTION: Activity
: FILE REFERENCE: 5470-183
: CURRENT APPLICATION NUMBER: US/09/118,748A
: CURRENT FILING DATE: 1998-07-17
: EARLIER APPLICATION NUMBER: 60/053,571
: EARLIER FILING DATE: 1997-07-21
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 415
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-118-748-2

```

|                             |       |               |            |            |
|-----------------------------|-------|---------------|------------|------------|
| Query Match                 | 44.5% | Score 85      | DB 10      | Length 415 |
| Best Local Similarity       | 39.5% | Pred. No.     | 8e-07      |            |
| Best Match 17; Conservative |       | 4; Mismatches | 22; Indels | 0; Gaps    |

**Oy**      2 NGFLXLLRNGSLRXCRXXLCSPAXAFYFRNNXRTRQFVSY 44  
         : | : | : | : | : | : |  
**Dd**     3 SGKLBEFYGNLEECMEERKCSFEAREVFENTETTEFFNKQY 45

```

RESULT 11
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
; TITLE OF INVENTION: with vesicle vector
; FILE REFERENCE: 6627-PA1170

```

```
;; CURRENT APPLICATION NUMBER: US/10/132,829
;; CURRENT FILING DATE: 2002-04-25
;; PRIOR APPLICATION NUMBER: 60/286,314
;; PRIOR FILING DATE: 2001-04-25
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 5
;; LENGTH: 461
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-132-829-5

Query March          44.5%; Score 85; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 8.8e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy      2  NGFLXLRNGSLXRCXRXLCGFXXAFFRXXXRTPQFWVS 44
Db      49  SGKLEFVQGNLERECMEKCSFEBAREVFEVTEVTEVFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17396
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/884,901
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-901-3

Query March          44.5%; Score 85; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 8.8e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy      2  NGFLXLRNGSLXRCXRXLCGFXXAFFRXXXRTPQFWVS 44
Db      49  SGKLEFVQGNLERECMEKCSFEBAREVFEVTEVTEVFWKQY 91

RESULT 13
US-09-759-1308-313
; Sequence 313, Application US/097591308
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarty, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
```

```
;; CURRENT FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: US 09/479,249
;; PRIOR FILING DATE: 2000-01-07
;; PRIOR APPLICATION NUMBER: US 09/559,497
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 09/578,063
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: US 09/333,159
;; PRIOR FILING DATE: 1999-06-14
;; PRIOR APPLICATION NUMBER: US 09/596,194
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 09/342,364
;; PRIOR FILING DATE: 1999-06-29
;; PRIOR APPLICATION NUMBER: US 09/608,452
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/393,996
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: US 09/602,871
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: US 09/420,707
;; PRIOR FILING DATE: 1999-10-19
;; NUMBER OF SEQ ID NOS: 460
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 313
;; LENGTH: 96
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-759-1308-313

Query March          35.1%; Score 67; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 0.00023;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy      11  GSLKXCRXXLCGFXXAFFRXXXRTPQFWVS 44
Db      46  GNLERECNEBLCNYEAREIVDDEKTIAPFWQY 79

RESULT 14
US-09-759-1308-312
; Sequence 312, Application US/097591308
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarty, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirtz, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
```



PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 312  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-130B-312

Query Match 35.1%; Score 67; DB 9; Length 209;  
Best Local Similarity 38.2%; Pred. No. 0.0005;  
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSIAXRCRXXLCSPXXAFXIFRNXXRTROPWVS 44  
DB 46 GNLERECNEELCNVEAREIFVDEKTIAPWQEX 79

## RESULT 15

US-09-759-130B-310  
Sequence 310, Application US/09759130B  
Publication No. US2003002279A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: McCarthy, Sean A  
APPLICANT: Fraser, Christopher C  
APPLICANT: Sharp, John D  
APPLICANT: Barnes, Thomas S  
APPLICANT: Kirst, Susan J  
APPLICANT: Mackay, Charles R  
APPLICANT: Myers, Paul S  
APPLICANT: Leiby, Kevin R  
APPLICANT: Wrighton, Nicolas  
APPLICANT: Goodearl, Andrew  
APPLICANT: Holtzman, Douglas A  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USGS.  
FILE REFERENCE: MP100-535OMNIM  
CURRENT APPLICATION NUMBER: US/09/759,130B  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: US 09/479,249  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/559,497  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 09/578,063  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/333,159  
PRIOR FILING DATE: 1999-06-14  
PRIOR APPLICATION NUMBER: US 09/596,194  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/342,364  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 310  
LENGTH: 226  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-759-130B-310

Query Match 35.1%; Score 67; DB 9; Length 226;  
Best Local Similarity 38.2%; Pred. No. 0.00055;  
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSIAXRCRXXLCSPXXAFXIFRNXXRTROPWVS 44  
DB 63 GNLERECNEELCNVEAREIFVDEKTIAPWQEX 96

Search completed: March 20, 2003, 13:30:20  
Job time : 9.375 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds  
(without alignments)  
186.869 Million cell updates/sec

Title: 10ASP28GLU\_4  
Perfect score: 190  
Sequence: 1 ANGFLXLRGSLRXCRXX.....XXAEXIFRNXXRTQFWVSX 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
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14: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
21: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
22: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
23: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 156   | 82.1        | 44     | AAV18306  | Bovine factor VII   |
| 2          | 156   | 82.1        | 44     | AAAB36396 | Bovine factor VII   |
| 3          | 130   | 68.4        | 44     | AAV18311  | Modified GLA domain |
| 4          | 126   | 66.3        | 44     | AAV18310  | Modified GLA domain |
| 5          | 123   | 64.7        | 44     | AAV18305  | Human factor VII G  |
| 6          | 123   | 64.7        | 44     | AAAB36395 | Human factor VII G  |
| 7          | 123   | 64.7        | 401    | AAAB4870  | Mutant blood coagu  |
| 8          | 123   | 64.7        | 401    | AAAB4871  | Mutant blood coagu  |
| 9          | 123   | 64.7        | 406    | AAAB3764  | Factor VII (VII).   |
| 10         | 123   | 64.7        | 406    | AAV14509  | Modified blood coa  |

|    |     |      |     |    |          |                    |
|----|-----|------|-----|----|----------|--------------------|
| 11 | 123 | 64.7 | 406 | 18 | AAV14510 | Modified blood coa |
| 12 | 123 | 64.7 | 406 | 22 | AAU77745 | Human factor VIIa  |
| 13 | 123 | 64.7 | 406 | 22 | AAV52171 | Human FVII SEQ ID  |
| 14 | 123 | 64.7 | 406 | 22 | AAV52172 | Mammalian expresse |
| 15 | 123 | 64.7 | 406 | 22 | AAV52181 | Human FVII mutant  |
| 16 | 123 | 64.7 | 406 | 22 | AAV52182 | Human FVII mutant  |
| 17 | 123 | 64.7 | 406 | 22 | AAV52183 | Human FVII mutant  |
| 18 | 123 | 64.7 | 406 | 22 | AAV52184 | Human FVII mutant  |
| 19 | 123 | 64.7 | 406 | 22 | AAV52185 | Human FVII mutant  |
| 20 | 123 | 64.7 | 406 | 22 | AAV52186 | Human FVII mutant  |
| 21 | 123 | 64.7 | 406 | 22 | AAV52187 | Human FVII mutant  |
| 22 | 123 | 64.7 | 406 | 22 | AAV52188 | Wild-type human bl |
| 23 | 123 | 64.7 | 406 | 22 | AAV52189 | Mutant blood coagu |
| 24 | 123 | 64.7 | 406 | 22 | AAV52190 | Mutant blood coagu |
| 25 | 123 | 64.7 | 406 | 22 | AAV52191 | Mutant blood coagu |
| 26 | 123 | 64.7 | 406 | 23 | AAV52192 | Human coagulation  |
| 27 | 123 | 64.7 | 406 | 23 | AAV52193 | Human coagulation  |
| 28 | 123 | 64.7 | 406 | 23 | AAV52194 | Human coagulation  |
| 29 | 123 | 64.7 | 406 | 23 | AAV52195 | Human coagulation  |
| 30 | 123 | 64.7 | 406 | 23 | AAV52196 | Human coagulation  |
| 31 | 123 | 64.7 | 406 | 23 | AAV52197 | Human coagulation  |
| 32 | 123 | 64.7 | 406 | 23 | AAV52198 | Human coagulation  |
| 33 | 123 | 64.7 | 406 | 23 | AAV52199 | Human coagulation  |
| 34 | 123 | 64.7 | 406 | 23 | AAV52200 | Human coagulation  |
| 35 | 123 | 64.7 | 406 | 23 | AAV52201 | Human coagulation  |
| 36 | 123 | 64.7 | 406 | 23 | AAV52202 | Human coagulation  |
| 37 | 123 | 64.7 | 406 | 23 | AAV52203 | Human coagulation  |
| 38 | 123 | 64.7 | 406 | 23 | AAV52204 | Human coagulation  |
| 39 | 123 | 64.7 | 406 | 23 | AAV52205 | Human coagulation  |
| 40 | 123 | 64.7 | 406 | 23 | AAV52206 | Human coagulation  |
| 41 | 123 | 64.7 | 406 | 23 | AAV52207 | Human coagulation  |
| 42 | 123 | 64.7 | 406 | 23 | AAV52208 | Human coagulation  |
| 43 | 123 | 64.7 | 406 | 23 | AAV52209 | Human coagulation  |
| 44 | 123 | 64.7 | 406 | 23 | AAV52210 | Human coagulation  |
| 45 | 123 | 64.7 | 406 | 23 | AAV52211 | Human coagulation  |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| AAV18306 | AAV18306 standard; peptide; 44 AA.                          |
| AC       | AAV18306;   |
| DT       | 17-AUG-1999 (first entry)                                   |
| XX       | Bovine factor VII GLA domain.                               |
| DE       |   |
| XX       | GLA domain; vitamin K-dependent protein; clotting disorder; |
| KM       | therapy.  |
| XX       |   |
| OS       | Bos taurus.   |
| XX       |   |
| XX       | Key   |
| FT       | Misc-difference 1..44                                       |
| FT       | /note= "Aaa= gamma-carboxyglutamic acid, or glutamic acid"  |
| XX       |   |
| XX       | MO9920767-A1.   |
| XX       |   |
| PD       | 29-APR-1999.  |
| XX       |   |
| XX       | 20-OCT-1998; 98WO-US22152.                                  |
| XX       |   |
| PR       | 23-OCT-1997; 97US-0955636.                                  |
| XX       |   |
| PA       | (MINU ) UNIV MINNESOTA.                                     |
| XX       |   |
| XX       | Neisestuen GI;  |
| PI       |   |
| XX       |   |
| DR       | WPI; 1999-288309/24.  |

```
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
PS
XX Disclosure; Page 15; 86pp; English.
CC
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
CC
XX Sequence 44 AA;
SQ
Query Match 82.1%; Score 156; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 8.1e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 ANGFLXLLRDSGLXRXCRXXLCSPFXAEXIFRNXXRTQFWVS Y 44
Db 1 ANGFLXLLRPSGLXRXCRXXLCSPFXAHXIFRNXXRTQFWVS Y 44
RESULT 2
AAB36396
ID AAB36396 standard; peptide; 44 AA.
XX
AC AAB36396;
XX
DT 27-FEB-2001 (first entry)
XX
DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
XX
KM Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KM factor X; prothrombin; enhanced membrane binding affinity;
KM clot formation; thrombolytic; haemostatic; bleeding disorder;
KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
KM liver disease.
XX
OS Bos taurus.
XX
PN WO200066753-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11416.
XX
PR 29-APR-1999; 99US-0302239.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Neiseetuen GL;
XX
DR WPI; 2001-007226/01.
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
PS Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
```

```
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
CC
XX Sequence 44 AA;
SQ
Query Match 82.1%; Score 156; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 8.1e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 ANGFLXLLRDSGLXRXCRXXLCSPFXAEXIFRNXXRTQFWVS Y 44
Db 1 ANGFLXLLRPSGLXRXCRXXLCSPFXAHXIFRNXXRTQFWVS Y 44
RESULT 3
AAV18311
ID AAV18311 standard; peptide; 44 AA.
XX
AC AAV18311;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KM therapy.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44 "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
PN WO9920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22152.
XX
PR 23-OCT-1997; 97US-0955636.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Neiseetuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
PS Disclosure; Page 80; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
CC
XX Sequence 44 AA;
SQ
Query Match 68.4%; Score 130; DB 20; Length 44;
Best Local Similarity 77.3%; Pred. No. 1.2e-13;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```



```

XX 28-APR-2000; 2000WO-US11416.
PF 29-APR-1999; 99US-0302239.
XX (MINU ) UNIV MINNESOTA.
PA
XX Nelssestuen GL;
PI
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
XX Disclosure; Page 12; 81pp; English.
PS
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can be thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX Sequence 44 AA;
SQ
Query Match 64.7%; Score 123; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLXLRDGLXRCXRLCSFXXAEXIFRNXXRTQFWVS 44
DB 1 ANAFPLXLRPGSLXRCXKXCSFXXARXIFPDARTKLFWISY 44
RESULT 7
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
XX AAB84870;
AC
XX 31-JUL-2001 (first entry)
DT
XX Mutant blood coagulant factor VII (FVII-31).
DE
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM mutant; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
PD
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
PA

```

```

XX WPI; 2001-310677/33.
DR N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
PT
XX Claim 14; Page 20-21; 29pp; Japanese.
PS
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 64.7%; Score 123; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.4e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLXLRDGLXRCXRLCSFXXAEXIFRNXXRTQFWVS 44
DB 1 ANAFLELRPGSLERECKEBCSFPEARIFPDARTKLFWISY 44
RESULT 8
AAB84871
ID AAB84871 standard; Protein; 401 AA.
XX
XX AAB84871;
AC
XX 31-JUL-2001 (first entry)
DT
XX Mutant blood coagulant factor VII (FVII-39).
DE
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM mutant; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 235..239
FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
FT Asp-Arg-Lys-Thr-Leu"
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
PD
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
DR N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
PT
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ

```

Query Match 64.7%; Score 123; DB 22; Length 401;  
Best Local Similarity 52.3%; Pred. No. 1.4e-11;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLXKRCXFXAXEIPRNXXRTROFWVS 44  
1 ANAFLEELRPQSLRECKEBCSFPEAREIFKDAERTLFWISY 44

RESULT 9  
AAR35764  
ID AAR35764 standard; protein; 406 AA.

XX AAR35764;  
XX 24-SEP-1993 (first entry)  
XX Factor VII (VII).

XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;  
XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;  
XX exosite; catalytic activity.

OS Homo sapiens.

XX Location/Qualifiers

PH Key 1..152

FT Region /note= "Factor VII light chain"

FT Region 153..406

FT Peptide /note= "Factor VII heavy chain"

FT Peptide 374..388

FT Peptide /note= "exosite 1"

FT Peptide 290..310

FT Peptide /note= "exosite 2"

FT Peptide 290..310

FT Peptide /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 374..388

FT Peptide /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 289..304

FT Peptide /note= "pref. PC polypeptide; claim 4, page 137"

FT Peptide 290..304

FT Peptide /note= "pref. PC polypeptide; claim 4, page 137"

FT Peptide 245..266

FT Peptide /note= "claim 9, page 138-139 describes an antibody  
that reacts with Factor VII; fragments  
289-304, 290-310, 374-388 and  
400-414 but not with fragment 245-266"

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

FT Peptide

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FT Peptide

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FT Peptide

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FT Peptide

FT Peptide

FT Peptide

CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described  
CC in the specification but have not yet been added to the SEQUENCE  
CC LISTING.  
XX Sequence 406 AA;

Qy 1 ANGFLXXLRDGLXKRCXFXAXEIPRNXXRTROFWVS 44  
1 ANAFLEELRPQSLRECKEBCSFPEAREIFKDAERTLFWISY 44

RESULT 10  
AAW14509  
ID AAW14509 standard; protein; 406 AA.

XX AAW14509;  
XX 14-MAY-1997 (first entry)  
XX Modified blood coagulation Factor VII (R290S).

XX Blood coagulation; factor 7; mutation; modification;  
XX thrombocytopenia; von Willebrand's disease; plasma substitute.

OS Homo sapiens.

XX Synthetic.

XX Key

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

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FT Modified-site

|    |   |                                     |  |
|----|---|-------------------------------------|--|
| FT | Modified-site   | 63                                  | /label= OTHER  |
| FT |   | /note= "beta-hydroxy-aspartic acid" |  |
| FT | Disulfide-bond  | 72..81                              |  |
| FT | Disulfide-bond  | 91..102                             |  |
| FT | Disulfide-bond  | 98..112                             |  |
| FT | Disulfide-bond  | 114..127                            |  |
| FT | Disulfide-bond  | 135..162                            |  |
| FT | Cleavage-site   | 143..144                            | /note= "proteolytic site"  |
| FT | Modified-site   | 145                                 | /note= "glycosylation site"  |
| FT | Disulfide-bond  | 159..164                            |  |
| FT | Disulfide-bond  | 178..194                            |  |
| FT | Active-site   | 193                                 |  |
| FT | Active-site   | 242                                 |  |
| FT | Active-site   | 344                                 |  |
| FT | Cleavage-site   | 290..291                            | /note= "proteolytic site in unmodified factor VII"   |
| FT | Misc-difference   | 290                                 | /note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond" |
| FT | Disulfide-bond  | 310..329                            |  |
| FT | Cleavage-site   | 315..316                            |  |
| FT | Modified-site   | 322                                 | /note= "proteolytic site"  |
| FT | Modified-site   | 322                                 | /note= "glycosylation site"  |
| FT | Disulfide-bond  | 340..368                            |  |
| FT | Cleavage-site   | 341..342                            | /note= "proteolytic site"  |
| FT | Cleavage-site   | 392..393                            | /note= "proteolytic site"  |
| FT | Cleavage-site   | 396..397                            | /note= "proteolytic site"  |
| FT | Cleavage-site   | 402..403                            | /note= "proteolytic site"  |
| XX | US5580560-A.  |                                     |  |
| XX | 03-DEC-1996.  |                                     |  |
| XX | 13-NOV-1989;  | 89US-0434149.                       |  |
| XX | 09-AUG-1993;  | 93US-0104509.                       |  |
| PR | 13-NOV-1989;  | 89US-0434149.                       |  |
| PR | 12-JUN-1992;  | 92US-0898248.                       |  |
| PR | 22-AUG-1994;  | 94US-0293778.                       |  |
| XX | (NOVO ) NOVO-NORDISK AS.  |                                     |  |
| XX | Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;   |                                     |  |
| XX | WPI: 1997-033523/03.  |                                     |  |
| XX | Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability  |                                     |  |
| XX | Example 3; Page -; 28pp; English.   |                                     |  |
| CC | Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys832, Lys838, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys832 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. The present sequence is a specific example of a modified factor VII protein. |                                     |  |
| XX | Sequence  | 406 AA;                             |  |

|                       |  |  |                                     |            |
|-----------------------|--|--|-------------------------------------|------------|
| Query Match           | 64.7%  | Score 123                                    | DB 18                               | Length 406 |
| Best Local Similarity | 52.3%  | Ped. No. 1.4e-11                             |                                     |            |
| Matches 23            | Conservative 5   | Mismatches 16                                | Indels 0                            |            |
| Qy                    | 1  | ANGFLXLRDGLXRXCRXXLCSFXAXEIRFXRXXTROFWY      | 44                                  |            |
|                       |  |  |                                     |            |
| Db                    | 1  | AAAFLEELRPSGLERCKEEOCSFEFARIRFXDAERTKULFWISY | 44                                  |            |
|                       |  |  |                                     |            |
| RESULT 11             |  |  |                                     |            |
| AAW14510              |  |  |                                     |            |
| ID                    | AAW14510   | standard; protein; 406 AA.                   |                                     |            |
| XX                    | AAW14510   |  |                                     |            |
| AC                    |  |  |                                     |            |
| XX                    |  |  |                                     |            |
| DT                    | 14-MAY-1997  | (first entry)                                |                                     |            |
| XX                    |  |  |                                     |            |
| DE                    | Modified blood coagulation Factor VII (R315S).               |  |                                     |            |
| XX                    |  |  |                                     |            |
| KW                    | Blood coagulation; factor 7; muten; mutation; modification;  |  |                                     |            |
| XX                    | thrombocytopenia; von Willebrand's disease; plasma substrate |  |                                     |            |
| XX                    |  |  |                                     |            |
| OS                    | Homo sapiens.  |  |                                     |            |
| XX                    | Synthetic.   |  |                                     |            |
| XX                    |  |  |                                     |            |
| FH                    | Key  | Location/Qualifiers                          |                                     |            |
| FT                    | Modified-site  | 6  | /label= OTHER                       |            |
| FT                    |  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 7  | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 14   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 16   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 19   | /note= "gamma-carboxylutamic acid"  |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 20   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 17..22                                       | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 25   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 26   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 29   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 32..33                                       | /note= "gamma-carboxylutamic acid"  |            |
| FT                    | Modified-site  | /note= "proteolytic site"                    |                                     |            |
| FT                    |  | 35   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "gamma-carboxylutamic acid"           |                                     |            |
| FT                    |  | 38..39                                       | /note= "proteolytic site"           |            |
| FT                    | Cleavage-site  | /note= "proteolytic site"                    |                                     |            |
| FT                    |  | 42..43                                       | /note= "proteolytic site"           |            |
| FT                    | Cleavage-site  | /note= "proteolytic site"                    |                                     |            |
| FT                    |  | 44..45                                       | /note= "proteolytic site"           |            |
| FT                    | Cleavage-site  | /note= "proteolytic site"                    |                                     |            |
| FT                    |  | 50..61                                       | /note= "proteolytic site"           |            |
| FT                    | Modified-site  | /note= "proteolytic site"                    |                                     |            |
| FT                    |  | 63   | /label= OTHER                       |            |
| FT                    | Modified-site  | /note= "beta-hydroxy-aspartic acid"          |                                     |            |
| FT                    |  | 72..81                                       | /note= "beta-hydroxy-aspartic acid" |            |
| FT                    | Disulfide-bond   | 91..102                                      | /note= "beta-hydroxy-aspartic acid" |            |
| FT                    | Disulfide-bond   | 98..112                                      | /note= "beta-hydroxy-aspartic acid" |            |







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XX 12-FEB-2001; 2001WO-DK00094.
PF 11-FEB-2000; 2000DK-0000218.
PR 18-OCT-2000; 2000DK-0001558.
XX (MAXY-) MAXYGEN APS.
PI Andersen KV, Pedersen AH, Bornaes C;
XX WPI; 2001-581807/65.
DR N-PSDB; AA199983.
XX
PT New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Disclosure; Page 85-86; 89pp; English.
XX
CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
SQ Sequence 406 AA;
XX
Query Match 64.7%; Score 123; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 1.4e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
XX
QY 1 ANGFLXXLRDGLKRXCXLCSPFXAXEIPRNXXRTQPNVSY 44
1 ANAFLLELRPGSLERCKEBOQCSFEAREIFKDAERTKLFMISY 44
Db
XX
RESULT 15
AAM52181
ID AAM52181 standard; Protein; 406 AA.
XX
AC AAM52181;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human FVII mutant T106N.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KM mutcin.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14 /note= "OTHER = gamma carboxyglutamic acid"

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FT /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Misc-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT Modified-site 52 /note= "O-glycosylated"
FT Modified-site 60 /note= "O-glycosylated"
FT Misc-difference 106 /note= "Wild-type Thr substituted by Asn"
FT Modified-site 145 /note= "N-glycosylated"
FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
FT /note= "to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT Modified-site 322 /note= "N-glycosylated"
XX
XX W0200158935-A2.
XX
PD 16-AUG-2001.
XX
PF 12-FEB-2001; 2001WO-DK00094.
XX
PR 11-FEB-2000; 2000DK-0000218.
PR 18-OCT-2000; 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
PI Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3; Page -; 89pp; English.
XX
CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10ASP28GLU\_4  
Perfect score: 190  
Sequence: 1 ANGFLXLDGSLRXRCRX.....XXAEXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 149   | 78.4        | 407    | 1 KFB07  | coagulation factor |
| 2          | 131   | 68.9        | 443    | 2 I46932 | coagulation factor |
| 3          | 123   | 64.7        | 466    | 1 KFH07  | coagulation factor |
| 4          | 109   | 57.4        | 461    | 1 JX0210 | protein C (activat |
| 5          | 107   | 56.3        | 461    | 1 S18994 | protein C (activat |
| 6          | 97    | 51.1        | 456    | 1 KXBO   | protein C (activat |
| 7          | 94    | 49.5        | 482    | 1 EXRT   | coagulation factor |
| 8          | 94    | 49.5        | 488    | 1 EXHU   | coagulation factor |
| 9          | 92    | 48.4        | 461    | 1 KXHU   | protein C (activat |
| 10         | 90    | 47.4        | 492    | 1 EXBO   | coagulation factor |
| 11         | 88    | 46.3        | 461    | 1 KFHU   | coagulation factor |
| 12         | 86    | 45.3        | 416    | 1 KFB0   | coagulation factor |
| 13         | 82    | 43.2        | 475    | 1 EXCH   | coagulation factor |
| 14         | 81    | 42.6        | 452    | 1 A30351 | coagulation factor |
| 15         | 81    | 42.6        | 459    | 2 JQ0419 | coagulation factor |
| 16         | 76    | 40.0        | 622    | 1 TBHU   | thrombin (EC 3.4.2 |
| 17         | 75    | 39.5        | 642    | 2 S53433 | thrombin (EC 3.4.2 |
| 18         | 73    | 38.4        | 617    | 2 S10511 | thrombin (EC 3.4.2 |
| 19         | 73    | 38.4        | 618    | 2 A35827 | thrombin (EC 3.4.2 |
| 20         | 70    | 36.8        | 642    | 2 S53434 | plasma protein S p |
| 21         | 70    | 36.8        | 676    | 1 KXBO   | plasma protein S p |
| 22         | 69    | 36.8        | 675    | 1 KKHUS  | plasma protein S p |
| 23         | 69    | 36.3        | 422    | 1 KKHU   | plasma protein S p |
| 24         | 69    | 36.3        | 645    | 2 S38819 | plasma protein S p |
| 25         | 67    | 35.3        | 625    | 1 TBBO   | thrombin (EC 3.4.2 |
| 26         | 67    | 35.3        | 675    | 1 KXRT   | plasma protein S p |
| 27         | 65    | 34.2        | 396    | 1 KXBO   | plasma protein S p |
| 28         | 60    | 31.6        | 675    | 1 KXMS   | plasma protein S p |
| 29         | 59    | 31.1        | 678    | 2 B48089 | growth arrest-spec |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 58   | 30.5 | 673  | 2 A48089 | growth arrest-spec  |
| 31 | 56   | 29.5 | 413  | 1 VHVNIH | nucleoprotein - in  |
| 32 | 56   | 29.5 | 674  | 2 I55476 | growth potentiatin  |
| 33 | 53   | 27.9 | 605  | 1 W1WLEB | E1 protein - bovin  |
| 34 | 53   | 27.9 | 620  | 1 W1WLEB | E1 protein - bovin  |
| 35 | 49.5 | 26.1 | 594  | 2 D84859 | probable MAP kinase |
| 36 | 49.5 | 26.1 | 603  | 2 C96575 | probable MAP kinase |
| 37 | 48.5 | 25.5 | 576  | 2 G96763 | probable MAP kinase |
| 38 | 48   | 25.3 | 267  | 2 JCI527 | coat protein - pot  |
| 39 | 46   | 24.2 | 204  | 2 E84173 | hypothetical prote  |
| 40 | 45   | 23.7 | 687  | 2 T08528 | probable DNA topoi  |
| 41 | 44   | 23.2 | 304  | 2 A30106 | SEC14 protein - ye  |
| 42 | 44   | 23.2 | 1217 | 2 T21403 | hypothetical prote  |
| 43 | 44   | 23.2 | 1337 | 2 T13948 | atypical protein k  |
| 44 | 43.5 | 22.9 | 952  | 2 AF2058 | ABC transporter At  |
| 45 | 43   | 22.6 | 219  | 2 AE2449 | hypothetical prote  |

ALIGNMENTS

RESULT 1

KFB07 Coagulation factor VIIa (EC 3.4.21.21) - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C/Accession: A31979; C20274

R/Keya, H.; Kawabata, S.; Nakagawa, K.; Yamachi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A/Title: Bovine factor VII. Its purification and complete amino acid sequence.

A/Reference number: A31979; PMID:89008362; PMID:3049594

A/Accession: A31979

A/Molecule type: protein

A/Residues: 1-407 <TRK>

R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A/Reference number: A20274; PMID:83308813; PMID:6688526

A/Accession: C20274

A/Molecule type: protein

A/Residues: 58-62 'X', 64-68 <MCM>

A/Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R/Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.

J. Biochem. 104, 867-868, 1988

A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A/Reference number: A44556; PMID:89213999; PMID:3149637

A/Contents: annotation

A/Note: structure and location of covalently bound carbohydrate

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser

gulation factor IX in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamu

F/1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F/1-44/Domain: Gla domain homology (fragment) <GLA>

F/50-81/Domain: EGF homology <EG1>

F/91-127/Domain: EGF homology <EG2>

F/153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F/153-387/Domain: trypsin homology <TRY>

F/6/7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F/17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/I

F/52/Binding site: carbohydrate (Ser) (covalent) #status experimental

F/63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental

F/145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F/152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental

F/193,242,344/Active site: His, Asp, Ser #status predicted

F/290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 78.4%; Score 149; DB 1; Length 407;  
Best Local Similarity 68.2%; Pred. No. 3; De-18;  
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```

Oy 1 ANGFLXXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWWSY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANGFLLELRPGSLERCKRELCSFEARAEVFOGTERTKQFWWSY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
146932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: I46932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: I46932; MUID:93190306; PMID:8383365
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:S56300; NID:9266294; PID:9266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <GLA>
F:189-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match 68.9%; Score 131; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 5.9e-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWWSY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 ANAFLELRPGSLERCKRELCSFEARAEVFOGTERTKQFWWSY 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
KFNH7
coagulation factor VIIa (BC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28322; A28319; A31186; B31362; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Inley, M.Y.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OHA>
A:Cross-references: GB:J02933; NID:9180333; PID:NAA51983.1; PID:9180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A28319; MUID:86205965; PMID:3486420
A:Accession: A28319
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M1323; NID:9182799; PID:NAA88040.1; PID:9182801
R:Thim, L.; Björn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Björn, S.; Foster, D.C.; Thim, L.; Wiber, F.C.; Christensen, M.; Komiyama, Y.; Pedersen
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations
A:Reference number: A40529; MUID:9150411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Peterson, E.; Petersen, L.C.

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Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy
A:Reference number: S63524; MUID:96096752; PMID:8539655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Gene: GDB:F7
C:Gene: F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domain: Gla domain homology <GLA>
F:61-112/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:110-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66,67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F:112/120/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-116 (coagulation factor XIra) #status experimental
F:253,302,404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 64.7%; Score 123; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 1.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWWSY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ANAFLELRPGSLERCKRELCSFEARAEVFOGTERTKQFWWSY 104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
JX0210
protein C (activated) (BC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tade, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:9220385; PID:NAA01235.1; PID:9220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
B.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <GLA>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <PC>
F:42-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:113-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

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F:212-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
 F:214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 57.4%; Score 109; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 4,4e-11;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCXKXLCSPFXAXEIXFRNXXRTQFWVS 44  
 Db 42 ANSFLBEMRPGSLERECMEICDFEBAQEIFQNVEDTLAFWIKY 85

RESULT 5  
 S18994

protein C (activated) (EC 3.4.21.69) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
 C:Accession: S18994; S24312  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 submitted to the EMBL Data Library, February 1992  
 A:Description: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S18994

A:Accession: S18994  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OKA>  
 A:Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 Biochim. Biophys. Acta 1131, 329-332, 1992

A:Title: The cDNA cloning and mRNA expression of rat protein C.

A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312

A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-461 <OKA2>

A:Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase  
 F:1-32/Domain: signal sequence #status predicted <SIG>

F:27-85/Domain: Gla domain homology <GLA>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-461/Product: protein C #status predicted <PRC>

F:91-130/Domain: EGF homology <EGF>

F:139-174/Domain: EGF homology <EG2>

F:213-445/Domain: trypsin homology <TRY>

F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat  
 F:215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 56.3%; Score 107; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 9.9e-11;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCXKXLCSPFXAXEIXFRNXXRTQFWVS 44  
 Db 42 ANSFLBEMRPGSLERECMEICDFEBAQEIFQNVEDTLAFWIKY 85

RESULT 6  
 KXBO

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)  
 N:Alternate names: autoproteolysin IIA, plasma protein C

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999

C:Accession: A26250; A18385; A00928

R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100

A:Accession: A26250  
 A:Molecule type: mRNA

A:Residues: 1-456 <LON>

R:Stenflo, J.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982

A:Title: Amino acid sequence of the light chain of bovine protein C.

A:Reference number: A18385; MUID:83007325; PMID:6896876

A:Accession: A18385

A:Molecule type: protein

A:Residues: 40-194 <PER>

A>Note: 82-Lys was also found

R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.

A:Reference number: A19316; MUID:83169769; PMID:6572939

A:Contents: annotation; revision to residue 110

R:Stenflo, J.; Fernlund, P.

J. Biol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine protein C.

A:Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386

A:Molecule type: protein

A:Residues: 197-454, 'PV' <STE>

R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.

J. Biol. Chem. 258, 5548-5553, 1983

A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p

A:Reference number: A37541; MUID:83213513; PMID:6304092

A:Contents: annotation; activation; calcium binding

R:Johnson, A.E.; Esmon, N.L.; Lane, T.M.; Esmon, C.T.

J. Biol. Chem. 258, 5554-5560, 1983

A:Title: Structural changes required for activation of protein C are induced by Ca<sup>2+</sup> bind

A:Reference number: A37542; MUID:83213514; PMID:6406503

A:Contents: annotation; activation; calcium binding

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

s.

C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c

bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stric

Cognition of the thrombin-chromodomin complex.

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>

F:24-83/Domain: Gla domain homology <GLA>

F:30-39/Domain: propeptide #status predicted <PRO>

F:40-194/Product: protein C light chain #status experimental <LCH>

F:98-128/Domain: EGF homology <EGF>

F:137-172/Domain: EGF homology <EG2>

F:157-456/Product: protein C heavy chain #status experimental <HCH>

F:157-210/Domain: activation peptide #status experimental <APT>

F:211-440/Domain: trypsin homology <TRY>

F:45,46,53,55,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:119/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119-128,137-148,144-157,159-172,180-318,237-253,368-387,393-421/Disulfide bonds: #stat

F:116,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:252,298,397/Active site: His, Asp, Ser #status predicted

F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.1%; Score 97; DB 1; Length 456;  
 Best Local Similarity 43.2%; Pred. No. 5.6e-09;  
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCXKXLCSPFXAXEIXFRNXXRTQFWVS 44  
 Db 40 ANSFLBEMRPGNVERECSEVCEFEAREIFQNTEDTMAFWFSY 83

RESULT 7  
 EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000  
C:Accession: 549075, UC4670, F50191, F50190, 162745  
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Thromb. Res. 80, 63-73, 1995  
A>Title: Evidence for competition between vitamin K-dependent clotting factors for intracellular binding sites  
A:Reference number: A58498; MUID:96093366; PMID:8578539  
A:Accession: 549075  
A:Molecule type: mRNA  
A:Residues: 1-482 <STAL>  
A:Cross-references: EMBL:X79807, NID:9506600; PIDN:CA56202.1; PID:9506601  
A:Experimental source: Cos-1 cell  
R:Enyoji, K.; Miyazaki, K.; Kato, H.  
J. Biochem. 109, 890-898, 1991  
A>Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat platelets  
A:Reference number: F50190; MUID:92041742; PMID:1718949  
A:Accession: F50191  
A:Molecule type: protein  
A:Residues: 41-58, 'X', 60-65 <ENJ1>  
A:Accession: F50190  
A:Molecule type: protein  
A:Residues: 183-186 'X', 188-207 <ENJ2>  
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
Eur. J. Haematol. 52, 167-169, 1994  
A>Title: Analysis of the partial nucleotide sequences and deduced primary structures of human factor X  
A:Reference number: I46196; MUID:94222160; PMID:8168596  
A:Accession: 162745  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 295-383, 'G', 385-455 <MUR>  
A:Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:9455396  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor Va  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:85-121/Product: coagulation factor X light chain #status predicted <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:120-164/Domain: EGF homology <EG2>  
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
F:183-231/Domain: activation peptide #status predicted <AP>  
F:233-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
F:233-460/Domain: trypsin homology <TRY>  
F:446, 47, 54, 56, 59, 60, 63, 66, 69, 72, 75/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <MOD>  
F:57-62, 90-101, 95-110, 112-120, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 434-440/Modified site: hydroxy-beta-hydroxyaspartic acid (Asp) #status predicted <MOD>  
F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:221-222/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted  
F:274, 350, 417/Active site: His, Asp, Ser #status predicted

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Query March 49.5% Score 94; DB 1; Length 483;
Best Local Similarity 36.4%; Pred. No. 2e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLLRDGSLKRXCRXXLCSFYXAEXIFPNXXRTQFWVSY 44
Db 41 ANSFEEIKKGNLRECEVEICISFEAREVFPEDNKETLEFNVKKY 84
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 8

EXHIBIT 8

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N:Alternate names: Stuart factor

C:Species: Homo sapiens (man)

C:Date: 15-Nov-1994 #sequence revision 02-May-1994 #text change 08-Dec-2000

C:Accession: A24478 JQ0917, A22485, A25533, A22268, A21284, A20362, S39415, I54051, A00184

R:Entry: S.P. Foster, D.C. Kuzach, K.; Davie, E.W.

Biochemistry 25, 5098-5102, 1986

A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization is

A:Reference number: A24478; MUID:87026600; PMID:3768336

A:Accession: A24478

A:Molecule type: DNA

A:Residues: 1-488 <LE>

A:Cross-references: GB:I29433; GB:M4327; NID:945809; PIDN:AAA52764.1; PID:g182831

R:Measler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X

A:Reference number: JQ0917; MUID:91216473; PMID:1992434

A:Accession: JQ0917

A:Molecule type: mRNA

A:Residues: 1-488 <MES>

A:Cross-references: GB:M57285; NID:g182389; PIDN:AAA5421.1; PID:g182390

R:Measler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A:Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor

A:Reference number: A42485; MUID:92218390; PMID:1313796

A:Accession: A42485

A:Molecule type: DNA

A:Residues: 1-15 <MTA>

A:Experimental source: liver

A:Note: Sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)

R:Kanal, R.K.; Hildebrand, B.; Robert, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A:Reference number: A25853; MUID:86221713; PMID:3011603

A:Accession: A25853

A:Molecule type: mRNA

A:Residues: 19-284, 'E', 289-488 <KAU>

A:Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336

R:Fung, M.R.; Hay, C.W.; Macgillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X

A:Reference number: A22208; MUID:85216545; PMID:2582420

A:Accession: A22208

A:Molecule type: mRNA

A:Residues: 13-441, 'S', 443-488 <FUN>

A:Cross-references: GB:K03194; NID:g182840; PIDN:AAA5490.1; PID:g182841

R:Levy, S.P.; Chung, D.W.; Kistiel, W.; Kuzach, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A:Title: Characterization of a cDNA coding for human factor X.

A:Reference number: A21284; MUID:84222026; PMID:6587384

A:Accession: A21284

A:Molecule type: mRNA

A:Residues: 13-284, 'E', 289-488 <LE2>

A:Cross-references: GB:K01866

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss

Biochemistry 22, 2875-2884, 1983

A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X

A:Reference number: A20362; MUID:83257207; PMID:6871167

A:Accession: A20362

A:Molecule type: protein

A:Residues: 41-179 <MCM>

R:Inoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A:Reference number: S39414; MUID:94062825; PMID:8243461

A:Accession: S39415

A:Molecule type: protein

A:Residues: 183-234 <INO>

A:Note: glycosylation sites

A:Note: Identification of O-linked oligosaccharide chains in the activation peptides of

R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusan, K.; Lyman, G.



Gene 84, 517-519, 1989  
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
A:Reference number: 154051; MUID:90128299; PMID:2612918  
A:Accession: 154051  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-references: GB:M33297; NID:9183860; PIDN:AAA52636.1; PID:9553330  
J:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blö  
J: Mol. Biol. 232, 947-966, 1993  
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A:Reference number: A49458; MUID:93360277; PMID:8355279  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
C:Comment: The two chains held together by one disulfide bond are formed from a single-C  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
C:Genetics:  
A:Gene: GDB:P10  
A:Cross-references: GDB:119890; OMIM:227600  
A:Map position: 13q34-13q34  
A:Insertions: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
A:Note: deficiency of this factor causes Stuart disease  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamat  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-119/Product: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:129-164/Domain: EGF homology <EG2>  
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
F:183-334/Domain: activation peptide #status experimental <APT>  
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
F:235-462/Domain: trypsin homology <TRY>  
F:46,47,54,56,59,60,65,66,67,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
F:57-63/Disulfide bonds: #status predicted  
F:90-101,99-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,339-404,415-443/  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:224-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 49.5%; Score 94; DB 1; Length 488;  
Best Local Similarity 36.4%; Pred. No. 2e-08;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRDGLRXCRXXLCSPFXAEXIFRNXXRTQFWVS 44  
Db 41 ANSFLEMKKHLERECMEETCSYEAREVFEDSDKTNEFMNKY 84

RESULT 9  
KXHU  
protein C (activated) (EC 3.4.21.69) precursor - human  
N:Alternate names: autoprothrombin IIA; plasma protein C  
C:Species: Homo sapiens (man)  
C>Date: 17-Mar-1997 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
C:Accession: A22311; A25426; A21781; A23789; A00927  
R:Forster, D.C.; Yoshitake, S.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
A:Title: The nucleotide sequence of the gene for human protein C.  
A:Reference number: A22311; MUID:85270390; PMID:2991887  
A:Accession: A22311  
A:Molecule type: DNA  
A:Residues: 1-461 <FOS1>  
A:Cross-references: GB:M1228; NID:9190333; PIDN:AAA60166.1; PID:9190334  
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
A:Title: Evolution and organization of the human protein C gene.  
A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426  
A:Molecule type: DNA  
A:Residues: 1-445; 'L', 446-461 <PLU>  
A:Cross-references: GB:M12712; NID:9190330; PIDN:AAA60165.1; PID:9190332  
R:Forster, D.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
A:Title: Characterization of a cDNA coding for human protein C.  
A:Reference number: A21781; MUID:84272714; PMID:6589623  
A:Accession: A21781  
A:Molecule type: mRNA  
A:Residues: 'Q', 107-461 <FOS2>  
A:Cross-references: GB:X02059; NID:9190322; PIDN:AAA60164.1; PID:9190323  
R:Beckmann, R.J.; Schmitt, R.J.; Santeirre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
Nucleic Acids Res. 13, 5233-5247, 1985  
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and it  
A:Reference number: A23789; MUID:85269633; PMID:2991889  
A:Accession: A23789  
A:Molecule type: mRNA  
A:Residues: 1-461 <BEC>  
A:Cross-references: GB:X02750; NID:935689; PIDN:CAA26528.1; PID:9763120  
R:Meitlich, J.P.; Broze Jr., G.J.  
J. Biol. Chem. 265, 11397-11404, 1990  
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me  
A:Reference number: A44605; MUID:90293094; PMID:1694179  
A:Contents: annotation; carboxylate binding sites; activation peptide  
A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
R:Harris, R.J.; Ling, V.T.; Spellman, M.W.  
J. Biol. Chem. 267, 5102-5107, 1992  
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor  
A:Reference number: A44606; MUID:92184750; PMID:1544894  
A:Contents: annotation; beta-hydroxyaspartic acid  
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also fe  
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is cl  
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
C:Genetics:  
A:Gene: GDB:PROC  
A:Cross-references: GDB:120317; OMIM:176860  
A:Map position: 2q13-2q21  
A:Insertions: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:27-86/Domain: Gla domain homology <GLA>  
F:33-42/Domain: propeptide #status predicted <PRO>  
F:43-197/Product: protein C light chain #status predicted <LCH>  
F:92-131/Domain: EGF homology <EG1>  
F:140-175/Domain: EGF homology <EG2>  
F:200-211/Product: protein C heavy chain #status predicted <HCH>  
F:212-445/Domain: trypsin homology <TRY>  
F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,338-354,373-387,398-426/D  
F:106-111/Disulfide bonds: #status predicted  
F:110/Binding site: carboxylate (Thr) (covalent) #status absent  
F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:211-212/Cleavage site: Arg-Leu (chrombin) #status experimental  
F:251,299,402/Active site: His, Asp, Ser #status predicted  
F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 48.4%; Score 92; DB 1; Length 461;  
Best Local Similarity 46.3%; Pred. No. 4.3e-08;  
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRDGLRXCRXXLCSPFXAEXIFRNXXRTQFW 41  
Db 43 ANSFLEMRHSLRRECEBECDFEAKETFGVNDTLAFW 83

RESULT 10  
EXBO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #next change 16-Jul-1999  
 A:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Func: M.R.; Campbell, R.M.; MacGillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; MUID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <GUN>  
 A:Cross-references: GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochemistry 19, 659-667, 1980  
 A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, 'N', 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T  
 A>Note: carboxylate binding sites and disulfide bonds were determined  
 R:Peterson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Slenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; MUID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A>Note: beta-hydroxyaspartic acid site  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196;199-209;216-233 <INO>  
 A>Note: carboxylate binding sites  
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D  
 Biochemistry 11, 4899-4903, 1972  
 A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal  
 A:Reference number: A12453; MUID:73053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Slenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic  
 A:Reference number: A38024; MUID:84185716; PMID:6546530  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of tw  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with seric  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Genetics:  
 A:Gene: P10  
 A:Map position: 13q34  
 C:Function:  
 A>Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PPO>  
 F:41-180/Domain: Gla domain homology <Gla>  
 F:129-121/Domain: BGF homology <BGF>  
 F:129-164/Domain: BGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <AP>  
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F:234-461/Domain: trypsin homology <TRY>  
 F:46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #s  
 F:57-62, 90, 101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #status p  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:208, 485/Binding site: sulfite (Tyr) (covalent) (partial) #status experimental  
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental  
 F:275, 321, 418/Active site: His, Asp, Ser #status predicted  
 Query Match 47.4%; Score 90; DB 1; Length 492;  
 Best Local Similarity 36.4%; Pred. No. 1e-07;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRDGLXCRXKLCSPXAXEIPFNKXRTQFWVS 44  
 DB 41 ANSFLEVKQGNLRECEACSLREAREVPEDADQTEFWSKY 84  
 RESULT 11  
 KFHU  
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
 N:Alternate names: antihemophilic factor B; Christmas factor  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #next change 15-Sep-2000  
 A:Accession: A00922; A37570; J03511; A32989; A22673; A21337; A37546; A30623; A60486; A20  
 R:Ioelentake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kutach, K.  
 Biochemistry 24, 3736-3750, 1985  
 A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).  
 A:Reference number: A00922; MUID:8600558; PMID:2994716  
 A:Accession: A00922  
 A:Molecule type: DNA  
 A:Residues: 1-461 <YOS>  
 A:Cross-references: GB:K02402; NID:G182612; PIDN:AMB59620.1; PID:G182613  
 R:Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro  
 EMBO J. 3, 1053-1060, 1984  
 A>Title: The gene structure of human anti-haemophilic factor IX.  
 A:Reference number: A37570; MUID:84236100; PMID:6328734  
 A:Accession: A37570  
 A:Molecule type: DNA  
 A:Residues: 1-461 <ANS>  
 A:Cross-references: GB:K02048  
 R:Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
 Blood 72, 1074-1076, 1988  
 A>Title: The putative factor IX gene promoter in hemophilia B Leyden.  
 A:Reference number: A30511; MUID:88327116; PMID:3416069  
 A:Accession: A30511  
 A:Molecule type: DNA  
 A:Residues: 8-24 <REI>  
 A:Cross-references: EMBL:X55008; NID:G311288; PIDN:CAB38245.2; PID:G4469253  
 R:Koeberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor  
 A:Reference number: A32989; MUID:88371752; PMID:2779337  
 A:Accession: A32989

A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 30-92 <NOE>  
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985  
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat  
 A:Reference number: A22673; MUID:85190593; PMID:3857619  
 A:Accession: A22673  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', 195-461 <MCG>  
 A:Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553  
 A:Note: the authors translated the codon ACA for residue 29 as Tyr  
 R:Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findell, A.; Tolstost  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A:Title: Isolation of a human anti-hemophilic factor IX cDNA clone using a unique 52-bp  
 A:Reference number: A21337; MUID:83220788; PMID:6687940  
 A:Accession: A21337  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', 195-461 <JAY>  
 A:Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611  
 R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I  
 A:Reference number: A37546; MUID:84300526; PMID:6089357  
 A:Accession: A37546  
 A:Molecule type: mRNA  
 A:Residues: 38-193, 'T', 195-326 <JAG>  
 A:Cross-references: GB:M35672  
 R:Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
 A:Title: Isolation and characterization of a cDNA coding for human factor IX.  
 A:Reference number: A30623; MUID:83065193; PMID:6959130  
 A:Accession: A30623  
 A:Molecule type: mRNA  
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',  
 A:Cross-references: GB:J00136; NID:g182608; PIDN:AAA8726.1; PID:g182609  
 A:Experimental source: liver  
 R:Tharakan, J.; Strickland, D.; Buggees, W.; Drohan, W.N.; Clark, D.B.  
 Vox Sang. 58, 21-29, 1990  
 A:Title: Development of an immunofluorescence process for factor IX purification.  
 A:Reference number: A60486; MUID:90194857; PMID:2316207  
 A:Accession: A60486  
 A:Molecule type: protein  
 A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Accession: A20274  
 A:Molecule type: protein  
 A:Residues: 105-109, 'X', 111-115 <MCM>  
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall  
 Eur. J. Biochem. 172, 565-572, 1988  
 A:Title: Characterisation of two differently processed forms of human recombinant factor  
 A:Reference number: S02527; MUID:88166735; PMID:3280312  
 A:Accession: S02527  
 A:Molecule type: protein  
 A:Residues: 29-63 <BAL>  
 A:Note: processed forms expressed in recombinant system  
 R:Jullar, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meullien,  
 EMBO J. 9, 3295-3301, 1990  
 A:Title: Characterization of recombinant human factor IX expressed in transgenic mice at  
 A:Reference number: S12058; MUID:91006024; PMID:2209546  
 A:Accession: S12058  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-68 <JAL>  
 A:Note: processed forms expressed in recombinant system  
 R:Handford, P.A.; Barton, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe  
 EMBO J. 9, 475-480, 1990  
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium  
 A:Reference number: S12377; MUID:90151623; PMID:2406129  
 A:Accession: S12377  
 A:Molecule type: protein

A:Residues: 92-130 <HAN>  
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system  
 R:de la Salle, C.; Charanfier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,  
 Thromb. Haemost. 70, 370-371, 1993  
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsib  
 A:Reference number: I59612; MUID:94054330; PMID:8236150  
 A:Accession: I59612  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 444-461 <RES>  
 A:Cross-references: GB:S66752; NID:g439773; PIDN:AA828588.1; PID:g439774  
 R:Stoffet, E.S.; Koebert, D.D.; Sarkar, G.; Sommer, S.S.  
 Science 239, 491-494, 1988  
 A:Title: Genomic amplification with transcript sequencing.  
 A:Reference number: I59529; MUID:88127096; PMID:3340835  
 A:Accession: I59529  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 290-359 <RE2>  
 A:Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623  
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.; Iw  
 Biochemistry 33, 5167-5171, 1994  
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically link  
 A:Reference number: A54255; MUID:94227047; PMID:8172892  
 A:Accession: A54255  
 A:Molecule type: protein  
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>  
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate  
 R:Di Sciipio, R.G.; Kurachi, K.; Davie, E.W.  
 J. Clin. Invest. 61, 1528-1538, 1978  
 A:Title: Activation of human factor IX (Christmas factor).  
 A:Reference number: A18483; MUID:78194509; PMID:659613  
 A:Contents: annotation; activation; active site; carbohydrate binding  
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
 Am. Soc. Hematol. Abstr. 64(Suppl. 1), 262a, 1984  
 A:Reference number: A37569  
 A:Contents: annotation  
 A:Note: 194-Thr was also found  
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
 J. Biol. Chem. 259, 5698-5704, 1984  
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
 A:Reference number: A37543; MUID:84185715; PMID:6425236  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
 J. Biol. Chem. 260, 2583, 1985  
 A:Reference number: A37544  
 A:Contents: annotation; calcium binding; correction  
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
 Cell 45, 343-348, 1986  
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation c  
 A:Reference number: A37545; MUID:86189947; PMID:3009023  
 A:Contents: annotation; signal sequence cleavage site  
 R:Shuho, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,  
 J. Biol. Chem. 264, 21257-21265, 1989  
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan  
 A:Reference number: A30622; MUID:90078229; PMID:2592373  
 A:Contents: annotation; sequence of mutant B(M) Nagoya  
 A:Note: carboxylation, glycosylation, and cleavage sites  
 R:Barton, M.; Norman, D.G.; Harvey, T.S.; Handford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee  
 submitted to the Brookhaven Protein Data Bank, November 1991  
 A:Reference number: A51252; PDB:1IXA  
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
 A:Note: recombinant form expressed in yeast  
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pro  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stron  
 C:Genetic: GDB:F9  
 A:Cross-references: GDB:119900; OMIM:306900  
 A:Map position: Xq27.1-Xq27.2  
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen

A.Pathway: blood coagulation intrinsic pathway  
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylutamic acid  
F.1-28/Domain: signal sequence #status predicted <SIG>  
F.29-46/Domain: propeptide #status experimental <PPT>  
F.31-91/Domain: Gla domain homology <GLA>  
F.47-191/Product: coagulation factor IXa light chain #status experimental <ALC>  
F.97-128/Domain: EGF homology <EG1>  
F.134-170/Domain: EGF homology <EG2>  
F.192-226/Domain: activation peptide #status experimental <ACT>  
F.227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F.227-454/Domain: trypsin homology <TRY>  
F.53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxylutamic acid (Glu) #  
F.64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D  
F.99/Binding site: carboxylate (Ser) (covalent) #status experimental  
F.110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F.191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental  
F.203-213/Binding site: carboxylate (Asn) (covalent) #status experimental  
F.205-215/Binding site: carboxylate (Thr) (covalent) #status experimental  
F.226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 46.3%; Score 88; DB 1; Length 461;  
Best Local Similarity 39.5%; Pred. No. 2,1e-07;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXLRDGSILXRCXKXLCSPXAXEYFRNXXRTQFWSY 44  
Db 49 SGLTEFVGNLERCKEKCSPFEAREVFENTERTTEFWKQY 91

RESULT 12

KRBO  
coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
N/Alternate names: Christmas factor  
C/Species: Bos primigenius taurus (catle)  
C/Date: 30-Nov-1980 #sequence revision 03-Aug-1994 #ext\_change 16-Jul-1999  
C/Accession: A14757; B20274; I45891; A00923  
R/Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; T  
Proc. Natl. Acad. Sci. U.S.A. 76; 4990-4994, 1979  
A/Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa  
A/Reference number: A14757; MUID:80056619; PMID:291916  
A/Accession: A14757  
A/Molecule type: protein  
A/Residues: 1-63, 'T', 65-416 <KAT>  
R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115; 8-14, 1983  
A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
A/Reference number: A20274; MUID:83308813; PMID:6688526  
A/Accession: B20274  
A/Molecule type: protein  
A/Residues: 59-63, 'X', 65-69 <MCM>  
R/Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
Nature 299; 178-180, 1982  
A/Title: Molecular cloning of the gene for human anti-hemophilic factor IX.  
A/Reference number: I45891; MUID:82272386; PMID:6287289  
A/Accession: I45891  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 52-139 <CHO>  
A/Cross-references: GB:J00007; NID:9163053; PIDN:AAA30520.1; PID:9163054  
R/Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,  
J. Biochem. 104; 867-868, 1988  
A/Title: A new triaccharide sugar chain linked to a serine residue in bovine blood coag  
A/Reference number: A44556; MUID:89213999; PMID:3149637  
A/Accession: A44556  
A/Content: annotation  
A/Note: structure and location of a carboxylate covalently bound to Ser  
C/Comment: Factor IX is activated by factor Xla, which excises the activation peptide pr  
C/Comment: The gamma-carboxylutamic acid residues arise by posttranslational, vitamin K  
C/Comment: Calcium binds to the gamma-carboxylutamic acid (Gla) residues and, with str  
C/Function:  
A/Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
A/Pathway: blood coagulation intrinsic pathway  
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylutamic acid  
F.1-146/Product: coagulation factor IXa light chain #status experimental <ALC>  
F.1-45/Domain: Gla domain homology (fragment) <GLA>  
F.51-82/Domain: EGF homology <EG1>  
F.88-124/Domain: EGF homology <EG2>  
F.147-181/Domain: activation peptide #status experimental <APR>  
F.182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F.182-409/Domain: trypsin homology <TRY>  
F.7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxylutamic acid (Glu) #sta  
F.18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide  
F.53/Binding site: carboxylate (Ser) (covalent) #status experimental  
F.64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F.158,168,173,261/Binding site: carboxylate (Asn) (covalent) #status experimental  
F.222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 45.3%; Score 86; DB 1; Length 416;  
Best Local Similarity 37.2%; Pred. No. 4.4e-07;  
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXLRDGSILXRCXKXLCSPXAXEYFRNXXRTQFWSY 44  
Db 3 SGLTEFVGNLERCKEKCSPFEAREVFENTERTTEFWKQY 45

RESULT 13

EXCH  
coagulation factor Xa (EC 3.4.21.6) precursor - chicken  
N/Alternate names: virus-activating proteinase  
C/Species: Gallus gallus (chicken)  
C/Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #ext\_change 16-Jul-1999  
C/Accession: S15838; S20380; S20381  
R/Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na  
FEBS Lett. 283; 281-285, 1991  
A/Title: Primary structure of the virus activating protease from chick embryo. Its ident  
A/Reference number: S15838; MUID:91257322; PMID:2044767  
A/Accession: S15838  
A/Status: not compared with conceptual translation  
A/Molecule type: protein  
A/Residues: 1-475 <SUG>  
A/Cross-references: DBJ:D00844; NID:9222869; PIDN:BAA00724.1; PID:9222870  
R/Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.  
FEBS Lett. 296; 274-278, 1992  
A/Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib  
A/Reference number: S20380; MUID:92164779; PMID:1537403  
A/Accession: S20380  
A/Molecule type: protein  
A/Residues: 41-55 <GO2>  
A/Accession: S20381  
A/Molecule type: protein  
A/Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>  
C/Function:  
A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A/Pathway: blood coagulation  
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylutamic acid  
F.1-20/Domain: signal sequence #status predicted <SIG>  
F.21-40/Domain: propeptide #status predicted <PRO>  
F.25-84/Domain: Gla domain homology <GLA>  
F.41-185/Product: coagulation factor X light chain #status experimental <LCH>  
F.90-121/Domain: EGF homology <EG1>  
F.129-167/Domain: EGF homology <EG2>  
F.186-475/Product: coagulation factor X heavy chain #status predicted <HCH>  
F.186-240/Domain: activation peptide #status predicted <APR>  
F.241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
F.241-468/Domain: trypsin homology <TRY>  
F.46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylutamic acid (Glu) #st  
F.57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42  
F.103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F.196,207,228,285/Binding site: carboxylate (Asn) (covalent) #status predicted  
F.282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 43.2%; Score 82; DB 1; Length 475;  
Best Local Similarity 34.1%; Pred. No. 2.5e-06;



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GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)  
328.082 Million cell updates/sec

Title: 10ASP28GLU\_4  
Perfect score: 190  
Sequence: 1 ANGFLXXLRDGSIXRXCRRX.....XXAEXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 149   | 78.4        | 407    | 1  | FA7_BOVIN   |
| 2          | 131   | 68.9        | 444    | 1  | FA7_RABIT   |
| 3          | 123   | 64.7        | 466    | 1  | FA7_HUMAN   |
| 4          | 109   | 57.4        | 461    | 1  | PRTC_MOUSE  |
| 5          | 108   | 56.8        | 218    | 1  | TMG1_HUMAN  |
| 6          | 107   | 56.3        | 461    | 1  | PRTC_RAT    |
| 7          | 106   | 55.8        | 446    | 1  | FA7_MOUSE   |
| 8          | 102   | 53.7        | 231    | 1  | TMG3_HUMAN  |
| 9          | 102   | 53.7        | 459    | 1  | PRTC_PIG    |
| 10         | 97    | 51.1        | 456    | 1  | PRTC_BOVIN  |
| 11         | 94    | 49.5        | 488    | 1  | FA10_HUMAN  |
| 12         | 92    | 48.4        | 461    | 1  | PRTC_HUMAN  |
| 13         | 92    | 48.4        | 490    | 1  | FA10_RABIT  |
| 14         | 90    | 47.4        | 492    | 1  | FA10_BOVIN  |
| 15         | 88    | 46.3        | 461    | 1  | FA9_HUMAN   |
| 16         | 86    | 45.3        | 416    | 1  | FA9_BOVIN   |
| 17         | 86    | 45.3        | 458    | 1  | PRTC_RABIT  |
| 18         | 82    | 43.2        | 475    | 1  | FA10_CHICK  |
| 19         | 81    | 42.6        | 452    | 1  | FA9_CANFA   |
| 20         | 76    | 40.0        | 459    | 1  | FA9_MOUSE   |
| 21         | 76    | 40.0        | 622    | 1  | THRB_HUMAN  |
| 22         | 73    | 38.4        | 617    | 1  | THRB_RAT    |
| 23         | 73    | 38.4        | 618    | 1  | THRB_MOUSE  |
| 24         | 71    | 37.4        | 202    | 1  | TMG2_HUMAN  |
| 25         | 70    | 36.8        | 226    | 1  | TMG4_HUMAN  |
| 26         | 70    | 36.8        | 649    | 1  | PRTS_MACAU  |
| 27         | 70    | 36.8        | 675    | 1  | PRTS_BOVIN  |
| 28         | 70    | 36.8        | 676    | 1  | PRTS_HUMAN  |
| 29         | 69    | 36.3        | 376    | 1  | FA10_TROCA  |
| 30         | 69    | 36.3        | 400    | 1  | PRTZ_HUMAN  |
| 31         | 69    | 36.3        | 446    | 1  | PRTS_RABIT  |
| 32         | 67    | 35.3        | 625    | 1  | THRB_BOVIN  |
| 33         | 67    | 35.3        | 675    | 1  | PRTS_RAT    |

|    |    |      |      |   |            |
|----|----|------|------|---|------------|
| 34 | 65 | 34.2 | 396  | 1 | PRTZ_BOVIN |
| 35 | 60 | 31.6 | 675  | 1 | PRTS_MOUSE |
| 36 | 56 | 29.5 | 413  | 1 | NCAPG_HNV  |
| 37 | 53 | 27.9 | 604  | 1 | VE1_BPv2   |
| 38 | 53 | 27.9 | 605  | 1 | VE1_BPv1   |
| 39 | 44 | 23.2 | 303  | 1 | SC14_YEAST |
| 40 | 43 | 22.6 | 302  | 1 | SC14_CANGA |
| 41 | 43 | 22.6 | 484  | 1 | SLT2_YEAST |
| 42 | 43 | 22.6 | 3061 | 1 | POLG_PVYHU |
| 43 | 42 | 22.1 | 330  | 1 | GSHB_BUCAI |
| 44 | 41 | 21.6 | 477  | 1 | FIBB_PETMA |
| 45 | 41 | 21.6 | 1275 | 1 | RFBC_MYXXA |

## ALIGNMENTS

RESULT 1  
FA7\_BOVIN STANDARD; PRT; 407 AA.  
AC P22457;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=9908362; PubMed=3049594;  
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,  
RA Iwanaga S.;  
RT "Bovine factor VII. Its purification and complete amino acid  
RT sequence.";  
RL J. Biol. Chem. 263:14868-14877(1988).  
RN [2]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=9921399; PubMed=1149637;  
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,  
RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in bovine  
RT blood coagulation factors VII and IX.";  
RL J. Biochem. 104:867-868(1988).  
RN [3]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the  
RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
CC CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIa, FACTOR IXa, OR  
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR  
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to  
CC form factor Xa.  
CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
CC BY A DISULFIDE BOND.  
CC -I- TISSUE SPECIFICITY: PLASMA.  
CC -I- PPM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
CC CALCIUM.  
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
DR PIR, A31979; A31979.  
DR HSSP, P08709; 1BF9.

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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFblood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 144
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT CARBOHYD 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 MW; 703B1EF0636F7F10 CRC64;

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Query Match 78.4%; Score 149; DB 1; Length 407;  
 Best Local Similarity 68.2%; Pred. No. 1,2e-19;  
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLRDGLXRXCRXXLCSFYXAXEIPRNXXRTQFWVS 44
Db 1 ANGFLLEELPLGSLERECEEELCSFEAAHIEIFNNEERTQFWVS 44

RESULT 2
ID -FA7 RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; Pubmed=8383365;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETEROIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; AAB37326.1; -.
DR HSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; blood coagulation; zymogen; glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
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FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
FT DISULFID 217 233
FT DISULFID 349 368
FT DISULFID 379 407
FT MOD_RES 45 45
FT MOD_RES 46 46
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FT MOD_RES 102 102
FT MOD_RES 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
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Query Match 68.9%; Score 131; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-16;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

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DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Ipratocog alfa).
CN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.U.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
[3]
RN SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
[4]
RN SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=8908153; PubMed=3264725;
RA Tim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RT Biochemistry 27:7785-7793(1988).
[5]
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Tim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RT J. Biol. Chem. 266:11051-11057(1991).
[6]
RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomitsu Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RT J. Biol. Chem. 264:20320-20325(1989).
[7]
RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RT Adv. Exp. Med. Biol. 281:121-131(1990).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RT Nature 380:41-46(1996).

```

[9] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RP MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPTT mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Murenji A., Finn B.E., Gierbert G.P., Forsten S., Stenflo J.,  
 RT Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RT Meade T.W.; Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,  
 RT Roderigo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7)." ;  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferrari M., Patrascchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms  
 RT (11His and 33Ser) in the human coagulation factor VII gene." ;  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamiya O., Kembell-Cook G., Martin D.M.A., Cooper D.N.,  
 RT von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII." ;  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RX MEDLINE=94264305; PubMed=8204879;  
 RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
 RT Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor." ;  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RT Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294Ala->Val) and X (334Ser->Pro)." ;  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohlwa M., Hayashi T., Wada H., Minami-Kawa K., Shirakawa S.,  
 RT Suzuki K.;  
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain." ;

Thromb. Haemost. 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule." ;  
 RL Blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,  
 RT Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency." ;  
 RL Hum. Mutat. 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Koroletsky M.,  
 RA Zaitov R., Seligson U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews." ;  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN [21]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=96112461; PubMed=9452082;  
 RA Alehinwi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene." ;  
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -1- PHARMACEUTICAL: Available under the names Niasate or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in  
 CC Query Match 64.7%; Score 123; DB 1; Length 466;  
 CC Best Local Similarity 52.3%; Pred. No. 8,1e-15;  
 CC Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 Qy 1 ANGFLXXLRDGSILXRCXRLCSFYXAEXIFRNXXRTROFWFSY 44  
 Db 61 ANAFLEELRPSGLERCKEKGCSFEERARIFDKARITKLFWSY 104  
 RESULT 4  
 PRTC MOUSE  
 ID PRTC MOUSE STANDARD; PRT; 461 AA.  
 AC P33587; O35498;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Mus musculus (Mouse).



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DB      42 ANSFLEMRPGSLERECMEICDFEBAQEIFQVEDTLAFWIKY 85
RESULT 5
ID      TMG1_HUMAN          STANDARD;          PRT;          218 AA.
AC      014668;
DT      15-JUN-2002 (rel. 41, Created)
DT      15-JUN-2002 (rel. 41, Last sequence update)
DT      15-JUN-2002 (rel. 41, Last annotation update)
DE      Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-
DE      rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein
DE      1).
GN      PRG1 OR TMG1 OR PRGP1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97404347; PubMed=9256434;
RA      Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT      "Primary structure and tissue distribution of two novel proline-rich
RT      gamma-carboxylglutamic acid proteins."
RL      Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062 (1997).
CC      -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC      -1- PTM: Gla residues are produced after subsequent posttranslational
CC      modifications of glutamic acid by a vitamin K-dependent gamma-
CC      carboxylase.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL, AF009242; AAB67070.1; -.
DR      HSP; P00740; ICFH.
DR      Genew; HGNC:9469; PRRG1.
DR      MIM: 604428; -.
DR      InterPro: IPR002383; GLA blood.
DR      InterPro: IPR000294; VitK_dep_GLA.
DR      InterPro: IPR000594; Gla; 1.
DR      Pfam; PF00594; Gla; 1.
DR      PRINTS; PR00001; GLABLOOD.
DR      SMART; SM00069; GLA; 1.
DR      PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR      KX      Gamma-carboxylglutamic acid; Vitamin K; Transmembrane.
FT      PROPEP      1      20      POTENTIAL.
FT      CHAIN      1      218      TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT      FT      DOMAIN      21      83      PROTEIN 1.
FT      TRANSMEM      84      106      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      107      218      POTENTIAL.
FT      DOMAIN      107      218      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      24      61      GLA-RICH.
FT      DOMAIN      131      135      POLY-PRO.
SQ      SEQUENCE      218 AA; 24947 MW; 26538A61AB0A9B98 CRC64;

Query Match      56.8%; Score 108; DB 1; Length 218;
Beet Local Similarity 38.6%; Pred. No. 2, 1e-12;
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-JUN-2002 (rel. 41, Last annotation update)
DE      Vitamin-K dependent protein C precursor (EC 3.4.21.65)
DE      (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE      factor XIV).
GN      PROC.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxId=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Mistart; TISSUE=Liver;
RX      MEDLINE=92329550; PubMed=1627650;
RA      Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT      "The cDNA cloning and mRNA expression of rat protein C."
RL      Biochim. Biophys. Acta 1131:329-332 (1992).
CC      -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC      REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIA
CC      IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC      -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC      and VIIa.
CC      -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC      INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC      BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC      TERRADCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS IS
CC      REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC      STRONGLY PROMOTED BY THROMBOMODULIN.
CC      -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC      -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC      GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC      -1- MISCELLANEOUS: CALCIUM ALSO BINDS. WITH STRONGER AFFINITY TO
CC      ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC      SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC      THROMBIN-THROMBOMODULIN COMPLEX.
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC      -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL, X64336; CAA45617.1; -.
DR      PIR; S18994; S18994.
DR      PIR; S24312; S24312.
DR      HSP; P04070; IFCU.
DR      MEROPS; S01.218; -.
DR      InterPro: IPR000152; Asx hydroxyl.
DR      InterPro: IPR001314; Chymotrypsin.
DR      InterPro: IPR000561; EGF-like.
DR      InterPro: IPR001881; EGF Ca.
DR      InterPro: IPR002383; GLA blood.
DR      InterPro: IPR001254; Ser-protease_Try.
DR      InterPro: IPR000294; VitK_dep_GLA.
DR      Pfam; PF00089; EGF; 2.
DR      Pfam; PF00089; trypsin; 1.
DR      Pfam; PF00594; gla; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      PRINTS; PR00001; GLABLOOD.
DR      SMART; SM00179; EGF_CA; 1.
DR      SMART; SM00001; EGF-like; 1.
DR      SMART; SM00069; GLA; 1.
DR      SMART; SM00020; Tryp_Spc; 1.
DR      PROSITE; PS00010; ASX_HYDROXYL; 1.
DR      PROSITE; PS00022; EGF_1; 1.
DR      PROSITE; PS01186; EGF_2; 2.
DR      PROSITE; PS01187; EGF_CA; 1.
DR      PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.

```

DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Blood coagulation; Glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 FT SIGNAL 1 32  
 FT PROPEP 33 41  
 FT CHAIN 42 196  
 FT CHAIN 199 461  
 FT PEPTIDE 199 212  
 FT SITE 212 213  
 FT DOMAIN 135 175  
 FT DOMAIN 213 461  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 254 254  
 FT ACT\_SITE 300 300  
 FT ACT\_SITE 402 402  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 320  
 FT DISULFID 239 255  
 FT DISULFID 373 387  
 FT CARBOHYD 215 215  
 FT CARBOHYD 291 291  
 FT CARBOHYD 355 355  
 SQ SEQUENCE 461 AA; 51912 MW; 844CF9364EDACD5 CRC64;

Query Match 56.3%; Score 107; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 7e-12;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXLRDGLKRXKXXLCSFYKXEXIRNNXXRTQFWVSY 44  
 DB 42 ANSFLEVRAGSLREKCEWIEICDFEEAOEIFQWEDTLAFWKY 85

RESULT 7  
 ID\_FAV MOUSE STANDARD; PRT; 446 AA.  
 AC P70375;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 conversion accelerator).  
 GN F7 OR CF7.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97127167; PubMed=8972017;  
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine blood  
 coagulation factor VII gene";  
 RL Thromb. Haemost. 76:957-964(1996).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS  
 CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIa, OR  
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC  
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 CC  
 CC EMBL; U66079; AAC33796.1; -.  
 DR HSSP; P08709; 1BF9.  
 DR MEROPS; S01.215; -.  
 DR MGD; MGI:109325; F7.  
 DR InterPro; IPR000152; Abs\_hydroxy1.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF-Ca.  
 DR InterPro; IPR002383; GLA\_Dlood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; YltK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; glaf\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KM EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 193  
 FT CHAIN 194 446  
 FT DOMAIN 47 76  
 FT DOMAIN 194 446  
 FT DOMAIN 47 76

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FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 128 169 EGF-LIKE 2.
FT DOMAIN 194 466 SERINE PROTEASE.
FT SITE 193 194 CLEAVAGE (BY FACTOR XA, FACTOR XIa,
  FACTOR IXa, OR THROMBIN) (BY SIMILARITY).
FT ACT_SITE 234 234 BY SIMILARITY.
FT ACT_SITE 283 283 BY SIMILARITY.
FT BINDING 379 379 BY SIMILARITY.
FT BINDING 385 385 SUBSTRATE (BY SIMILARITY).
FT BINDING 399 399 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
FT DISULFID 113 122 BY SIMILARITY.
FT DISULFID 132 143 BY SIMILARITY.
FT DISULFID 139 153 BY SIMILARITY.
FT DISULFID 155 168 BY SIMILARITY.
FT DISULFID 176 203 BY SIMILARITY.
FT DISULFID 200 205 BY SIMILARITY.
FT DISULFID 219 235 BY SIMILARITY.
FT DISULFID 351 370 BY SIMILARITY.
FT DISULFID 381 409 BY SIMILARITY.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 146 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45CBC96E CRC64;

Query Match 55.8%; Score 106; DB 1; Length 446;
Beet Local Similarity 47.7%; Pred. No. 1e-11;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGLXRXCRXXLCSPXXAEXIFRNXXRTPOFWVS 44
Db 42 ANSLLELWPGSLERECNEQCSFEERARETFKSPERTKQWIVY 85

RESULT 8
TM33_HUMAN STANDARD; PRT; 231 AA.
AC O9BBD7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid precursor.
GN TM33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RX MEDLINE=21117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
  proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375 (2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
  modifications of glutamic acid by a vitamin K-dependent gamma-
  carboxylase.
CC -----
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CC -----
DR EMBL; AF326350; AAK0955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
  PROTEIN 3.
FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 79 101 POTENTIAL.
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MW; 8A373B484890D81 CRC64;

Query Match 53.7%; Score 102; DB 1; Length 231;
Beet Local Similarity 38.6%; Pred. No. 2.8e-11;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGLXRXCRXXLCSPXXAEXIFRNXXRTPOFWVS 44
Db 20 ANEFLLELRQGTIERECMEICSYEEVKEVFENKKEIFWNGY 63

RESULT 9
PRTC_PIG ID PRTC_PIG STANDARD; PRT; 459 AA.
AC O9GFP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Anticoagulant protein C) (blood coagulation
  factor XIV).
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
  Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
  protein modeling of membrane binding sites and comparative anatomy of
  protein domains.";
RL Cell. Mol. Life Sci. 58:148-159 (2001).
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
  regulates blood coagulation by inactivating factors Va and VIIIa
  in the presence of calcium ions and phospholipids.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
  and VIIIa.
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
  into a light chain and a heavy chain held together by a disulfide
  bond. The enzyme is then activated by thrombin, which cleaves a
  tetradecapeptide from the amino end of the heavy chain; this
  reaction, which occurs at the surface of endothelial cells, is
  strongly promoted by thrombomodulin.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
  residues allows the modified protein to bind calcium.
CC -----
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CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
CC another site, beyond the GLA domain. This GLA-independent binding  
CC site is necessary for the recognition of the  
CC thrombin-thrombomodulin complex.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC -----  
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CC -----  
DR EMBL: AF191307; AAC28380.1; -.  
DR HSSP: P04070; 1PCU.  
DR MEROPS: S01.218; -.  
DR InterPro: IPR000152; Aex hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR001881; EGF-Ca.  
DR InterPro: IPR002383; GLA\_Blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VltK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00089; trypsin\_1.  
DR Pfam: PF00594; gla\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00001; EGF-like\_2.  
DR SMART: SM00069; GLA\_1.  
DR SMART: SM00020; TRY\_P\_Src; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_CA; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PSS0240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KM Blood coagulation; Glycoprotein; Serine protease;  
KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
FT SIGNAL 1 18  
FT PROPEP 19 41  
FT CHAIN 42 459  
FT CHAIN 42 196  
FT CHAIN 199 459  
FT CHAIN 199 213  
FT PEPTIDE 199 213  
FT SITE 213 214  
FT DOMAIN 96 131  
FT DOMAIN 135 175  
FT DOMAIN 214 459  
FT MOD\_RES 47 47  
FT MOD\_RES 48 48  
FT MOD\_RES 48 48  
FT MOD\_RES 55 55  
FT MOD\_RES 57 57  
FT MOD\_RES 60 60  
FT MOD\_RES 61 61  
FT MOD\_RES 66 66  
FT MOD\_RES 67 67  
FT MOD\_RES 67 67

FT MOD\_RES 70 70  
FT MOD\_RES 112 112  
FT ACT\_SITE 255 255  
FT ACT\_SITE 301 301  
FT ACT\_SITE 400 400  
FT ACT\_SITE 400 400  
FT DISULFID 58 63  
FT DISULFID 91 110  
FT DISULFID 100 105  
FT DISULFID 104 115  
FT DISULFID 121 130  
FT DISULFID 139 150  
FT DISULFID 146 159  
FT DISULFID 161 174  
FT DISULFID 182 321  
FT DISULFID 240 256  
FT DISULFID 371 385  
FT DISULFID 396 424  
FT CARBOHYD 138 138  
FT CARBOHYD 292 292  
FT CARBOHYD 353 353  
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CCL6D09 CRC64;  
Query Match 53.7%; Score 102; DB 1; Length 459;  
Best Local Similarity 45.5%; Pred. No. 5.8e-11;  
Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;  
OY 1 ANGFLXXLRDGLXRCXKXICSYXAXEIPFNXXRTROFVSY 44  
Db 42 ANSFLEELRPSLSRECKEETCFEAREIFQNTENTWAFWSKY 85  
RESULT 10  
PRTC\_BOVIN STANDARD; PRT; 456 AA.  
ID P00745;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
DE (Autoproteolytic protein C) (Blood coagulation  
DE factor XIV) (Fragment).  
GN PROC.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_Taxid=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014826; PubMed=6091100;  
RA Long G.L., Balasage R.M., McGilivray R.T.A.;  
RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
RN [2]  
RP SEQUENCE OF 40-194.  
RX MEDLINE=83007325; PubMed=6896876;  
RA Fernlund P., Stenflo J.;  
RT "Amino acid sequence of the light chain of bovine protein C";  
RL J. Biol. Chem. 257:12170-12179(1982).  
RN [3]  
RP REVISION TO 110.  
RX MEDLINE=83169769; PubMed=6572939;  
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;  
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
RN [4]  
RP SEQUENCE OF 197-456.  
RX MEDLINE=83007326; PubMed=6896877;  
RA Stenflo J., Fernlund P.;  
RT "Amino acid sequence of the heavy chain of bovine protein C";  
RL J. Biol. Chem. 257:12180-12190(1982).

```

RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmon N.L., Debaule L.E., Esmon C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RL domainless protein C.";
RJ J. Biol. Chem. 258:5548-5553 (1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RJ J. Biol. Chem. 258:5554-5560 (1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CC EMBL, K02435; AAA30685.1; -.
CC PIR, A00928; KXBO.
CC HSSP, P04070; LPCU.
CC MEROPS, S01.218; -.
CC InterPro, IPR000152; Asx_hydroxyl.
CC InterPro, IPR000561; EGF-like.
CC InterPro, IPR001881; EGF_Ca.
CC InterPro, IPR001254; Ser_protease_Try.
CC InterPro, IPR000294; VitK_dep_GLA.
CC Pfam, PF00008; EGF_2.
CC Pfam, PF00089; cypsin; 1.
CC Pfam, PF00594; gla; 1.
CC SMART, SM00181; EGF; 2.
CC SMART, SM00069; GLA; 1.
CC SMART, SM00020; TYP_SPC; 1.
CC PROSITE, PS00010; ASK_HYDROXYL; 1.
CC PROSITE, PS00022; EGF_1; 1.
CC PROSITE, PS01186; EGF_2; 2.
CC PROSITE, PS01187; EGF_Ca; 1.
CC PROSITE, PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE, PS00240; TRYPSIN_DOM; 1.
CC PROSITE, PS00134; TRYPSIN_HIS; FALSE_NEG.
CC PROSITE, PS00135; TRYPSIN_SER; 1.
CC Blood coagulation, Glycoprotein, Serine protease;
CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
CC EGF-like domain; Repeat; Endothelial cell; Hydroxylase; Signal.
FT SIGNL 1 1
FT NON_TER 1 1
FT 30 29
FT PROPEP 30 39

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FT CHAIN 40 194
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FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
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FT CARBOHYD 350 350
FT CARBOHYD 366 366
FT VARIANT 82 82
FT VARIANT 455 455
SQ SEQUENCE 456 AA; 51407 MW; CAAF6833F894C209 CRC64;

Query Match 51.1%; Score 97; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 4;8e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRDGLXLRXCRLXLCSPYXAEIIFRNXXRTROFWYSY 44
Db 40 ANSFLELRPGNVERECSEVCFEPEARITFONDTMAFNSFY 83

RESULT 11
FA10 HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor) .
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Webster T.U., Pileman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";
RL Gene 99:291-294 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;

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RA Leytus S.P., Foester D.C., Kurachi K., Davie E.W.;  
RT "Gene for human factor X: a blood coagulation factor whose gene  
RT organization is essentially identical with that of factor IX and  
RT protein C.";  
RN Biochemistry 25:5098-5102(1986).  
[3]  
RX SEQUENCE OF 13-488 FROM N.A.  
RX MEDLINE=85216545; PubMed=2582420;  
RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
RT "Characterization of an almost full-length cDNA coding for human  
RT blood coagulation factor X.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
[4]  
RP SEQUENCE OF 19-488 FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=86221713; PubMed=3011603;  
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
RT "Isolation and characterization of human blood-coagulation factor X  
RT cDNA.";  
RL Gene 41:311-314(1986).  
[5]  
RP SEQUENCE OF 41-179.  
RX MEDLINE=83257207; PubMed=6871167;  
RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,  
RA Kwa B.Y., Weinstein B.;  
RT "Complete amino acid sequence of the light chain of human blood  
RT coagulation factor X: evidence for identification of residue 63 as  
RT beta-hydroxyaspartic acid.";  
RL Biochemistry 22:2875-2884(1983).  
[6]  
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
RP TISSUE=Liver;  
RC MEDLINE=84222026; PubMed=658784;  
RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
RT "Characterization of a cDNA coding for human factor X.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
[7]  
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=94062825; PubMed=8243461;  
RA Inoue K., Morita T.;  
RT "Identification of O-linked oligosaccharide chains in the activation  
RT peptides of blood coagulation factor X. The role of the carbohydrate  
RT moieties in the activation of factor X.";  
RL Eur. J. Biochem. 218:153-163(1993).  
[8]  
RP SEQUENCE OF 1-23 FROM N.A.  
RX MEDLINE=90128299; PubMed=2612918;  
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
RT "Cloning and characterization of the 5' end (exon 1) of the gene  
RT encoding human factor X.";  
RL Gene 84:517-519(1989).  
[9]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
RX MEDLINE=93360277; PubMed=8355279;  
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
RL J. Mol. Biol. 232:947-966(1993).  
[10]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
RX MEDLINE=98283982; PubMed=9618463;  
RA Kamata K., Kawamoto H., Homma T., Iwama T., Kim S.H.;  
RT "Structural basis for chemical inhibition of human blood coagulation  
RT factor Xa.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
CC converts prothrombin to thrombin in the presence of factor Va,  
CC calcium and phospholipid during blood clotting.  
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
CC Arg-|-Ile bonds in prothrombin to form thrombin.  
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
CC MORE DISULFIDE BONDS.

CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
CC CALCIUM.  
CC -1- PTM: N- AND O-GLYCOSYLATED.  
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE  
CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC -----  
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CC -----  
DR EMBL; K03194; AAA52490.1; -;  
DR EMBL; M57285; AAA52421.1; -;  
DR EMBL; L29433; AAA52764.1; -;  
DR EMBL; L00390; AAA52764.1; JOINED.  
DR EMBL; L00391; AAA52764.1; JOINED.  
DR EMBL; L00392; AAA52764.1; JOINED.  
DR EMBL; L00393; AAA52764.1; JOINED.  
DR EMBL; L00394; AAA52764.1; JOINED.  
DR EMBL; L00395; AAA52764.1; JOINED.  
DR EMBL; L00396; AAA52764.1; JOINED.  
DR EMBL; M22613; AAA51984.1; -;  
DR EMBL; K01886; AAA52486.1; -;  
DR EMBL; M33297; AAA52636.1; -;  
DR PIR; A00924; EXHU.  
DR PIR; A25853; A25853.  
DR PIR; A24478; A24478.  
DR PDB; 1HCG; 08-MAY-95.  
DR PDB; 1FAX; 29-OCT-97.  
DR PDB; 1FXY; 17-JUN-98.  
DR PDB; 1XKA; 23-MAR-99.  
DR PDB; 1XKB; 23-MAR-99.  
DR MEROPS; S01.216; -;  
DR GLYCOSULEDB; P00742; -;  
DR Genew; HGNC:3528; F10.  
DR MIM; 134530; -;  
DR MIM; 227600; -;  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; Bgf-like.  
DR InterPro; IPR000742; Bgf-like.  
DR InterPro; IPR001881; EGF Ca.  
DR InterPro; IPR002383; GLA blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00089; trypsin\_1.  
DR Pfam; PF00594; Gla\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA\_1.  
DR SMART; SM00069; GLA\_1.  
DR SMART; SM00020; TRY\_P\_SPC\_1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA\_1.  
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM\_1.  
DR PROSITE; PS00134; TRYPSIN\_HIS\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER\_1.  
KW Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.  
FT SIGNAL 1 31 POTENTIAL.

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FT PROPEP      32      40
FT CHAIN       41      179
FT CHAIN       183     488
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FT DOMAIN      86      122
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FT MOD_RES     103     103
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FT CARBOHYD     221     221
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FT CARBOHYD     231     231
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FT DISULFID     90      101
FT DISULFID     95      110
FT DISULFID     112     121
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Query Match  Best Local Similarity 36.4%; Pred. No. 1.8e-09;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

      1 ANGFLXXLRDGLRXCRXXLCSFXXAEXIFRNXXRTGFWVSY 44
      41 ANSFLEEMKKGHLRECMETGCTCYEARREVFEDSDKTNERWNNY 84

RESULT 12
PRTC HUMAN STANDARD; PRT; 461 AA.
AC P04070; O16001; O15190; O15189;
AC 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
CN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85270390; PubMed=2991897;
RA Foster D.C., Yoshitake S., Davie E.W.;
RA "The nucleotide sequence of the gene for human protein C.";
RA Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Santee R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RA "The structure and evolution of a 461 amino acid human protein C
RA precursor and its messenger RNA, based upon the DNA sequence of
RT cloned human liver cDNAs";
RT Nucleic Acids Res. 13:5233-5247(1985).

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RA "Evolution and organization of the human protein C gene.";
RA Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.U., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RA Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RA "Characterization of a cDNA coding for human protein C.";
RA Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J. Jr.;
RA "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cytosine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RA "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RA "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Matner T., Oganessyan V., Hof P., Huber R., Foundling S., Eamon C.,
RA Bode W.;
RA "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reltsma P.H., Poort S.R., Bernardi F., Gandille S., Long G.L.,
RA Sala N., Cooper D.N.;
RA "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [11]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
RA Leonard A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Corvase R.;
RA "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098506; PubMed=2602169;
RA Grundy C.B., Chiccole A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RA "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [13]

```

RP VARIANT CYS-272.  
 RX MEDLINE=91329836; PubMed=1868249;  
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;  
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with  
 RT symptomatic protein C deficiency type I: heterogeneity and founder  
 RT effects.";  
 RL Blood 78:890-894(1991).  
 RN [14]  
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.  
 RX MEDLINE=92190481; PubMed=1347706.  
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,  
 RA Rainville I.R., Long G.L.;  
 RT "Protein C variant: symptomatic type II protein C deficiency  
 RT associated with two GLA domain mutations.";  
 RL Blood 79:1456-1465(1992).  
 RN [15]  
 RP VARIANT ASP-418 (HONG KONG-2).  
 RX MEDLINE=92305321; PubMed=1611081;  
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;  
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C  
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and  
 RT a missense mutation.";  
 RL Blood 80:126-133(1992).  
 RN [16]  
 RP VARIANT LEU-289.  
 RX MEDLINE=92380660; PubMed=1511988;  
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;  
 RT "A novel homozygous missense mutation in the protein C (PROC) gene  
 RT causing recurrent venous thrombosis.";  
 RL Hum. Genet. 89:683-684(1992).  
 RN [17]  
 RP VARIANTS GLN-220 AND TRP-220.  
 RX MEDLINE=92380661; PubMed=1511989;  
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;  
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)  
 RT gene causing recurrent venous thrombosis.";  
 RL Hum. Genet. 89:685-686(1992).  
 RN [18]  
 RP VARIANT GLN-220.  
 RX MEDLINE=93250852; PubMed=1301959;  
 RA Gaudrille S., Vidard M., Alach M., Albenc-Gelas M., Fischer A.M.,  
 RA Gouault-Heilman M., Toulon P., Plessinger J.N., Goossens M.;  
 RT "Two novel mutations responsible for hereditary type I protein C  
 RT deficiency: characterization by denaturing gradient gel  
 RT electrophoresis.";  
 RL Hum. Mutat. 1:491-500(1992).  
 RN [19]  
 RP VARIANT SER-334.  
 RX MEDLINE=92276939; PubMed=1593215;  
 RA Yamamoto K., Matsumura T., Sugitara I., Takamatsu J., Iwasaki E.,  
 RA Wada H., Deguchi K., Shirakawa S., Saio H.;  
 RT "Homozygous protein C deficiency: identification of a novel missense  
 RT mutation that causes impaired secretion of the mutant protein C.";  
 RL J. Lab. Clin. Med. 119:682-689(1992).  
 RN [20]  
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.  
 RX MEDLINE=93313192; PubMed=8124221;  
 RA Gaudrille S., Albenc-Gelas M., Gausem P., Aillaud M.-F., Dupuy E.,  
 RA Juhán-Vague I., Alach M.;  
 RT "Five novel mutations located in exons III and IX of the protein C  
 RT gene in patients presenting with defective protein C anticoagulant  
 RT activity.";  
 RL Blood 82:159-168(1993).  
 RN [21]  
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND  
 RP V-388.  
 RX MEDLINE=93271391; PubMed=8499565;  
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,  
 RA Bertina R.M.;  
 RT "Twelve novel and two recurrent mutations in 14 Austrian families  
 RT with hereditary protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).  
 RN [22]

RP VARIANT TRP-57.  
 RX MEDLINE=93271396; PubMed=8499568;  
 RA Miller D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,  
 RA Kakkar V.V., Cooper D.N.;  
 RT "A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene  
 RT causing type 2 protein C deficiency and recurrent venous  
 RT thrombosis.";  
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).  
 RN [23]  
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.  
 RX MEDLINE=94122325; PubMed=8292730;  
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,  
 RA Koepfer M.A., Coughlin J., Griffin J.H.;  
 RT "Genetic mutations in ten unrelated American patients with  
 RT symptomatic type I protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).  
 RN [24]  
 RP VARIANT SER-423.  
 RX MEDLINE=94001606; PubMed=8398832;  
 RA Marchetti G., Patrascchini P., Gemmati D., Castaman G., Rodeghiero F.,  
 RA Macey A., Cooper D.N., Tuddenham E.G., Bernardi F.;  
 RT "Symptomatic type II protein C deficiency caused by a missense  
 RT mutation (Gly 361-->Ser) in the substrate-binding pocket.";  
 RL Br. J. Haematol. 84:285-289(1993).  
 RN [25]  
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).  
 Query Match 48.4%; Score 92; DB 1; Length 461;  
 Best Local Similarity 46.3%; Pred. No. 4e-09;  
 Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;  
 Oy 1 ANGFLXXLRDGLKRCXKXLCSPFXAEXIPRNXXRTROFW 41  
 Db 43 ANSFLELRHSLRECEICEICEDEEAKELFQNVDTLAFW 83  
 RESULT 13  
 ID \_P410\_RABIT STANDARD; PRT; 490 AA.  
 AC 019045;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN P10.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97256311; PubMed=9101642;  
 RA Penduth U.R., Anderson K.D., James H.L.;  
 RT "Characterization of a full-length cDNA for rabbit factor X.";  
 RL Thromb. Res. 85:503-514(1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)  
 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF003200; AAB62542.1; -  
 CC HSSP: P00742; IHCG.  
 DR MEMOPS: S01.216; -  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF 2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; Vtck\_dep\_GLA.  
 DR Pfam: PF00008; EGF; 2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; gla; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_like; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
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 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KM Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
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 FT CHAIN 21 180  
 FT CHAIN 41 180  
 FT PROPEP 184 490  
 FT CHAIN 184 490  
 FT CHAIN 233 490  
 FT DOMAIN 86 122  
 FT DOMAIN 125 165  
 FT DOMAIN 233 490  
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 FT MOD\_RES 54 54  
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 FT MOD\_RES 59 59  
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 FT MOD\_RES 65 65  
 FT MOD\_RES 66 66  
 FT MOD\_RES 69 69  
 FT MOD\_RES 72 72  
 FT MOD\_RES 75 75  
 FT MOD\_RES 79 79

FT MOD\_RES 103 103  
 FT ACT\_SITE 274 274  
 FT ACT\_SITE 320 320  
 FT ACT\_SITE 417 417  
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 FT DISULFID 95 110  
 FT DISULFID 112 121  
 FT DISULFID 129 140  
 FT DISULFID 136 149  
 FT DISULFID 151 164  
 FT DISULFID 172 340  
 FT DISULFID 239 244  
 FT DISULFID 359 275  
 FT DISULFID 388 402  
 FT CARBOHYD 413 441  
 FT CARBOHYD 61 61  
 FT CARBOHYD 187 187  
 FT CARBOHYD 205 205  
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;  
 Query Match 48.4%; Score 92; DB 1; Length 490;  
 Best Local Similarity 38.6%; Pred. No. 4.3e-09;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRDGLSLRXCRXLCSFXXAEIFRNXXRTQFWWSY 44  
 DB 41 ANSFLEELKGNLRERCWENCSEYEEALVEFDRKRTNPFMKY 84  
 RESULT 14  
 PA10\_BOVIN STANDARD; PRT; 492 AA.  
 ID PA10\_BOVIN  
 AC P00743;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxId:9913;  
 RN (1)  
 RP SEQUENCE OF 1-487 FROM N.A.  
 RX MEDLINE=84247315; PubMed=6330671;  
 RA Fung M.R., Campbell R.M., McGallivray R.T.A.;  
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain  
 RT containing a prepro leader sequence."  
 RL Nucleic Acids Res. 12:4481-4492(1984).  
 RN (2)  
 RP SEQUENCE OF 41-180.  
 RX MEDLINE=80130563; PubMed=6766735;  
 RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,  
 RA Titani K.;  
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart  
 RT factor)."  
 RL Biochemistry 19:659-667(1980).  
 RN (3)  
 RP REVISION TO 103.  
 RX MEDLINE=83508813; PubMed=6688526;  
 RA McMullen B.A., Fujikawa K., Kisiel W.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
 RT K-dependent blood coagulation zymogens."  
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
 RN (4)  
 RP SEQUENCE OF 163-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RX MEDLINE=76053069; PubMed=1059093;  
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,  
 RA Neurath H.;  
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RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).  
 RN [5]  
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [6]  
 RP ACTIVE SITE.  
 RX MEDLINE=73053314; PubMed=4264286;  
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,  
 RA Neurath H., Davie E.W.;  
 RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology  
 RT with mammalian serine proteases.";  
 RL Biochemistry 11:4899-4903(1972).  
 RN [7]  
 RP PROCESSING.  
 RX MEDLINE=76053121; PubMed=1059122;  
 RA Fujikawa K., Titani K., Davie E.W.;  
 RT "Activation of bovine factor X (Stuart factor): conversion of factor  
 RT Xa-alpha to factor Xa-beta.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).  
 RN [8]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185716; PubMed=6546930;  
 RA Sugo T., Bjoerck I., Holmgren A., Stenflo J.;  
 RT "Calcium-binding properties of bovine factor X lacking the gamma-  
 RT carboxyglutamic acid-containing region.";  
 RL J. Biol. Chem. 259:5705-5710(1984).  
 RN [9]  
 RP SULFATION.  
 RX MEDLINE=86140210; PubMed=3949800;  
 RA Morita T., Jackson C.M.;  
 RT "Localization of the structural difference between bovine blood  
 RT coagulation factors XI and X2 to tyrosine 18 in the activation  
 RT peptide.";  
 RL J. Biol. Chem. 261:4008-4014(1986).  
 RN [10]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=91084483; PubMed=2261466;  
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;  
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of  
 RT the amino-terminal epidermal growth factor like domain in coagulation  
 RT factor X.";  
 RL Biochemistry 29:8111-8118(1990).  
 RN [11]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=92329412; PubMed=1627540;  
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,  
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 RT "Three-dimensional structure of the apo form of the N-terminal  
 RT EGF-like module of blood coagulation factor X as determined by NMR  
 RT spectroscopy and simulated folding.";  
 RL Biochemistry 31:5974-5983(1992).  
 RN [12]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=92406922; PubMed=1527084;  
 RA Selander M., Ullner M., Persson E., Teleman O.,  
 RA Stenflo J., Drakenberg T.;  
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High  
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-  
 RT like domain in coagulation factor X.";  
 RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sumnerhagen M., Olah G.A., Stenflo J., Foren S., Drakenberg T.,  
 RA Trewhella J.;  
 RT "The relative orientation of Gla and EGF domains in coagulation  
 RT factor X is altered by Ca2+ binding to the first EGF domain. A  
 RT combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg1-Thr and then  
 CC Arg1-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC -----  
 DR EMBL; X00673; CA025286.1; -.  
 DR PIR; A00925; EXBO.  
 DR PDB; 1APO; 31-JAN-94.  
 DR PDB; 1CCF; 31-MAY-94.  
 DR PDB; 1MHE; 15-MAY-97.  
 DR PDB; 1MHE; 15-MAY-97.  
 DR MEROPS; S01.216; -.  
 DR GLYCOSULEDB; P00743; -.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR Pfam; PF00594; Gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
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 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3d-structure.  
 FT SIGNAL 1 23  
 FT PROPEP 24 40  
 FT CHAIN 41 180  
 FT CHAIN 183 492  
 FT PROPEP 183 233  
 FT CHAIN 234 492  
 FT PROPEP 476 492  
 FT DOMAIN 86 122  
 FT  
 FT FACTOR X LIGHT CHAIN.  
 FT FACTOR X HEAVY CHAIN.  
 FT ACTIVATION PEPTIDE.  
 FT ACTIVATED FACTOR XA, HEAVY CHAIN.  
 FT MAY BE REMOVED BUT IS NOT NECESSARY FOR  
 FT ACTIVATION.  
 FT EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 125 165 EGF-LIKE 2.  
FT 234 492 SERINE PROTEASE.  
FT ACT SITE 275 275 CHARGE RELAY SYSTEM.  
FT ACT SITE 321 321 CHARGE RELAY SYSTEM.  
FT ACT SITE 418 418 CHARGE RELAY SYSTEM.  
FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

Query Match 47.4%; Score 90; DB 1; Length 492;  
Best Local Similarity 36.4%; Pred. No. 1e-08;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRDGLXRCXKXLCGFFXAXEYFRXXXTQGFVY 44  
Db 41 ANSFLFEEVXQGNLERECLEBACSLBEAREVEFDADQTDPMKY 84

RESULT 15.  
FR9\_HUMAN STANDARD; PRT; 461 AA.  
ID PA9\_HUMAN  
AC P00740;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).  
GN F9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RP MEDLINE=8600558; PubMed=2994716;  
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;  
RT "Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).";  
RL Biochemistry 24:3736-3750(1985).  
RN [2]  
RP MEDLINE=85190593; PubMed=3857619;  
RA McGraw R.A., Davie L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,  
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RN [3]  
RP MEDLINE=84236100; PubMed=6329734;  
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RT "The gene structure of human anti-haemophilic factor IX.";  
RL EMBO J. 3:1053-1060(1984).  
RN [4]  
RP MEDLINE=8320788; PubMed=6687940;  
RA Jaye M., de la Salle H., Schamber F., Ballard A., Kohl V.,  
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-base synthetic oligonucleotide probe deduced from the amino acid sequence of bovine factor IX.";  
RL Nucleic Acids Res. 11:2325-2335(1983).  
RN [5]  
RP MEDLINE=84300526; PubMed=6089357;  
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RN [6]  
RP MEDLINE=88127096; PubMed=3340835;  
RA Stoflet E.S., Koebler D.D., Sarkar G., Sommer S.S.;  
RT "Genomic amplification with transcript sequencing.";  
RL Science 239:491-494(1988).  
RN [7]  
RP MEDLINE=94054330; PubMed=8236150;  
RA de la Salle C., Chauxantier J.L., Baes M.J., Schwartz A.,  
RT "A deletion located in the 3' non translated part of the factor IX gene responsible for mild haemophilia B.";  
RL Thromb. Haemost. 70:370-371(1993).  
RN [8]  
RP MEDLINE=90078229; PubMed=2592373;  
RA Sueniro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by tryptophan and its activation by alpha-chymotrypsin and rat mast cell chymase.";  
RL J. Biol. Chem. 264:21257-21265(1989).  
RN [9]  
RP HYDROXYLATION OF ASP-110.  
RX MEDLINE=83308813; PubMed=6688526;  
RA McMullen B.A., Fujikawa K., Kistel W.;  
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation zymogens.";  
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
RN [10]  
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=78194509; PubMed=659613;  
RA di Scipio R.G., Kurachi K., Davie E.W.;  
RT "Activation of human factor IX (Christmas factor).";  
RL J. Clin. Invest. 61:1528-1538(1978).  
RN [11]  
RP CALCIUM-BINDING DATA.  
RX MEDLINE=84185715; PubMed=6425296;  
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
RT "Derivatives of blood coagulation factor IX contain a high affinity Ca<sup>2+</sup>-binding site that lacks gamma-carboxyglutamic acid.";  
RL J. Biol. Chem. 259:5698-5704(1984).  
RN [12]  
RP ERRATUM.  
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
RL J. Biol. Chem. 260:2583-2583(1985).  
RN [13]  
RP SIGNAL SEQUENCE CLEAVAGE SITE.  
RX MEDLINE=86189947; PubMed=3009023;  
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
RT "Defective propeptide processing of blood clotting factor IX caused by mutation of arginine to glutamine at position -4.";  
RL Cell 45:343-348(1986).  
RN [14]  
RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
RX MEDLINE=90062160; PubMed=2511201;  
RA Nishimura H., Kawabata S., Kistel W., Hase S., Ikenaka T.,  
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl<sub>2</sub>-Glc) O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.";  
RL J. Biol. Chem. 264:20320-20325(1989).  
RN [15]  
RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kistel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).

[16]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-107.  
 RX MEDLINE=92386094; PubMed=1517205.  
 RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;  
 RT "Human factor IX has a tetraaccharide O-glycosidically linked to  
 RT serine 61 through the fucose residue."  
 RL J. Biol. Chem. 267:17520-17525(1992).  
 RN [17]  
 RP PHOSPHORYLATION OF SER-114.  
 RA Harris R.J., Papac D.I., Truong L., Smith K.J.;  
 RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX."  
 RL (in) Abstracts of 11th international conference on methods in protein  
 RL structure analysis, pp.50-50, Annecy (1996).  
 RN [18]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=20575397; PubMed=11133752;  
 RA Arruda V.R., Hagstrom J.N., Delich J., Helman-Patterson T.,  
 RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
 RA Larson P.J., High K.A.;  
 RT "Posttranslational modifications of recombinant myotube-synthesized  
 RT human factor IX."  
 RL Blood 97:130-138(2001).  
 RN [19]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=95229607; PubMed=7713897;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich  
 RT binding region of factor IX by two-dimensional NMR spectroscopy."  
 RL J. Biol. Chem. 270:7980-7987(1995).  
 RN [20]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96032604; PubMed=7547952;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
 RT domain of factor IX."  
 RL Biochemistry 34:12126-12137(1995).  
 RN [21]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96279169; PubMed=8663165;  
 RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
 RA Furie B.;  
 RT "Identification of the phospholipid binding site in the vitamin K-  
 RT dependent blood coagulation protein factor IX."  
 RL J. Biol. Chem. 271:16227-16236(1996).  
 RN [22]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=97199336; PubMed=9047312;  
 RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,  
 RA Smith H., Hiskey R.G., Pedersen L.G.;  
 RT "Refinement of the NMR solution structure of the  
 RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
 RT molecular dynamics simulation with initial Ca<sup>2+</sup> positions determined  
 RT by a genetic algorithm."  
 RL Biochemistry 36:2132-2138(1997).  
 RN [23]  
 RP STRUCTURE BY NMR OF 91-133.  
 RX MEDLINE=91308127; PubMed=1854745;  
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;  
 RT "Sequence-specific 1H NMR assignments, secondary structure, and  
 RT location of the calcium binding site in the first epidermal growth  
 RT factor like domain of blood coagulation factor IX."  
 RL Biochemistry 30:7402-7409(1991).  
 RN [24]  
 RP STRUCTURE BY NMR OF 92-130.  
 RX MEDLINE=93284090; PubMed=1304885;  
 RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,  
 RA Tee A.G.D., Brownlee G.G., Campbell I.D.C.;  
 RT "The three-dimensional structure of the first EGF-like module of  
 RT human factor IX: comparison with EGF and TGF-alpha."  
 RL Protein Sci. 1:81-90(1992).  
 RN [25]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
 RX MEDLINE=95330802; PubMed=7606779;

RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;  
 RT "The structure of a Ca(2+)-binding epidermal growth factor-like  
 RT domain: its role in protein-protein interactions."  
 RL Cell 82:131-141(1995).  
 RN [26]  
 RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 46.3%; Score 88; DB 1; Length 461;  
 Best local Similarity 39.5%; Pred. No. 2,2e-08;  
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXLRDGLKRXCRXXLCSFYXAEIIPNXXRIPQFVSY 44  
 Db 49 SGKLEFVQGNLRECEMEKCSFEAREVFENRTETFEWKQY 91

Search completed: March 19, 2003, 14:52:55  
 Job time : 6.625 secs

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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(without alignments)  
196.288 Million cell updates/sec

Title: 10ASP28GLU\_4  
Perfect score: 190  
Sequence: 1 ANGFLXLRGSLXRCRX...XXAEXIPRNXXRRQFWVS 44

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPRMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 123   | 64.7        | 701    | 4 Q96PQ8  | Q96PQ8 homo sapien |
| 2          | 109   | 57.4        | 460    | 11 Q91WN8 | Q91WN8 mus musculu |
| 3          | 106   | 55.8        | 446    | 11 Q61109 | Q61109 mus musculu |
| 4          | 103   | 54.2        | 460    | 11 Q99PC6 | Q99PC6 mus musculu |
| 5          | 99    | 52.1        | 456    | 6 Q8TTR0  | Q8TTR0 canis faml  |
| 6          | 94    | 49.5        | 482    | 11 Q63207 | Q63207 rattus norv |
| 7          | 91    | 47.9        | 481    | 11 Q54740 | Q54740 mus musculu |
| 8          | 91    | 47.9        | 481    | 11 Q99L32 | Q99L32 mus musculu |
| 9          | 91    | 47.9        | 481    | 11 Q88947 | Q88947 mus musculu |
| 10         | 88    | 46.3        | 456    | 4 Q14316  | Q14316 homo sapien |
| 11         | 88    | 46.3        | 461    | 6 Q95ND7  | Q95ND7 pan troglod |
| 12         | 88    | 46.3        | 461    | 6 Q95ND6  | Q95ND6 pan troglod |
| 13         | 87    | 45.8        | 469    | 6 Q9GMD9  | Q9GMD9 ornithorhyn |
| 14         | 86    | 45.3        | 49     | 6 Q95ME8  | Q95ME8 bos taurus  |
| 15         | 81    | 42.6        | 138    | 6 Q28994  | Q28994 sus scrofa  |
| 16         | 80    | 42.1        | 433    | 13 Q90YK1 | Q90YK1 brachydanio |

|    |      |      |      |           |                    |
|----|------|------|------|-----------|--------------------|
| 17 | 76   | 40.0 | 100  | 4 Q15253  | Q15253 homo sapien |
| 18 | 76   | 40.0 | 608  | 13 Q9PTW7 | Q9PTW7 struthio ca |
| 19 | 75   | 39.5 | 648  | 6 Q29094  | Q29094 sus scrofa  |
| 20 | 74   | 38.9 | 399  | 11 Q9COW3 | Q9COW3 mus musculu |
| 21 | 71.5 | 37.6 | 542  | 5 Q8T6T3  | Q8T6T3 halocynthia |
| 22 | 71   | 37.4 | 179  | 4 Q8TAS3  | Q8TAS3 homo sapien |
| 23 | 71   | 37.4 | 198  | 11 Q8R182 | Q8R182 mus musculu |
| 24 | 70   | 36.8 | 650  | 4 Q9NSD0  | Q9NSD0 homo sapien |
| 25 | 70   | 36.8 | 650  | 4 Q16519  | Q16519 homo sapien |
| 26 | 64   | 33.7 | 607  | 13 Q91001 | Q91001 gallus gall |
| 27 | 59   | 31.1 | 678  | 4 Q14393  | Q14393 homo sapien |
| 28 | 58   | 30.5 | 673  | 11 Q61592 | Q61592 mus musculu |
| 29 | 58   | 30.5 | 674  | 11 Q99K57 | Q99K57 mus musculu |
| 30 | 57   | 30.0 | 98   | 13 P82807 | P82807 notechis sc |
| 31 | 56   | 29.5 | 25   | 11 Q9OVH6 | Q9OVH6 rattus sp.  |
| 32 | 56   | 29.5 | 674  | 11 Q63772 | Q63772 rattus sp.  |
| 33 | 52   | 27.4 | 1159 | 13 Q9Y1A6 | Q9Y1A6 cyprinus ca |
| 34 | 50.5 | 26.6 | 575  | 10 Q94E17 | Q94E17 oryza sativ |
| 35 | 50.5 | 26.6 | 608  | 10 Q9XFX6 | Q9XFX6 medicago sa |
| 36 | 50   | 26.3 | 472  | 13 Q988U5 | Q988U5 gasteroste  |
| 37 | 50   | 26.3 | 613  | 13 Q988U6 | Q988U6 gasteroste  |
| 38 | 50   | 26.3 | 910  | 13 Q988U7 | Q988U7 gasteroste  |
| 39 | 49.5 | 26.1 | 196  | 10 Q04284 | Q04284 belaginelia |
| 40 | 49.5 | 26.1 | 567  | 10 Q8W4J2 | Q8W4J2 arabidopsis |
| 41 | 49.5 | 26.1 | 603  | 10 Q9LPG7 | Q9LPG7 arabidopsis |
| 42 | 49.5 | 26.1 | 606  | 10 Q95JG9 | Q95JG9 arabidopsis |
| 43 | 49.5 | 26.1 | 651  | 10 Q852I8 | Q852I8 oryza sativ |
| 44 | 48.5 | 25.5 | 431  | 10 Q94EY5 | Q94EY5 arabidopsis |
| 45 | 48.5 | 25.5 | 492  | 10 Q95MJ7 | Q95MJ7 cicor arlet |

## ALIGNMENTS

RESULT 1

| ID | Q96PQ8   | PREDIMINARY: | PRT: | 701 AA. |
|----|--|--------------|------|---------|
| AC | Q96PQ8:  |              |      |         |
| DT | 01-DEC-2001 (TREMURel. 19, Last sequence update)                       |              |      |         |
| DT | 01-DEC-2001 (TREMURel. 19, Last sequence update)                       |              |      |         |
| DT | 01-MAR-2002 (TREMURel. 20, Last annotation update)                     |              |      |         |
| DT | Factor VII active site mutant immunocognate.                           |              |      |         |
| OS | Homo sapiens (Human).  |              |      |         |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                |              |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.            |              |      |         |
| OX | NCBI_TaxId=9606;   |              |      |         |
| RN | [1]  |              |      |         |
| RP | SEQUENCE FROM N.A.   |              |      |         |
| RX | MEDLINE=21477448; PubMed=11593034;                                     |              |      |         |
| RA | Hu Z., Garen A.;   |              |      |         |
| RT | "Targeting tissue factor on tumor vascular endothelial cells and tumor |              |      |         |
| RT | cells for immunotherapy in mouse models of prostatic cancer.";         |              |      |         |
| RL | Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).                    |              |      |         |
| DR | EMBL; AF272774; AAKS6866.1; -  |              |      |         |
| DR | InterPro; IPR000152; Asx hydroxyl.                                     |              |      |         |
| DR | InterPro; IPR000561; BGF-like.   |              |      |         |
| DR | InterPro; IPR000742; BGF_2.  |              |      |         |
| DR | InterPro; IPR001881; BGF_Ca.   |              |      |         |
| DR | InterPro; IPR003061; IG_MHC.   |              |      |         |
| DR | InterPro; IPR001254; Ser protease_Try.                                 |              |      |         |
| DR | InterPro; IPR00294; VitK_dep_GLA.                                      |              |      |         |
| DR | Pfam; PF00008; EGF_2.  |              |      |         |
| DR | Pfam; PF00594; gla; 1.   |              |      |         |
| DR | Pfam; PF00047; Ig; 2.  |              |      |         |
| DR | Pfam; PF00089; trypsin; 1.   |              |      |         |
| DR | SMART; SM00181; EGF; 2.  |              |      |         |
| DR | PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.                             |              |      |         |
| DR | PROSITE; PS00022; EGF_1; UNKNOWN_1.                                    |              |      |         |
| DR | PROSITE; PS01185; EGF_2; UNKNOWN_1.                                    |              |      |         |
| DR | PROSITE; PS01187; EGF_CA; UNKNOWN_1.                                   |              |      |         |
| DR | PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.                        |              |      |         |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN_1.                                   |              |      |         |
| DR | PROSITE; PS00240; TRYPSIN_DOM; 1.                                      |              |      |         |

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CBB42CC992F CRC64;

Query Match 64.7%; Score 123; DB 4; Length 701;  
 Best Local Similarity 52.3%; Pred. No. 45e-14;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGSIXRXCXLLCSFXAXEXIFRNXXRTROPFWVS 44  
 DB 61 ANAFLEELRPGSLERECMEQCSFEERAREIFKDAERTKLFWISY 104

## RESULT 2

O91WN8 PRELIMINARY; PRT; 460 AA.  
 AC O91WN8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Similar to protein C.  
 GN PROC.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013896; AAH13896.1; -.

DR MGI; MGI:97771; Proc.

DR InterPro; IPR000152; Asx hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR001254; Ser protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.

DR Pfam; PF00008; EGF\_2.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.

DR PROSITE; PS01187; EGF Ca; UNKNOWN\_1.

DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN\_1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.

KW Hydrolyase; Serine protease.

SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FC274 CRC64;

Query Match 57.4%; Score 109; DB 11; Length 460;  
 Best Local Similarity 45.5%; Pred. No. 1.2e-11;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGSIXRXCXLLCSFXAXEXIFRNXXRTROPFWVS 44  
 DB 42 ANSFLEMRPGSLERECMEICDPEERAOEIFQNVETLAWIRY 85

RESULT 3  
 O61109 PRELIMINARY; PRT; 446 AA.  
 AC O61109;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Coagulation factor VII.  
 GN F7 OR FVII.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=96276538; PubMed=8701412;

RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,

RA Castellino F.J.; "Characterization of a cDNA encoding murine coagulation factor VII.";

RT Thromb. Haemost. 75:481-487(1996).

CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE

TRYPSIN FAMILY.

DR EMBL; U44795; AAC52570.1; -.

DR HSSP; P08709; IFAK.

DR MEROPS; S01.215; -.

DR MGI; MGI:109325; F7.

DR InterPro; IPR002086; Aldehyde dehydr.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR002383; GLA\_blood.

DR InterPro; IPR001254; Ser protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.

DR Pfam; PF00008; EGF\_2.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF\_CA; 1.

DR SMART; SM00001; EGF-like; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp\_Spc; 1.

DR PROSITE; PS00070; ALDEHYDE DEHYDR\_CYS; UNKNOWN\_1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS01187; EGF Ca; 1.

DR PROSITE; PS00011; GLU CARBOXYLATION; 1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;

KW Serine protease.

SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 55.8%; Score 106; DB 11; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 4e-11;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGSIXRXCXLLCSFXAXEXIFRNXXRTROPFWVS 44  
 DB 42 ANSLLELMPGSLERECNEQCSFEERAREIFKSPERTKQFWIVY 85

RESULT 4  
 O99PC6 PRELIMINARY; PRT; 460 AA.  
 AC O99PC6;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Anticoagulant protein C.

GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL;  
 RA Korf I.;

```

RT "Complete sequence of UC72A01."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR01254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ
SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 54.2%; Score 103; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 1.5e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRDGLKRXCRXXLCSFYXAEIIFRNXXRTQFWVS 44
Db 42 ANSFLEEMRPGSLERECEIEICDLEAQEIFQNVEDTLAFWIKY 85

RESULT 5
Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Depe A., Breen M., Matlis U., Brunberg L.,
RT "Molecular characterization and chromosomal assignment of the canine
RT protein C gene."
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Depe A., Breen B.;
RT "Analysis of canine protein C gene polymorphisms."
RL Annu. Genet. 30:237-238(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

```

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DR EMBL; AJ001979; CAA05126.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR01254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
SQ
SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 52.1%; Score 99; DB 6; Length 456;
Best Local Similarity 43.2%; Pred. No. 8.2e-10;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRDGLKRXCRXXLCSFYXAEIIFRNXXRTQFWVS 44
Db 43 ANSFLEIRAGSLERECEIEICDLEAKEIFQNVDDTLAWISKY 86

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase."
RL Thromb. Res. 80:63-73(1995).
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000294; VitK_dep_GLA.

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DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; Chymotrypsin.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_1like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

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Query Match 49.5%; Score 94; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 7.4e-09;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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QY 1 ANGFLXLLRDGSLXRCXKXLCSPXAXEYIFRNXXRTQFWWSY 44
Db 41 ANSFEEIFKGNLERECVEEICSEFBAREVFEDEKTEFWTKY 84

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RESULT 7

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OS4740 PRELIMINARY; PRT; 481 AA.
ID OS4740
AC OS4740;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F10.
OS Mus musculus (Mouse).
OC Plasmid pBluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAAL0933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; F10.
DR MGD; MGI:103107; F10.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR00134; Chymotrypsin.
DR InterPro; IPR000561; EGF_1like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; Chymotrypsin.
DR PRINTS; PR00001; GLABLOOD.

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DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_1like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D7AE CRC64;

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Query Match 47.9%; Score 91; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 2.7e-08;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

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```

QY 1 ANGFLXLLRDGSLXRCXKXLCSPXAXEYIFRNXXRTQFWWSY 44
Db 41 ANSFEEIFKGNLERECVEEICSEFBAREVFEDEKTEFWTKY 84

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RESULT 8

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Q99LJ2 PRELIMINARY; PRT; 481 AA.
ID Q99LJ2
AC Q99LJ2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; F10.
DR MGD; MGI:103107; F10.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR00134; Chymotrypsin.
DR InterPro; IPR000561; EGF_1like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR00138; EGF_1I.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; Chymotrypsin.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_1like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

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DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
 KM Serine protease.  
 SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;  
 Best Local Similarity 31.8%; Pred. No. 2,7e-08;  
 Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLXRCXKXCSFXAXEIPRNXXRTROFVNSY 44  
 Db 41 ANSFEEFKGNLERECMEICSYEVRVETFEDEKTEYWKY 84

## RESULT 9

088947 PRELIMINARY; PRT; 481 AA.  
 AC 088947;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Coagulation factor X precursor.  
 GN F10.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL6 X CBA; TISSUE=LIVER;  
 RX MEDLINE=98347933; PubMed=9684791;  
 RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,  
 RA Castellino F.J., Rosen E.D.;  
 RT "Cloning and characterization of a cDNA encoding murine coagulation  
 RT factor X.";  
 RL Thromb. Haemost. 80:87-91(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SJ;  
 RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;  
 RT "Cloning and characterization of the Murine Factor X Gene.";  
 RL Thromb. Haemost. 0:0-0(2000).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL; AF087644; AAC36345.1; -.  
 DR EMBL; AF211347; AAF22980.1; -.  
 DR HSSP; P00742; IKA.  
 DR MEROPS; S01.216; -.  
 DR MGD; MGI:103107; F10.  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR002383; GLA\_Blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
 KM Serine protease; Signal.  
 FT SIGNAL 1 40  
 FT CHAIN 41 481  
 SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E9FD271E CRC64;

Query Match 47.9%; Score 91; DB 11; Length 481;  
 Best Local Similarity 31.8%; Pred. No. 2,7e-08;  
 Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLXRCXKXCSFXAXEIPRNXXRTROFVNSY 44  
 Db 41 ANSFEEFKGNLERECMEICSYEVRVETFEDEKTEYWKY 84

## RESULT 10

014316 PRELIMINARY; PRT; 456 AA.  
 AC 014316;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-AUG-1999 (TReMBLrel. 11, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas  
 DE disease, HAEMOPHILIA B) (Factor IX)).  
 GN F9 OR FACTOR IX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bird C.;  
 RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 3-19 FROM N.A.  
 RX MEDLINE=88327116; PubMed=3416069;  
 RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,  
 RA Briet E.;  
 RT "The putative factor IX gene promoter in hemophilia B Leyden.";  
 RL Blood 72:1074-1076(1988).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL; AL033403; CAA21954.1; -.  
 DR EMBL; X55008; CAB38245.2; -.  
 DR HSSP; P00740; ICFH.  
 DR MEROPS; S01.214; -.  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR002383; GLA\_Blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGF\_BLOOD.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.

DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
KW Serine protease.  
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 46.3%; Score 88; DB 4; Length 456;  
Best Local Similarity 39.5%; Pred. No. 9.1e-08;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRDGSILRXCRXXLCSPFXAEXIFRNXXRTROPFWVSY 44  
Db 44 SGKLEEFVQGNLERECMEKCSFEARBEVFENTERTERTEFWKQY 86

## RESULT 11

ID Q95ND7 PRELIMINARY; PRT; 461 AA.

AC Q95ND7; 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Coagulation factor XI.

GN F9.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

OX NCBI\_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=504;

RA Satta Y.;

RT "Comparison of DNA and protein polymorphisms between humans and

RT chimpanzees."

RL Genes Gene. Syst. 0.0-0.0(2001).

DR EMBL; AB062470; BAB58885.1; -.

DR EMBL; AB062458; BAB58885.1; JOINED.

DR EMBL; AB062460; BAB58885.1; JOINED.

DR EMBL; AB062462; BAB58885.1; JOINED.

DR EMBL; AB062464; BAB58885.1; JOINED.

DR EMBL; AB062466; BAB58885.1; JOINED.

DR EMBL; AB062468; BAB58885.1; JOINED.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.

DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.

DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.

DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN\_1.

DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.

DR Hydrolase; Serine protease.

KW SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 46.3%; Score 88; DB 6; Length 461;  
Best Local Similarity 39.5%; Pred. No. 9.2e-08;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRDGSILRXCRXXLCSPFXAEXIFRNXXRTROPFWVSY 44  
Db 49 SGKLEEFVQGNLERECMEKCSFEARBEVFENTERTERTEFWKQY 91

## RESULT 12

ID Q95ND6 PRELIMINARY; PRT; 461 AA.

AC Q95ND6; 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Coagulation factor XI.

GN F9.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

OX NCBI\_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=505;

RA Satta Y.;

RT "Comparison of DNA and protein polymorphisms between humans and

RT chimpanzees."

RL Genes Gene. Syst. 0.0-0.0(2001).

DR EMBL; AB062471; BAB58886.1; -.

DR EMBL; AB062459; BAB58886.1; JOINED.

DR EMBL; AB062461; BAB58886.1; JOINED.

DR EMBL; AB062463; BAB58886.1; JOINED.

DR EMBL; AB062465; BAB58886.1; JOINED.

DR EMBL; AB062467; BAB58886.1; JOINED.

DR EMBL; AB062469; BAB58886.1; JOINED.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.

DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.

DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.

DR PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN\_1.

DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.

DR Hydrolase; Serine protease.

KW SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 46.3%; Score 88; DB 6; Length 461;  
Best Local Similarity 39.5%; Pred. No. 9.2e-08;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRDGSILRXCRXXLCSPFXAEXIFRNXXRTROPFWVSY 44  
Db 49 SGKLEEFVQGNLERECMEKCSFEARBEVFENTERTERTEFWKQY 91

## RESULT 13

ID Q9GMD9 PRELIMINARY; PRT; 469 AA.

AC Q9GMD9; 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Coagulation factor X.

OS Ornithorhynchus anatinus (Duckbill platypus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.

OX NCBI\_TaxID=9258;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21015017; PubMed=1132153;

RA Poorafshar M., Aveskog M., Munday B., Hellman L.;

RT "Identification and structural analysis of four serine proteases in a

```
RT monotreme, the platypus, Ornithorhynchus anatinus."
RL Immunogenetics 52:19-28 (2000).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
   TRYPSIN FAMILY.
DR EMBL; AF275554; AAC00453.1; -.
DR HSPSP; P00742; IKB.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_CA; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Sec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_2; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Hydroxase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C23D0758F6A CRC64;

Query Match 45.8%; Score 87; DB 6; Length 469;
Best Local Similarity 34.1%; Pred. No. 1.4e-07;
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ANGLXLRDGSILKRCXKXLCSPFXAEXIFRNXXRTROFWVS 44
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 41 ANSLFEELKGNLRECEKNEETCSYEAREVEFDTKTNEFWNIY 84

RESULT 14
Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RN SEQUENCE FROM N.A.
RP Mizlata M.N., Amaral E.J.;
RT "Partial sequence of bovine f9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF394598; AAK77556.1; -.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6023 MW; DISC6D89CCBA4A14 CRC64;

Query Match 45.3%; Score 86; DB 6; Length 49;
Best Local Similarity 37.2%; Pred. No. 2.2e-08;
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Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXLRDGSILKRCXKXLCSPFXAEXIFRNXXRTROFWVS 44
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 SGKLEFPVFNGLRECEKNEKCSFEAREVFENTKTEFWKQY 48

RESULT 15
Q28994 PRELIMINARY; PRT; 138 AA.
ID Q28994
AC Q28994;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mature porcine factor IX (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=LIVER.
RC MEDLINE=96003866; PubMed=7568220.
RX Brandstetter H., Bauer M., Huber R., Lollar P., Bode W.;
RT "X-ray structure of clotting factor IXa: active site and module
   structure related to Xase activity and hemophilia B.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9796-9800(1995).
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U51135; AAA96318.1; -.
DR HSPSP; P00740; IEDM.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00010; EGFBLLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15515 MW; 793BABDR4D5FAFAD CRC64;

Query Match 42.6%; Score 81; DB 6; Length 138;
Best Local Similarity 41.2%; Pred. No. 5.3e-07;
Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 11 GSLKRCXKXLCSPFXAEXIFRNXXRTROFWVS 44
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 4 GNLERCEIEKCSFEAREVENTKTEFWKQY 37

Search completed: March 19, 2003, 15:13:37
Job time : 47.3125 secs
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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10ASP28GLU\_4  
Perfect score: 190  
Sequence: 1 ANGFLXXLRDGLRXCRXX.....XAXEYIFRNXXRTQFVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
|------------|-------|-------------|--------|-------|------------------|
| 1          | 156   | 82.1        | 44     | 3     | US-08-955-636-4  |
| 2          | 130   | 68.4        | 44     | 3     | US-08-955-636-27 |
| 3          | 126   | 66.3        | 44     | 3     | US-08-955-636-26 |
| 4          | 123   | 64.7        | 44     | 3     | US-08-955-636-3  |
| 5          | 123   | 64.7        | 406    | 1     | US-08-293-778-24 |
| 6          | 123   | 64.7        | 406    | 1     | US-08-295-411-5  |
| 7          | 123   | 64.7        | 406    | 2     | US-08-955-471-5  |
| 8          | 123   | 64.7        | 406    | 5     | PCT-US92-10242-5 |
| 9          | 123   | 64.7        | 444    | 1     | US-08-475-845-2  |
| 10         | 123   | 64.7        | 444    | 2     | US-08-327-690-2  |
| 11         | 123   | 64.7        | 444    | 2     | US-08-660-289-2  |
| 12         | 123   | 64.7        | 444    | 2     | US-08-537-807-2  |
| 13         | 123   | 64.7        | 444    | 2     | US-08-871-003-2  |
| 14         | 123   | 64.7        | 444    | 3     | US-08-464-233-2  |
| 15         | 123   | 64.7        | 444    | 4     | US-09-189-607-2  |
| 16         | 123   | 64.7        | 444    | 4     | US-09-378-907-2  |
| 17         | 123   | 64.7        | 444    | 5     | PCT-US94-05779-2 |
| 18         | 123   | 64.7        | 466    | 1     | US-07-882-202A-4 |
| 19         | 123   | 64.7        | 466    | 1     | US-08-021-615A-4 |
| 20         | 123   | 64.7        | 466    | 1     | US-08-321-777-4  |
| 21         | 123   | 64.7        | 466    | 4     | US-09-009-217-14 |
| 22         | 123   | 64.7        | 466    | 4     | US-09-009-656-14 |
| 23         | 123   | 64.7        | 466    | 5     | PCT-US93-04493-4 |
| 24         | 122   | 64.2        | 44     | 3     | US-08-955-636-30 |
| 25         | 120   | 62.6        | 44     | 3     | US-08-955-636-28 |
| 26         | 119   | 62.6        | 44     | 3     | US-08-955-636-29 |
| 27         | 109   | 57.4        | 41     | 1     | US-08-229-280-4  |

|    |    |      |     |   |                  |                   |
|----|----|------|-----|---|------------------|-------------------|
| 28 | 99 | 52.1 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appli |
| 29 | 99 | 52.1 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appli |
| 30 | 99 | 52.1 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appli |
| 31 | 99 | 52.1 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appli |
| 32 | 99 | 52.1 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appli |
| 33 | 99 | 52.1 | 437 | 1 | US-08-487-037-3  | Sequence 2, Appli |
| 34 | 99 | 52.1 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appli |
| 35 | 97 | 51.1 | 44  | 3 | US-08-955-636-2  | Sequence 2, Appli |
| 36 | 97 | 51.1 | 44  | 3 | US-08-955-636-23 | Sequence 2, Appli |
| 37 | 95 | 50.0 | 44  | 3 | US-08-955-636-35 | Sequence 3, Appli |
| 38 | 94 | 49.5 | 448 | 1 | US-08-295-411-3  | Sequence 3, Appli |
| 39 | 94 | 49.5 | 448 | 1 | US-08-955-471-3  | Sequence 3, Appli |
| 40 | 94 | 49.5 | 448 | 5 | PCT-US92-10068-1 | Sequence 1, Appli |
| 41 | 94 | 49.5 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appli |
| 42 | 93 | 48.9 | 44  | 3 | US-08-955-636-22 | Sequence 2, Appli |
| 43 | 93 | 48.9 | 44  | 3 | US-08-955-636-24 | Sequence 2, Appli |
| 44 | 92 | 48.4 | 41  | 1 | US-08-229-280-5  | Sequence 5, Appli |
| 45 | 92 | 48.4 | 42  | 2 | US-08-745-254A-2 | Sequence 2, Appli |

## ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa-gamma carboxylutamic acid or glutamic acid
US-08-955-636-4

Query Match      82.1%; Score 156; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 2e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGLRXCRXXLCSPXAXEYIFRNXXRTQFVSY 44
Db 1 ANGFLXXLRDGLRXCRXXLCSPXAXEYIFRNXXRTQFVSY 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD.RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-27

Query Match 68.4%; Score 130; DB 3; Length 44;  
Best Local Similarity 77.3%; Pred. No. 4, 6e-15;  
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWVS 44  
Db 1 ANAFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWIS 44

## RESULT 3

US-08-955-636-26  
Sequence 26, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD.RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-26

Query Match 66.3%; Score 126; DB 3; Length 44;  
Best Local Similarity 75.0%; Pred. No. 2, 2e-14;  
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWVS 44  
Db 1 ANAFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWIS 44

## RESULT 4

US-08-955-636-3  
Sequence 3, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD.RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-3

Query Match 64.7%; Score 123; DB 3; Length 44;  
Best Local Similarity 75.0%; Pred. No. 6, 9e-14;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWVS 44  
Db 1 ANAFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWIS 44

## RESULT 5

US-08-293-778-24  
Sequence 24, Application US/08293778  
Patent No. 5580560  
GENERAL INFORMATION:  
APPLICANT: Nicolaissen, Else M.  
APPLICANT: Bjorn, Soren E.  
APPLICANT: Wiberg, Finn C.  
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.  
STREET: 405 Lexington Avenue, 62nd floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,778  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,509  
FILING DATE:

APPLICATION NUMBER: DK 3235/87  
FILING DATE: 25-JUN-1987

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/434,149  
FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DR8/00103  
FILING DATE: 24-JUN-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3129, 224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 64.7%; Score 123; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 6, 7e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWVS 44  
Db 1 ANAFLLXLRDGLXRCXKXLCSPFXAEXIFRNXXRTQFWIS 44

RESULT 6  
US-08-293-411-5



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: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/10242
: FILING DATE: 19921118
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,989
: FILING DATE: 18-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SC80472P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152
: OTHER INFORMATION: /note= "Factor VII Light Chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 153..406
: OTHER INFORMATION: /note= "Factor VII Heavy Chain"
: PCT-US92-10242-5

Query Match 64.7%; Score 123; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.7e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLXRXCRXXLCSPXXAEXIFRNXXRTROPWVS 44
Db 1 ANAFLELRPGSLERCKEQCSFEARBEIFKDAERTKLFWISY 44

RESULT 9
US-08-475-845-2
: Sequence 2, Application US/08475845
: Patent No. 5788965
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stewart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
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: APPLICATION NUMBER: US/08/475,845
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920
: FILING DATE: 28-FEB-1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 13952-8-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-475-845-2

Query Match 64.7%; Score 123; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 7.3e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLXRXCRXXLCSPXXAEXIFRNXXRTROPWVS 44
Db 39 ANAFLELRPGSLERCKEQCSFEARBEIFKDAERTKLFWISY 82

RESULT 10
US-08-327-690-2
: Sequence 2, Application US/08327690
: Patent No. 5817788
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stewart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920
```

FILING DATE: 28-FEB-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-327-690-2

Query Match 64.7%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 7.3e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGLXKRCXXICSFXXAEXIFRNXXRTQFWVS 44  
DB 39 ANAFLELRPGSLERCKEKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 11  
US-08-660-289-2  
Sequence 2, Application US/08660289  
Patent No. 5833982  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,289  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,845  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-660-289-2

Query Match 64.7%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 7.3e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGLXKRCXXICSFXXAEXIFRNXXRTQFWVS 44  
DB 39 ANAFLELRPGSLERCKEKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12  
US-08-537-807-2  
Sequence 2, Application US/08537807  
Patent No. 5861374  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,807  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05779  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 08/065,725  
FILING DATE: 21-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 64.7%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 7.3e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGLXKRCXXICSFXXAEXIFRNXXRTQFWVS 44  
DB 39 ANAFLELRPGSLERCKEKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5997864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.

APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 64.7%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 7.3e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGSIXRXCXXLCSPFXXAEXIFRXXRTPQFWVS 44  
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14  
US-08-464-233-2  
Sequence 2, Application US/08464233  
Patent No. 6039944  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,233  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-233-2

Query Match 64.7%; Score 123; DB 3; Length 444;  
Best Local Similarity 52.3%; Pred. No. 7.3e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXXLRDGSIXRXCXXLCSPFXXAEXIFRXXRTPQFWVS 44  
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15  
US-09-189-607-2  
Sequence 2, Application US/09189607  
Patent No. 6168789  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,607  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/660,289  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/662,920  
 FILING DATE: 28-FEB-1991  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parmelee, Steven W.  
 REGISTRATION NUMBER: 31,990  
 REFERENCE/DOCKET NUMBER: 13952-8-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-467-9600  
 TELEFAX: 415-543-5043  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 444 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-189-607-2

Query Match 64.7%; Score 123; DB 4; Length 444;  
 Best Local Similarity 52.3%; Pred. No. 7.3e-13;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
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 Db 39 ANAPLELRPGSLRECKEEOCSFEAREIFRDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:18  
 Job time: 10.75 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds  
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Perfect score: 190  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries  
Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB pep:\*  
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14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 123   | 64.7        | 406    | 9  | US-10-109-498-1    |
| 2          | 93    | 48.9        | 419    | 9  | US-10-182-263-6    |
| 3          | 92    | 48.4        | 419    | 9  | US-10-182-263-1    |
| 4          | 92    | 48.4        | 419    | 9  | US-10-182-263-3    |
| 5          | 92    | 48.4        | 419    | 9  | US-10-182-263-4    |
| 6          | 92    | 48.4        | 419    | 9  | US-10-182-263-5    |
| 7          | 92    | 48.4        | 419    | 9  | US-09-978-917A-4   |
| 8          | 92    | 48.4        | 461    | 9  | US-10-182-263-2    |
| 9          | 92    | 48.4        | 461    | 9  | US-09-978-917A-2   |
| 10         | 88    | 46.3        | 415    | 10 | US-09-118-748-2    |
| 11         | 88    | 46.3        | 461    | 9  | US-10-132-829-5    |
| 12         | 88    | 46.3        | 461    | 10 | US-09-884-901-3    |
| 13         | 70    | 36.8        | 96     | 9  | US-09-759-130B-313 |
| 14         | 70    | 36.8        | 209    | 9  | US-09-759-130B-310 |
| 15         | 70    | 36.8        | 226    | 9  | US-09-758-130B-310 |
| 16         | 53    | 27.9        | 95     | 9  | US-09-759-130B-356 |
| 17         | 53    | 27.9        | 208    | 9  | US-09-759-130B-355 |
| 18         | 53    | 27.9        | 225    | 9  | US-09-759-130B-353 |
| 19         | 44    | 23.2        | 744    | 10 | US-09-862-179A-1   |

|    |      |      |      |    |                    |                   |
|----|------|------|------|----|--------------------|-------------------|
| 20 | 44   | 23.2 | 1337 | 10 | US-09-757-781-62   | Sequence 62, Appl |
| 21 | 43   | 22.6 | 484  | 10 | US-09-801-368-334  | Sequence 334, App |
| 22 | 41   | 21.6 | 135  | 10 | US-09-925-301-1491 | Sequence 1491, Ap |
| 23 | 41   | 21.6 | 273  | 9  | US-09-764-868-968  | Sequence 968, App |
| 24 | 41   | 21.6 | 1266 | 9  | US-09-931-969A-2   | Sequence 2, Appli |
| 25 | 41   | 21.6 | 1266 | 9  | US-10-079-699-2    | Sequence 2, Appli |
| 26 | 41   | 21.6 | 1266 | 10 | US-09-757-781-63   | Sequence 63, Appl |
| 27 | 41   | 21.6 | 1356 | 10 | US-09-757-781-2    | Sequence 2, Appli |
| 28 | 41   | 21.6 | 1663 | 10 | US-09-875-519A-22  | Sequence 22, App  |
| 29 | 40.5 | 21.3 | 197  | 9  | US-10-076-622-516  | Sequence 516, App |
| 30 | 40.5 | 21.3 | 197  | 12 | US-10-007-805-516  | Sequence 516, App |
| 31 | 40.5 | 21.3 | 232  | 9  | US-10-076-622-517  | Sequence 517, App |
| 32 | 40.5 | 21.3 | 232  | 12 | US-10-007-805-517  | Sequence 517, App |
| 33 | 40.5 | 21.3 | 243  | 9  | US-09-938-418-7    | Sequence 7, Appli |
| 34 | 40.5 | 21.3 | 243  | 9  | US-10-045-992-4    | Sequence 4, Appli |
| 35 | 40.5 | 21.3 | 243  | 9  | US-10-063-547-122  | Sequence 122, App |
| 36 | 40.5 | 21.3 | 243  | 9  | US-10-174-590-366  | Sequence 366, App |
| 37 | 40.5 | 21.3 | 243  | 9  | US-10-176-758-366  | Sequence 366, App |
| 38 | 40.5 | 21.3 | 243  | 9  | US-10-063-616-122  | Sequence 122, App |
| 39 | 40.5 | 21.3 | 243  | 9  | US-10-175-737-366  | Sequence 366, App |
| 40 | 40.5 | 21.3 | 243  | 9  | US-10-063-502-122  | Sequence 122, App |
| 41 | 40.5 | 21.3 | 243  | 9  | US-10-076-622-514  | Sequence 514, App |
| 42 | 40.5 | 21.3 | 243  | 9  | US-10-173-706-366  | Sequence 366, App |
| 43 | 40.5 | 21.3 | 243  | 9  | US-10-175-738-366  | Sequence 366, App |
| 44 | 40.5 | 21.3 | 243  | 9  | US-10-175-752-366  | Sequence 366, App |
| 45 | 40.5 | 21.3 | 243  | 9  | US-10-176-482-366  | Sequence 366, App |

ALIGNMENTS

RESULT 1  
US-10-109-498-1  
; Sequence 1, Application US/10109498  
; Publication No. US200304908A1  
; GENERAL INFORMATION:  
; APPLICANT: Persson, Egon  
; TITLE OF INVENTION: Coagulation Factor VII Derivatives  
; FILE REFERENCE: 6286, 200-US  
; CURRENT APPLICATION NUMBER: US/10/109,498  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/281,261  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: PA 2001 00477  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(406)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-109-498-1  
Query Match 64.7%; Score 123; DB 9; Length 406;  
Best Local Similarity 75.0%; Pred. No. 1.5e-13;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
OY 1 ANGFLLXLRDGLRXCRXXLCSPFXAEXIFRNXXRTROFWVSY 44  
Db 1 ANAFLLXLRDGLRXCRXXLCSPFXAEXIFRNXXRTROFWVSY 44  
RESULT 2  
US-10-182-263-6  
; Sequence 6, Application US/10182263  
; Publication No. US20030022354A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlitz, Bruce E  
; APPLICANT: Jones, Bryan E

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          48.9%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 2.5e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCRXXLCFFXXAEXIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFW 41

RESULT 3
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          48.4%; Score 92; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 3.8e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

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Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFQVDDTLAFW 41

RESULT 4
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          48.4%; Score 92; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 3.8e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCRXXLCFFXXAEXIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFW 41

RESULT 5
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          48.4%; Score 92; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 3.8e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCRXXLCFFXXAEXIFRNXXRTROFW 41
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFW 41

RESULT 6
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-182-263-5

Query Match 48.4%; Score 92; DB 9; Length 419;  
Best Local Similarity 46.3%; Pred. No. 3.8e-08;  
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRXCXKXLCSPFXAXEYIFRNXXRTROFW 41  
DB 1 ANSFLEELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 41

## RESULT 7

US-09-978-917A-4  
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; Publication No. US20030027299A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Abs; Maxygen Holdings  
; TITLE OF INVENTION: Protein C or activated protein C-like molecules  
; FILE REFERENCE: 0219us310 - protein C  
; CURRENT APPLICATION NUMBER: US/09/978,917A  
; CURRENT FILING DATE: 2001-10-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 419  
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; ORGANISM: Homo sapiens  
US-09-978-917A-4

Query Match 48.4%; Score 92; DB 9; Length 419;  
Best Local Similarity 46.3%; Pred. No. 3.8e-08;  
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

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DB 1 ANSFLEELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 41

## RESULT 8

US-10-182-263-2  
; Sequence 2, Application US/10182263  
; Publication No. US20030022354A1  
; GENERAL INFORMATION:  
; APPLICANT: Getlitz, Bruce E  
; APPLICANT: Jones, Bryan E  
; APPLICANT: Grinnell, Brian W  
; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
; FILE REFERENCE: X-13611  
; CURRENT APPLICATION NUMBER: US/10/182,263  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: 60/181948  
; PRIOR FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: 60/189199  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-182-263-2

Query Match 48.4%; Score 92; DB 9; Length 461;  
Best Local Similarity 46.3%; Pred. No. 4.1e-08;  
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRXCXKXLCSPFXAXEYIFRNXXRTROFW 41  
DB 43 ANSFLEELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 83

## RESULT 9

US-09-978-917A-2  
; Sequence 2, Application US/09978917A  
; Publication No. US20030027299A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Abs; Maxygen Holdings  
; TITLE OF INVENTION: Protein C or activated protein C-like molecules  
; FILE REFERENCE: 0219us310 - protein C  
; CURRENT APPLICATION NUMBER: US/09/978,917A  
; CURRENT FILING DATE: 2001-10-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(42)  
; FEATURE:  
; NAME/KEY: CHAIN  
; LOCATION: (43)...(461)  
US-09-978-917A-2

Query Match 48.4%; Score 92; DB 9; Length 461;  
Best Local Similarity 46.3%; Pred. No. 4.1e-08;  
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRXCXKXLCSPFXAXEYIFRNXXRTROFW 41  
DB 43 ANSFLEELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 83

## RESULT 10

US-09-118-748-2  
; Sequence 2, Application US/09118748A  
; Patent No. US20020031799A1  
; GENERAL INFORMATION:  
; APPLICANT: Stafford, Darrel W.  
; APPLICANT: Chang, Jinli  
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 5470-183  
; CURRENT APPLICATION NUMBER: US/09/118,748A  
; CURRENT FILING DATE: 1998-07-17  
; EARLIER APPLICATION NUMBER: 60/053,571  
; EARLIER FILING DATE: 1997-07-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-118-748-2

Query Match 46.3%; Score 88; DB 10; Length 415;  
Best Local Similarity 39.5%; Pred. No. 1.8e-07;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXXLRDGSIXRXCXKXLCSPFXAXEYIFRNXXRTROFW 44  
DB 3 SGLBEFVQNLRECEMEKESFEAREVFENTERTEFWKQY 45

## RESULT 11

US-10-132-829-5  
; Sequence 5, Application US/10132829  
; Publication No. US20030044982A1  
; GENERAL INFORMATION:  
; APPLICANT: Chien, Kenneth R  
; APPLICANT: Hoshijima, Masahiko  
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII  
; FILE REFERENCE: 6627-PA1170

```

; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          46.3%; Score 88; DB 9; Length 461;
Best Local Similarity 39.5%; Pred. No. 2,1e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLRDGSIXRXCXXLCSEFXAEXIFRXXRRQFWVS 44
Db 49 SGLKEEFVQGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US2002076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1,1736
; CURRENT APPLICATION NUMBER: US/09/884,901
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-901-3

Query Match          46.3%; Score 88; DB 10; Length 461;
Best Local Similarity 39.5%; Pred. No. 2,1e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Oy 2 NGFLXXLRDGSIXRXCXXLCSEFXAEXIFRXXRRQFWVS 44
Db 49 SGLKEEFVQGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiret, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
```

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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          36.8%; Score 70; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 5,7e-05;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 11 GSLRXRCRXLCSEFXAEXIFRXXRRQFWVS 44
Db 46 GNLRECNELCNVEAREIFVDEDKITAFWOEY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiret, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/393,996  
 ; PRIOR FILING DATE: 1999-09-10  
 ; PRIOR APPLICATION NUMBER: US 09/602,871  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: US 09/420,707  
 ; PRIOR FILING DATE: 1999-10-19  
 ; NUMBER OF SEQ ID NOS: 460  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 312  
 ; LENGTH: 209  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-759-130B-312

Query Match 36.8%; Score 70; DB 9; Length 209;  
 Best Local Similarity 38.2%; Pred. No. 0.00013;  
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXCRXXLCSPFXAEXIFRNXXRTQFWVSY 44  
 DB 46 GNLERECNEBLCNFEARELIFVDEDKTIAFWQEX 79

RESULT 15

; US-09-759-130B-310  
 ; Sequence 310, Application US/09759130B  
 ; Publication No. US2003022279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: McCarthy, Sean A  
 ; APPLICANT: Fraser, Christopher C  
 ; APPLICANT: Sharp, John D  
 ; APPLICANT: Barnes, Thomas S  
 ; APPLICANT: Kirst, Susan J  
 ; APPLICANT: Mackay, Charles R  
 ; APPLICANT: Myers, Paul S  
 ; APPLICANT: Leiby, Kevin R  
 ; APPLICANT: Wrighton, Nicolas  
 ; APPLICANT: Goodearl, Andrew  
 ; APPLICANT: Holtzman, Douglas A  
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
 ; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
 ; TITLE OF INVENTION: USES.  
 ; FILE REFERENCE: MPI00-535OMNIM  
 ; CURRENT APPLICATION NUMBER: US/09/759,130B  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: US 09/479,249  
 ; PRIOR FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/559,497  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: US 09/578,063  
 ; PRIOR FILING DATE: 2000-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/333,159  
 ; PRIOR FILING DATE: 1999-06-14  
 ; PRIOR APPLICATION NUMBER: US 09/596,194  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 09/342,364  
 ; PRIOR FILING DATE: 1999-06-29  
 ; PRIOR APPLICATION NUMBER: US 09/608,452  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/393,996  
 ; PRIOR FILING DATE: 1999-09-10  
 ; PRIOR APPLICATION NUMBER: US 09/602,871  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: US 09/420,707  
 ; PRIOR FILING DATE: 1999-10-19  
 ; NUMBER OF SEQ ID NOS: 460  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 310  
 ; LENGTH: 226  
 ; TYPE: PRT

; ORGANISM: Homo sapiens  
 ; US-09-759-130B-310

Query Match 36.8%; Score 70; DB 9; Length 226;  
 Best Local Similarity 38.2%; Pred. No. 0.00014;  
 Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXCRXXLCSPFXAEXIFRNXXRTQFWVSY 44  
 DB 63 GNLERECNEBLCNFEARELIFVDEDKTIAFWQEX 96

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID      | Description         |
|------------|-------|-------------|--------|---------|---------------------|
| 1          | 155   | 81.2        | 44     | AA18306 | Bovine factor VII   |
| 2          | 155   | 81.2        | 44     | AA18306 | Bovine factor VII   |
| 3          | 129   | 67.5        | 44     | AA18312 | Modified GLA domain |
| 4          | 127   | 66.5        | 44     | AA18311 | Modified GLA domain |
| 5          | 123   | 64.4        | 44     | AA18310 | Modified GLA domain |
| 6          | 120   | 62.8        | 44     | AA18305 | Human factor VII G  |
| 7          | 120   | 62.8        | 44     | AA18305 | Human factor VII G  |
| 8          | 120   | 62.8        | 401    | AA18470 | Mutant blood coagu  |
| 9          | 120   | 62.8        | 401    | AA18471 | Mutant blood coagu  |
| 10         | 120   | 62.8        | 406    | AA18471 | Factor VII (VII).   |

|    |     |      |     |    |         |                    |
|----|-----|------|-----|----|---------|--------------------|
| 11 | 120 | 62.8 | 406 | 18 | AA14509 | Modified blood coa |
| 12 | 120 | 62.8 | 406 | 18 | AA14510 | Modified blood coa |
| 13 | 120 | 62.8 | 406 | 22 | AAU7745 | Human factor VIIa  |
| 14 | 120 | 62.8 | 406 | 22 | AA15217 | Human FVII SEQ ID  |
| 15 | 120 | 62.8 | 406 | 22 | AA15217 | Mammalian expresse |
| 16 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 17 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 18 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 19 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 20 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 21 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 22 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 23 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 24 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 25 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 26 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 27 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 28 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 29 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 30 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 31 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 32 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 33 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 34 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 35 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 36 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 37 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 38 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 39 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 40 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 41 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 42 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 43 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 44 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |
| 45 | 120 | 62.8 | 406 | 22 | AA15218 | Human FVII mutant  |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| AA18306  | AA18306 standard; peptide; 44 AA.                           |
| XX       |   |
| AC       | AA18306;  |
| XX       |   |
| DT       | 17-AUG-1999 (first entry)                                   |
| XX       |   |
| DE       | Bovine factor VII GLA domain.                               |
| XX       |   |
| KW       | GLA domain; vitamin K-dependent protein; clotting disorder; |
| KM       | therapy.  |
| XX       |   |
| OS       | Bos taurus.   |
| XX       |   |
| PH       | Key   |
| FT       | Misc-difference 1..44                                       |
| FT       | Location/Qualifiers   |
| FT       | /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"  |
| XX       |   |
| PD       | MO9920767-A1.   |
| XX       |   |
| PD       | 29-APR-1999.  |
| XX       |   |
| PP       | 20-OCT-1998; 98WO-US22152.                                  |
| XX       |   |
| PR       | 23-OCT-1997; 97US-0955636.                                  |
| XX       |   |
| PA       | (MINU) UNIV MINNESOTA.                                      |
| XX       |   |
| PI       | Neisestuen GL;  |
| XX       |   |
| DR       | WPI, 1999-288309/24.  |

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 15; 86pp; English.  
XX  
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 81.2%; Score 155; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2,2e-18;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1 ANGFLXXLRDGLRXCRXXLCSPXXAFXIFRNXXRTQPFWSY 44  
1 ANGFLXXLRPGLRXCRXXLCSPXXAHXIFRNXXRTQPFWSY 44  
DB  
XX  
RESULT 2  
AAB36396  
ID AAB36396 standard; peptide; 44 AA.  
XX  
XX AAB36396;  
XX  
DT 27-FEB-2001 (first entry)  
XX  
XX Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.  
DE  
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;  
KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;  
KM factor X; prothrombin; enhanced membrane binding affinity;  
KM clot formation; thrombolytic; haemostatic; bleeding disorder;  
KM thrombosis; clotting disorder; haemophilia A; haemophilia B;  
KM liver disease.  
XX  
XX Bos taurus.  
OS  
XX WO200066753-A2.  
PN  
XX 09-NOV-2000.  
PD  
XX 28-APR-2000; 2000WO-US11416.  
PF  
XX 29-APR-1999; 99US-0302239.  
PR  
XX (MINU ) UNIV MINNESOTA.  
PA  
XX Nelsestuen GL;  
PI  
XX Nelsestuen GL;  
PS  
XX WPI; 2001-007226/01.  
DR  
XX  
XX Novel vitamin K-dependent polypeptide useful for treating clotting  
PT disorders such as thrombosis and hemophilia, comprises modified  
PT gamma-carboxy glutamic acid domain that enhances membrane binding  
PT affinity -  
XX  
XX Disclosure; Page 12; 81pp; English.  
PS  
XX The present invention describes a vitamin K-dependent polypeptide (I)  
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having  
CC at least one amino acid substitution, that enhances membrane binding  
CC affinity and the activity of the polypeptide relative to a corresponding  
CC native vitamin K-dependent polypeptide and inhibits clot formation.  
CC (I) can have thrombolytic and haemostatic activities, and can be used  
CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified  
CC GLA domain is useful for increasing clot formation and for treating a  
CC bleeding disorder, including thrombosis and clotting disorders such as  
CC haemophilia A, haemophilia B and liver disease. The present sequence  
CC represents a wild type bovine factor VII GLA domain sequence, given in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 81.2%; Score 155; DB 22; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2,2e-18;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1 ANGFLXXLRDGLRXCRXXLCSPXXAFXIFRNXXRTQPFWSY 44  
1 ANGFLXXLRPGLRXCRXXLCSPXXAHXIFRNXXRTQPFWSY 44  
DB  
XX  
RESULT 3  
AA18312  
ID AA18312 standard; peptide; 44 AA.  
XX  
XX AA18312;  
AC  
XX  
DT 17-AUG-1999 (first entry)  
XX  
XX Modified GLA domain of vitamin K-dependent protein.  
DE  
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KM therapy.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 1..44  
FT acid" "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT  
XX WO9920767-A1.  
PN  
XX 29-APR-1999.  
PD  
XX 20-OCT-1998; 98WO-US22152.  
PF  
XX 23-OCT-1997; 97US-0955636.  
PR  
XX (MINU ) UNIV MINNESOTA.  
PA  
XX Nelsestuen GL;  
PI  
XX Nelsestuen GL;  
PS  
XX WPI; 1999-288309/24.  
DR  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
PT  
XX  
XX Disclosure; Page 80; 86pp; English.  
PS  
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 67.5%; Score 129; DB 20; Length 44;  
Best Local Similarity 77.3%; Pred. No. 4.6e-14;  
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;





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XX 29-APR-1999.
PD gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity -
XX
XX 20-OCT-1996; 98WO-US22152.
PF Disclosure; Page 12; 81pp; English.
XX
XX 23-OCT-1997; 97US-0955636.
PR The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX CC affinity and the activity of the polypeptide relative to a corresponding
XX CC native vitamin K-dependent polypeptide and inhibits clot formation.
XX CC (I) can have thrombolytic and haemostatic activities, and can be used
XX CC as an inhibitor of clot formation. (I) is useful for decreasing clot
XX CC formation in a mammal, a factor VII or factor IX containing a modified
XX CC GLA domain is useful for increasing clot formation and for treating a
XX CC bleeding disorder, including thrombosis and clotting disorders such as
XX CC haemophilia A, haemophilia B and liver disease. The present sequence
XX CC represents a wild type human factor VII GLA domain sequence, given in
XX CC the exemplification of the present invention.
PS Sequence 44 AA;
SQ

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```

Query Match 62.8%; Score 120; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLXXLRDGSIXRXCXXLCSPFXAAXIFRNXXRTQFWVS 44
1 ANAFXXLRPGSLXRXCKXXQCSFXAXRXIFDXAXRTKLFWISY 44
DB

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```

RESULT 7
AAB36395
AAB36395 standard; peptide; 44 AA.

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```

AC AAB36395;
DT 27-FEB-2001 (first entry)
XX

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```

DE Human factor VII gamma-carboxylutamic acid domain SEQ ID NO:3.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxylutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX

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OS Homo sapiens.
XX
XX WO200066753-A2.
XX

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XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.
XX

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XX (MINU ) UNIV MINNESOTA.
XX

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XX Nelsestuen GL;
XX

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XX WPI; 2001-007226/01.
XX

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XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
PT

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PT gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity -
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX CC affinity and the activity of the polypeptide relative to a corresponding
XX CC native vitamin K-dependent polypeptide and inhibits clot formation.
XX CC (I) can have thrombolytic and haemostatic activities, and can be used
XX CC as an inhibitor of clot formation. (I) is useful for decreasing clot
XX CC formation in a mammal, a factor VII or factor IX containing a modified
XX CC GLA domain is useful for increasing clot formation and for treating a
XX CC bleeding disorder, including thrombosis and clotting disorders such as
XX CC haemophilia A, haemophilia B and liver disease. The present sequence
XX CC represents a wild type human factor VII GLA domain sequence, given in
XX CC the exemplification of the present invention.
XX

```

```

Query Match 62.8%; Score 120; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ANGFLXXLRDGSIXRXCXXLCSPFXAAXIFRNXXRTQFWVS 44
1 ANAFXXLRPGSLXRXCKXXQCSFXAXRXIFDXAXRTKLFWISY 44
DB

```

```

RESULT 8
AAB84870
AAB84870 standard; Protein; 401 AA.

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XX AAB84870;
XX

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```

DT 31-JUL-2001 (first entry)
XX

```

```

DE Mutant blood coagulant factor VII (FVII-31).
XX

```

```

XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX

```

```

XX Homo sapiens.
XX
XX Synthetic.
XX

```

```

XX Key Location/Qualifiers
XX

```

```

XX Misc-difference 311..317
XX /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX

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XX JP2001061479-A.
XX

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XX 13-MAR-2001.
XX

```

```

XX 24-AUG-1999; 99JP-0237610.
XX

```

```

XX 24-AUG-1999; 99JP-0237610.
XX

```

```

XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX

```

```

XX WPI; 2001-310677/33.
XX

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XX N-PSDB; AAH19463.
XX

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```

XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX

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XX Claim 14; Page 20-21; 29pp; Japanese.
XX

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```

XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX

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```
XX Sequence 401 AA;
SQ Query Match 62.8%; Score 120; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.3e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRLDGLXRXCRXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 1 ANAFLEELRPGSLERCKECCSFEEAREIFDARTKLFWISY 44

RESULT 9
AAB84871
ID AAB84871 standard; Protein; 401 AA.
XX
AC AAB84871;
XX
AC 31-JUL-2001 (first entry)
XX
DE Mutant blood coagulant factor VII (FVII-39).
XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutain.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Misc-difference 235..239
FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
FT Asp-Arg-Lys-Thr-Leu"
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT Misc-difference 311..317
FT /note= "Wild-type substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ Query Match 62.8%; Score 120; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 1.3e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRLDGLXRXCRXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 1 ANAFLEELRPGSLERCKECCSFEEAREIFDARTKLFWISY 44

RESULT 10
AAR35764
ID AAR35764 standard; protein; 406 AA.
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XX AAR35764;
AC 24-SEP-1993 (first entry)
XX
DT Factor VII (VII).
XX
DE PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
KW exosite; catalytic activity.
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FH Region 1..152
FT /note= "Factor VII light chain"
FT /note= "Factor VII heavy chain"
FT Region 153..406
FT /note= "Factor VII heavy chain"
FT Peptide 374..388
FT /note= "exosite 1"
FT Peptide 290..310
FT /note= "exosite 2"
FT Peptide 290..310
FT /note= "pref. PC polypeptide; claim 2, page 136"
FT Peptide 374..388
FT /note= "pref. PC polypeptide; claim 2, page 136"
FT Peptide 289..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 290..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 245..266
FT /note= "claim 9, page 138-139 describes an antibody
FT that reacts with Factor VII; fragments
FT 289-304, 290-304, 290-310, 374-388 and
FT 400-414 but not with fragment 245-266"
XX
XX MO309804-A.
XX
XX 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US10242.
XX
XX 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Griffin JH, Westers RM;
XX
XX WPI; 1993-182244/22.
XX
XX Serine protease derived-polypeptide(s) and anti-peptide
XX antibodies - for inhibiting coagulation and assaying for the
XX presence of serine protease in fluid samples
XX
XX Disclosure; Page 133-135; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit
XX coagulation (they prevent binding of serine protease to natural
XX substrates), esp. when admin. to give an intravascular blood
XX concn. of 0.1-100 (pref. 0.5-10) microm.
XX
XX NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
XX in the specification but have not yet been added to the SEQUENCE
XX LISTING.
XX
XX Sequence 406 AA;
SQ Query Match 62.8%; Score 120; DB 14; Length 406;
Best Local Similarity 52.3%; Pred. No. 1.3e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANGFLXLRLDGLXRXCRXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 1 ANAFLEELRPGSLERCKECCSFEEAREIFDARTKLFWISY 44
```

|           |   |
|-----------|---|
| RESULT 11 |   |
| AAW14509  |   |
| ID        | AAW14509 standard; protein; 406 AA.                           |
| XX        |   |
| AC        | AAW14509;   |
| XX        |   |
| DT        | 14-MAY-1997 (first entry)                                     |
| XX        |   |
| DE        | Modified blood coagulation Factor VII (R290S).                |
| XX        |   |
| KW        | Blood coagulation; factor 7; muteln; mutation; modification;  |
| KM        | thrombocytopenia; von Willebrand's disease; plasma substitute |
| XX        |   |
| OS        | Homo sapiens.   |
| OS        | Synthetic.  |
| XX        |   |
| FH        | Key   |
| FT        | Modified-site   |
| FT        | 6   |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 7   |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 14  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 16  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 19  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 20  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 17..22  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 25  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 26  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 29  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 33..33  |
| FT        | /note= "proteolytic site"                                     |
| FT        | 35  |
| FT        | /label= OTHER   |
| FT        | /note= "gamma-carboxyglutamic acid"                           |
| FT        | 38..39  |
| FT        | /note= "proteolytic site"                                     |
| FT        | 42..43  |
| FT        | /note= "proteolytic site"                                     |
| FT        | 44..45  |
| FT        | /note= "proteolytic site"                                     |
| FT        | 50..61  |
| FT        | 55..70  |
| FT        | 63  |
| FT        | /label= OTHER   |
| FT        | /note= "beta-hydroxy-aspartic acid"                           |
| FT        | 72..81  |
| FT        | 91..102   |
| FT        | 98..112   |
| FT        | 114..127  |
| FT        | 135..162  |
| FT        | 143..144  |
| FT        | /note= "proteolytic site"                                     |
| FT        | 145   |
| FT        | /note= "glycosylation site"                                   |
| FT        | 159..164  |
| FT        | Disulfide-bond  |

```

FT FT Disulfide-bond 178..194
FT FT Active-site 193
FT FT Active-site 242
FT FT Active-site 344
FT FT Cleavage-site 290..291
FT FT Misc-difference /note= "proteolytic site in unmodified factor VII"
FT FT bond"/
FT FT Disulfide-bond 310..329
FT FT Cleavage-site /note= "proteolytic site"
FT FT Modified-site /note= "glycosylation site"
FT FT Disulfide-bond 340..368
FT FT Cleavage-site /note= "proteolytic site"
FT FT Cleavage-site /note= "proteolytic site"
FT FT Cleavage-site /note= "proteolytic site"
FT FT Cleavage-site /note= "proteolytic site"
FT FT Cleavage-site /note= "proteolytic site"
FT FT Cleavage-site /note= "proteolytic site"
XX XX US5580560.A.
XX XX PD 03-DEC-1996.
XX PE 13-NOV-1989; 89US-0434149.
XX PR 09-AUG-1993; 93US-0104509.
XX PR 13-NOV-1989; 89US-0434149.
XX PR 12-JUN-1992; 92US-0898248.
XX PR 22-AUG-1994; 94US-0293778.
PA (NOVO ) NOVO-NORDISK AS.
XX BIjorn SE, Nicolajsen EM, Wiberg FC, Woodbury R;
XX WPI; 1997-033523/03.
DR PT Mutated human factor VII or VIIA proteins - with amino acid
PT substitutions to improve proteolytic stability
PS Example 3; Page -: 28pp; English.
CC Modified human factor VII or VIIA proteins are stabilised against
CC proteolytic cleavage by substitution of one of the residues Lys32,
CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
CC Lys341 by an amino acid that provides a proteolytically more stable
CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC bleeding disorders such as thrombocytopenia and von Willebrand's
CC disease. They are also suitable for addition to plasma substitutes.
CC The present sequence is a specific example of a modified factor VII
CC protein.
SQ Sequence 406 AA;
Query Match 62.8%; Score 120; DB 18; Length 406;
Beat Local Similarity 52.3%; Pred.No. 1,3e-11;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
OY 1 ANGFLXALPDGSLKRCRXXLCSPFXAXIRNNXXRTQFWMSY 44
DB 1 ANAFLEELRPGSLERECKEEOCSFEAREIFXDARITLFWISY 44
RESULT 12
ID AAW14510 standard; protein; 406 AA.
XX
```

AC AAW14510;  
 XX 14-MAY-1997 (first entry)  
 XX Modified blood coagulation Factor VII (R315S).  
 DE Blood coagulation; factor 7; mutein; mutation; modification;  
 KW thrombocytopenia; von Willebrand's disease; plasma substitute.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 FH Key  
 FT Modified-site  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 7  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 14  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 16  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 19  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 20  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 17..22  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 26  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 29  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 32..33  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 35  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 38..39  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 42..43  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 44..45  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 50..61  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 55..70  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 63  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 72..81  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 91..102  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 98..112  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 114..127  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 135..162  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 143..144  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 145  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 159..164  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 178..194  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 193  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 242  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 344  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT 290..291  
 FT /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"

FT Disulfide-bond 310..329  
 FT Cleavage-site 315..316  
 FT /note= "proteolytic site in unmodified factor VII"  
 FT Misc-difference 315  
 FT /note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"  
 FT Modified-site 322  
 FT /note= "glycosylation site"  
 FT Disulfide-bond 340..368  
 FT Cleavage-site 341..342  
 FT /note= "proteolytic site"  
 FT Cleavage-site 392..393  
 FT /note= "proteolytic site"  
 FT Cleavage-site 396..397  
 FT /note= "proteolytic site"  
 FT Cleavage-site 402..403  
 FT /note= "proteolytic site"  
 FT US5580560-A.  
 FT 03-DEC-1996.  
 FT 13-NOV-1989;  
 FT 09-AUG-1993;  
 FT 13-NOV-1989;  
 FT 12-JUN-1992;  
 FT 22-AUG-1994;  
 FT (NOVO ) NOVO-NORDISK AS.  
 FT Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;  
 FT WPI; 1997-033523/03.  
 FT Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability  
 FT Example 4; Page -; 28pp; English.  
 FT Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes.  
 FT The present sequence is a specific example of a modified factor VII protein.  
 FT Sequence 406 AA;  
 SQ  
 Query Match 62.8%; Score 120; DB 18; Length 406;  
 Best Local Similarity 52.3%; Pred. No. 1.3e-11;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRDGSIXRXCXFXLCSFYXAFIFRNXXRTQFWVS 44  
 DB 1 ANAFLELRPGSLERCKEKCSPFEAREIFPDARTKLFWSY 44  
 RESULT 13  
 AAU77745  
 ID AAU77745 standard; protein; 406 AA.  
 AC AAU77745;  
 XX 05-JUN-2002 (first entry)  
 DT Human factor VIIa active site mutant.  
 XX

|    |   |  |
|----|---|--|
| KM |   | Factor VIIa; human; shock heat treatment; protein stability; |
| XX |   | protein manufacture; protein conformation; mutant; muten.    |
| XX |   | Homo sapiens.  |
| OS |   | Synthetic.   |
| XX |   |  |
| FH | Key   | Location/Qualifiers  |
| FT | Active-site   | 193  |
| FT | /note= "Member of the factor VIIa catalytic triad"                        |  |
| FT | Active-site   | 242  |
| FT | /note= "Member of the factor VIIa catalytic triad"                        |  |
| FT | Active-site   | 344  |
| FT | /note= "Member of the factor VIIa catalytic triad"                        |  |
| FT | Misc-difference   | 344  |
| FT | /label= Gly, Met, Thr   |  |
| FT | /note= "Preferably Ala. Wild type Ser"                                    |  |
| PN | MO200177141-AI.   |  |
| XX |   |  |
| PD | 18-OCT-2001.  |  |
| XX |   |  |
| PF | 06-APR-2001; 2001WO-DK00234.  |  |
| XX |   |  |
| PR | 06-APR-2000; 2000DK-0000573.  |  |
| PR | 17-APR-2000; 2000US-197650P.  |  |
| XX | (NOVO ) NOVO NORDISK AS.  |  |
| PA |   |  |
| XX |   |  |
| PI | Matthesen F;  |  |
| XX |   |  |
| DR | WPI; 2001-657162/75.  |  |
| XX |   |  |
| PT | Stabilisation of a polypeptide e.g. in a pharmaceutical composition       |  |
| PS | Involves a shock heat treatment -   |  |
| XX |   |  |
| PS | Disclosure; Page -: 22pp; English.  |  |
| CC | The invention describes a method of stabilising a polypeptide involving   |  |
| CC | shock heat treatment of the polypeptide. The method is useful in a        |  |
| CC | pharmaceutical composition, in the industrial or large scale method of    |  |
| CC | manufacturing a polypeptide, also as a unit operation during preparation, |  |
| CC | purification, recovery and/or formulation of polypeptides. The shock heat |  |
| CC | treatment improves the protein stability without substantial loss of      |  |
| CC | biological activity. The method can be applied to change polypeptide      |  |
| CC | conformation in a very fast and non-invasive manner. The polypeptide      |  |
| CC | formed is stable. The method is also useful for decreasing the            |  |
| CC | association of the polypeptide. This sequence represents a modified       |  |
| CC | human factor VIIa protein, mutated at the catalytic site, described       |  |
| CC | in the invention.   |  |
| CC | Note: This sequence does not appear in the specification but has          |  |
| CC | been obtained using information given in the invention.                   |  |
| CC |   |  |
| XX |   |  |
| SQ | Sequence 406 AA:  |  |
|    |   |  |
|    | Query Match 62.8%; Score 120; DB 22; Length 406;                          |  |
|    | Best Local Similarity 52.3%; Pred. No. 1,3e-11;                           |  |
|    | Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0,              |  |
| OY | 1 ANGFLXLLDGLSLRXRCRXLLCSFFXAFAIFRNXXXTROFWISY 44                         |  |
|    | :           :   |  |
| Dd | 1 ANAFLELRPGSLPERCKEEOCSFEAREIRFKDAERTKLFWISY 44                          |  |
|    | :           :   |  |
|    |   |  |
|    | RESULT 14   |  |
| ID | AAMS2171  |  |
| AC | AAMS2171 standard; Protein; 406 AA.                                       |  |
| XX |   |  |
| XX | AAMS2171;   |  |
| DT | 07-FEB-2002 (first entry)   |  |
| XX |   |  |
| DE | Human FVII SEQ ID NO 1.   |  |
| XX |   |  |

|    |   |
|----|---|
| KW | Factor VII; FVII; Factor VIIa; FVIIa; hemostatic; thrombolytic;   |
| KM | cardiac; hepatocentric; cerebroprotective; haemophilia; liver disease;  |
| KW | myocardial infarction; thrombotic stroke; deep-vein thrombosis.   |
| XX |   |
| OS | Homo sapiens.   |
| XX |   |
| XX | Key   |
| FT | Misc-difference 6   |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 7   |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 14  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 16  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 19  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 20  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 25  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 26  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 29  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 35  |
| FT | /label= Glu, OTHER  |
| FT | /note= "OTHER = gamma carboxyglutamic acid"   |
| FT | Misc-difference 52  |
| FT | /label= "O-glycosylated"  |
| FT | /note= "O-glycosylated"   |
| FT | Misc-difference 60  |
| FT | /label= "O-glycosylated"  |
| FT | /note= "O-glycosylated"   |
| FT | Misc-difference 145   |
| FT | /label= "N-glycosylated"  |
| FT | /note= "N-glycosylated"   |
| FT | Misc-difference 152..153  |
| FT | /label= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"  |
| FT | Misc-difference 322   |
| FT | /label= "N-glycosylated"  |
| XX |   |
| PN | WO200158935-A2.   |
| XX |   |
| PN | 16-AUG-2001.  |
| XX |   |
| XX | 12-FEB-2001; 2001WO-DK00094.  |
| XX |   |
| XX | 11-FEB-2000; 2000DK-0000218.  |
| XX | 18-OCT-2000; 2000DK-0001558.  |
| XX |   |
| XX | (MAXY-) MAXYGEN APS.  |
| XX |   |
| XX | Andersen KV, Pedersen AH, Bornaaes C;   |
| XX |   |
| XX | WPI; 2001-581807/65.  |
| XX |   |
| XX | N-PSDB; AA199982.   |
| XX |   |
| XX | New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis; comprises non-polypeptide group covalently attached to polypeptide group - |
| XX |   |
| XX | Claim 1; Page 81-83; 89pp; English.   |
| XX |   |

CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.

XX  
SQ Sequence 406 AA;

Query Match 62.8%; Score 120; DB 22; Length 406;  
Best Local Similarity 75.0%; Pred. No. 1.3e-11;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGPLXLRDGLXRXCRXXLCSPFXAXFIFRNXXRTQFWVS 44  
Db 1 ANAPFLXLRPGSLRXCRXXQCSPFXARXIFXDAXRTKLFWIS 44

RESULT 15  
AAM52172  
ID AAM52172 standard; Protein; 406 AA.  
XX  
AC AAM52172;  
XX  
DT 07-FEB-2002 (first entry)  
XX  
DE Mammalian expressed human FVII SEQ ID NO 3.  
XX  
KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;  
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 52  
FT /note= "O-glycosylated"  
FT Modified-site 60  
FT /note= "O-glycosylated"  
FT Modified-site 145  
FT /note= "N-glycosylated"  
FT Cleavage-site 152..153  
FT /note= "proteolytic cleavage site converting FVII zymogen  
FT to an activated form, comprising two chains  
FT linked by a single disulphide bridge"  
FT Modified-site 322  
FT /note= "N-glycosylated"  
XX  
WO200158935-A2.  
XX  
PN 16-AUG-2001.  
XX  
PD 12-FEB-2001; 2001WO-DK00094.  
XX  
PE 11-FEB-2000; 2000DK-0000218.  
PR 18-OCT-2000; 2000DK-0001558.  
XX  
PA (MAXY-) MAXYGEN APS.  
XX  
PI Andersen KV, Pedersen AH, Bornaes C;  
XX  
XX WPI; 2001-581807/65.  
XX  
XX N-PSDB; AAI99983.

PT New conjugate, useful for treating Factor VIIa related diseases or  
PT disorders such as haemophilia, liver disease, myocardial infarction and  
PT deep-vein thrombosis, comprises non-polypeptide group covalently  
PT attached to polypeptide group -  
XX  
PS Disclosure; Page 85-86; 89pp; English.  
XX  
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.

XX  
SQ Sequence 406 AA;

Query Match 62.8%; Score 120; DB 22; Length 406;  
Best Local Similarity 52.3%; Pred. No. 1.3e-11;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGPLXLRDGLXRXCRXXLCSPFXAXFIFRNXXRTQFWVS 44  
Db 1 ANAPFLXLRPGSLRXCRXXQCSPFXARXIFXDAXRTKLFWIS 44

Search completed: March 19, 2003, 14:51:16  
Job time : 32.4375 secs

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GenCore version 5.1.4.P5.4578  
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# OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10ASP28PHE\_4  
Perfect score: 191  
Sequence: 1 ANGFLXXLRDGSIXRCRX.....XXAFXIPRXRXRTQFMVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: PIR 73:.\*  
2: pir1:.\*  
3: pir2:.\*  
4: pir3:.\*  
5: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 148   | 77.5        | 407    | 1 KRB07  | coagulation factor |
| 2          | 128   | 67.0        | 443    | 2 I46932 | coagulation factor |
| 3          | 120   | 62.8        | 466    | 1 KPHU7  | coagulation factor |
| 4          | 104   | 54.5        | 461    | 1 JX0210 | protein C (activat |
| 5          | 102   | 53.4        | 461    | 1 S18994 | protein C (activat |
| 6          | 94    | 49.2        | 456    | 1 KXBO   | protein C (activat |
| 7          | 91    | 47.6        | 482    | 1 EXRT   | coagulation factor |
| 8          | 91    | 47.6        | 488    | 1 EXHU   | coagulation factor |
| 9          | 88    | 46.1        | 461    | 1 KXBO   | protein C (activat |
| 10         | 87    | 45.5        | 492    | 1 KPHU   | coagulation factor |
| 11         | 85    | 44.5        | 461    | 1 KPHU   | coagulation factor |
| 12         | 85    | 44.5        | 622    | 1 TBHU   | thrombin (EC 3.4.2 |
| 13         | 83    | 43.5        | 416    | 1 KRB0   | coagulation factor |
| 14         | 82    | 42.9        | 617    | 2 S10511 | thrombin (EC 3.4.2 |
| 15         | 82    | 42.9        | 618    | 2 A35827 | thrombin (EC 3.4.2 |
| 16         | 79    | 41.4        | 475    | 1 EXCH   | coagulation factor |
| 17         | 78    | 40.8        | 452    | 1 A30351 | coagulation factor |
| 18         | 78    | 40.8        | 459    | 2 J00419 | coagulation factor |
| 19         | 76    | 39.8        | 625    | 1 TBBO   | thrombin (EC 3.4.2 |
| 20         | 72    | 37.7        | 642    | 2 S53433 | plasma protein S p |
| 21         | 67    | 35.1        | 642    | 1 S53434 | plasma protein S p |
| 22         | 67    | 35.1        | 675    | 1 KXBOS  | plasma protein S p |
| 23         | 67    | 35.1        | 676    | 1 KXHU   | plasma protein S p |
| 24         | 66    | 34.6        | 422    | 1 KXHU   | plasma protein S p |
| 25         | 66    | 34.6        | 646    | 2 S38819 | plasma protein S - |
| 26         | 64    | 33.5        | 675    | 1 KXRTS  | plasma protein S - |
| 27         | 62    | 32.5        | 396    | 1 KXBOZ  | plasma protein S p |
| 28         | 57    | 29.8        | 675    | 1 KXMS   | growth arrest-spec |
| 29         | 56    | 29.3        | 678    | 2 B48089 |                    |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 55   | 28.8 | 673  | 2 A48089 | growth arrest-spec  |
| 31 | 53   | 27.7 | 674  | 2 I55476 | growth potentialin  |
| 32 | 52   | 27.2 | 605  | 1 W1MLEB | E1 protein - bovin  |
| 33 | 52   | 27.2 | 620  | 1 W1MLB2 | E1 protein - bovin  |
| 34 | 48   | 25.1 | 413  | 1 VHAVNH | nucleoprotein - in  |
| 35 | 46.5 | 24.3 | 594  | 2 D84859 | probable MAP kinase |
| 36 | 46.5 | 24.3 | 603  | 2 C96575 | probable MAP kinase |
| 37 | 46   | 24.1 | 204  | 2 E84173 | hypothetical prote  |
| 38 | 45.5 | 23.8 | 576  | 2 G96763 | probable MAP kinase |
| 39 | 45.5 | 23.8 | 2133 | 2 T42763 | coagulation factor  |
| 40 | 45   | 23.6 | 448  | 2 T18710 | hypothetical prote  |
| 41 | 45   | 23.6 | 687  | 2 T08528 | probable DNA topoi  |
| 42 | 44   | 23.0 | 1217 | 2 T21403 | hypothetical prote  |
| 43 | 43.5 | 22.8 | 304  | 2 AF2942 | 5-dehydro-4-deoxyg  |
| 44 | 43.5 | 22.8 | 304  | 2 D98340 | 5-dehydro-4-deoxyg  |
| 45 | 43   | 22.5 | 536  | 2 E70066 | hypothetical prote  |

## ALIGNMENTS

### RESULT 1

KRB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C/Accession: A31979; C20274

R/Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

U. Biol. Chem. 263, 14868-14877, 1988

A>Title: Bovine factor VII. Its purification and complete amino acid sequence.

A/Reference number: A31979; MUID:89008362; PMID:3049594

A/Accession: A31979

A/Molecule type: protein

A/Residues: 1-407 <TRX>

R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A/Reference number: A20274; MUID:83308813; PMID:6688526

A/Accession: C20274

A/Molecule type: protein

A/Residues: 58-62, 'X', 64-68 <MCM>

A/Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R/Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A>Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A/Reference number: A44556; MUID:89213959; PMID:3149637

A/Contents: annotation

A/Note: structure and location of covalently bound carbohydrate

C/Function: A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

gulation factor IX in the presence of calcium and tissue factor

A/Pathway: blood coagulation extrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylutam

F.1-152/Product: coagulation factor VIIa light chain #status experimental <MA>

F.1-44/Domain: Gla domain homology (fragment) <GLA>

F.50-81/Domain: EGF homology <EGL>

F.91-127/Domain: EGF homology <EG1>

F.153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F.153-387/Domain: trypsin homology <TRY>

F.67.14.16.19.20.25.26.29.34.35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F.17.22.50.61.55-70.72-81.91-102.98-112.114-127.135-262.159-164.178-194.310-329.340-368/

F.152/Binding site: carbohydrate (Ser) (covalent) #status experimental

F.163/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment

F.145-153/Binding site: carbohydrate (Asn) (covalent) #status experimental

F.152-153/Cleavage site: Arg-Ile (coagulation factor XIa) #status experimental

F.193.242.344/Active site: His, Asp, Ser #status predicted

F.290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 77.5% ; Score 148 ; DB 1 ; Length 407 ;  
Best Local Similarity 68.2% ; Pred. No. 2.8e-18 ;  
Matches 30 ; Conservative 0 ; Mismatches 14 ; Indels 0 ; Gaps 0 ;

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Qy 1 ANGFLXXLRDGLRXCRXXLCSFXXAFXIFRNXXTRQFWVS 44
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANGFLEELRPGSLERCKEELCSFEERAEVQSTERTKQFWISY 44

RESULT 2
146932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #ext_change 12-Feb-1999
C:Accession: I46932
R:Brothers, A.B.; Clarke, B.U.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: I46932; PMID:93190306; PMID:8383365
A:Accession: I46932
A:Status: preliminary; translated from GB/EMBL/DDJJ
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:I56300; NID:g266294; PID:g266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <GLA>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match 67.0%; Score 128; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 1,1e-14;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCRXXLCSFXXAFXIFRNXXTRQFWVS 44
    ||||| ||||| ||||| ||||| ||||| |||||
Db 40 ANGFLEELRPGSLERCKEELCSFEERAEVQSTERTKQFWISY 83

RESULT 3
KHHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1994 #ext_change 08-Dec-2000
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.U.; Haldeman, B.A.; Gray, C.L.; Imley, M.Y.; Hagen, F.S.; Murt
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; PMID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OHA>
A:Cross-references: GB:J02933; NID:g180333; PIDN:AAAS1983.1; PID:g180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.U.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; PMID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M13232; NID:g182799; PIDN:AA88040.1; PID:g182801
R:Thim, L.; Björn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a
A:Reference number: A90539; PMID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THR>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TR2>
R:Björn, S.; Foster, D.C.; Thim, L.; Wibeberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations
A:Reference number: A40529; PMID:91250411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Pedersen, E.; Petersen, L.C.

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Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A:Reference number: S63524; PMID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PBR>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:65-104/Domain: Gla domain homology <GLA>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA>
F:151-187/Domain: EGF homology <EG1>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66-67;74;76;79;80;85;86;89;95/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:77-82;110-121;115-130;132-141;151-162;158-172;174-187;195-322;219-224;238-254;370-389,
F:112/Binding site: carboxylate (Ser) (covalent) #status experimental
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205;382/Binding site: carboxylate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-Ile (coagulation factor XIIIa) #status experimental
F:253;302;404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor XIa) #status predicted

Query Match 62.8%; Score 120; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 3e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGLRXCRXXLCSFXXAFXIFRNXXTRQFWVS 44
    ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ANGFLEELRPGSLERCKEELCSFEERAEVQSTERTKQFWISY 104

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 16-Jun-2000
C:Accession: JX0210
R:Pada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; PMID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:g220385; PIDN:BA01225.1; PID:g220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
8.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <GLA>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196;199-461/Product: protein C #status predicted <PRC>
F:91-130/Domain: light chain #status predicted <PCL>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

```



C>Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #text\_change 08-Dec-2000  
 C/Accession: S49075; J04670; P50191; P50190; I62745  
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 C/Title: Evidence for competition between vitamin K-dependent clotting factors for intra-  
 Thromb. Res. 80, 63-73, 1995  
 A/Reference number: A58498; MUID:96093366; PMID:8578539  
 A/Accession: S49075  
 A/Molecule type: mRNA  
 A/Residues: 1-482 <STAI>  
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601  
 A/Note: submitted to the EMBL Data Library, June 1994  
 A/Note: neither the complete nucleic acid sequence nor the complete translation are shown  
 R/Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
 Gene 169, 269-273, 1996  
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
 A/Reference number: J04670; MUID:96194815; PMID:8647460  
 A/Accession: J04670  
 A/Molecule type: mRNA  
 A/Residues: 1-482 <STAI>  
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601  
 A/Experimental source: Cos-1 cell  
 R/Enlyoji, K.; Miyazaki, K.; Kato, H.  
 J. Biochem. 109, 890-898, 1991  
 A/Title: Characterization of rat factors X and XI: demonstration of factor Xa in rat platelets  
 A/Reference number: P50190; MUID:92041742; PMID:1718949  
 A/Accession: P50191  
 A/Molecule type: protein  
 A/Residues: 41-58, 'X', 60-65 <ENJI>  
 A/Accession: P50190  
 A/Molecule type: protein  
 A/Residues: 183-186, 'X', 188-207 <ENJ2>  
 R/Mutakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
 A/Reference number: I62745; MUID:94222160; PMID:8168596  
 A/Accession: I62745  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 295-383, 'G', 385-455 <MUR>  
 A/Cross-references: GB:D12125; NID:9415309; PIDN:BAA04756.1; PID:9455396  
 C/Function:  
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor Xa  
 A/Pathway: blood coagulation  
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
 F.1-23/Domain: signal sequence #status predicted <SIG>  
 F.24-40/Domain: signal sequence #status predicted <PRO>  
 F.25-84/Domain: Gla domain homology <GLA>  
 F.41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F.129-164/Domain: EGF homology <EG1>  
 F.183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F.183-231/Domain: activation peptide #status predicted <APR>  
 F.232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F.232-460/Domain: trypsin homology <TRY>  
 F.46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted  
 F.57-62, 90-101, 95-110, 112-121, 123-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 411  
 F.103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F.1208/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F.208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F.218/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F.231-232/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #status predicted  
 F.274, 320, 417/Active site: His, Asp, Ser #status predicted

Query Match 47.6%; Score 91; DB 1; Length 482;  
 Best Local Similarity 36.4%; Pred. No. 4, 4e-08;  
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

1 ANGFLLXRLDGSILRXKCRXXLXSPXAFIFRNXXRTROFWASY 44  
 DB 41 ANSFEEIKGNLRECEVERICSEFEAREVFNEDNEKTTETWNTK 84

RESULT 8  
 EXHU  
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human  
 N/Alternate names: Stuart factor  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
 C/Accession: A24478; J00917; A24485; A25853; A22208; A21284; A20362; S39415; I54051; A00  
 R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
 Biochemistry 25, 5098-5102, 1986  
 A/Title: Gene for human Factor X: a blood coagulation factor whose gene organization is  
 A/Reference number: A24478; MUID:87026600; PMID:3768336  
 A/Accession: A24478  
 A/Molecule type: DNA  
 A/Residues: 1-488 <LEV>  
 A/Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:g182831  
 R/Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.  
 Gene 99, 291-294, 1991  
 A/Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X  
 A/Reference number: J00917; MUID:91216473; PMID:1902434  
 A/Accession: J00917  
 A/Molecule type: mRNA  
 A/Residues: 1-488 <MES>  
 A/Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:g182390  
 U. Biol. Chem. 267, 7395-7401, 1992  
 A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor  
 A/Reference number: A24485; MUID:92218390; PMID:1313796  
 A/Accession: A24485  
 A/Molecule type: DNA  
 A/Residues: 1-15 <MIA>  
 A/Experimental source: liver  
 A/Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)  
 R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
 Gene 41, 311-314, 1986  
 A/Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
 A/Reference number: A25853; MUID:86221713; PMID:3011603  
 A/Accession: A25853  
 A/Molecule type: mRNA  
 A/Residues: 19-284, 'E', 289-488 <KAU>  
 A/Cross-references: GB:M2613; NID:9180335; PIDN:AAA51984.1; PID:g180336  
 R/Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
 A/Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X  
 A/Reference number: A22208; MUID:85216545; PMID:2582420  
 A/Accession: A22208  
 A/Molecule type: mRNA  
 A/Residues: 13-441, 'S', 443-488 <FUN>  
 A/Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:g182841  
 R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
 A/Title: Characterization of a cDNA coding for human factor X.  
 A/Reference number: A21284; MUID:84222026; PMID:6587384  
 A/Accession: A21284  
 A/Molecule type: mRNA  
 A/Residues: 13-284, 'E', 289-488 <LE2>  
 A/Cross-references: GB:K01886  
 R/McMillan, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss  
 Biochemistry 22, 2875-2884, 1983  
 A/Title: Complete amino acid sequence of the light chain of human blood coagulation factor X  
 A/Reference number: A20362; MUID:83257207; PMID:6871167  
 A/Accession: A20362  
 A/Molecule type: protein  
 A/Residues: 41-179 <MCW>  
 R/Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X  
 A/Reference number: S39414; MUID:94062825; PMID:823461  
 A/Accession: S39415  
 A/Molecule type: protein  
 A/Residues: 183-234 <INO>  
 A/Note: glycosylation sites  
 A/Note: identification and characterization of beta-hydroxyaspartic acid  
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.D.; Hamsabhusanam, K.; Lyman, G.

Gene 84, 517-519, 1989  
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
A:Reference number: 154051; MUID:90128299; PMID:2612918  
A:Accession: 154051  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-references: GB:M3297; NID:g183860; PIDN:AAA52636.1; PID:g553330  
J:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla  
J. Mol. Biol. 232, 947-966, 1993  
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A:Reference number: A49458; MUID:93360277; PMID:8355279  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
C:Genetics:  
A:Gene: GDB:F10  
A:Cross-references: GDB:119890; OMIM:227600  
A:Map position: 13q34-13q34  
A:Insertions: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
A:Note: deficiency of this factor causes Stuart disease  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-119/Product: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:129-164/Domain: EGF homology <EG2>  
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <APR>  
F:235-462/Domain: trypsin homology <TRY>  
F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
F:57-62/Disulfide bonds: #status predicted  
F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:119,211/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F:216,222,419/Active site: His, Asp, Ser #status experimental

Query Match 47.6%; Score 91; DB 1; Length 488;  
Best Local Similarity 36.4%; Pred. No. 4.4e-08;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

1 ANGFLLXLRDGLXRCXKXLCSPFXAFPIFNXXRTQFWVS 44  
41 ANSFLEMKKHLEKRECEBETCSYEAREVEFSDKTEPFMKY 84

RESULT 9

KXHU  
protein C (activated) (EC 3.4.21.6) precursor - human  
N:Alternate names: autoprothrombin IIA; plasma protein C  
C:Species: Homo sapiens (man)  
C>Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
A:Accession: A22331; A25426; A21781; A23789; A00927  
R:Forster, D.C.; Yoshitake, S.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
A:Title: The nucleotide sequence of the gene for human protein C.  
A:Reference number: A22331; MUID:85270390; PMID:2991887  
A:Accession: A22331  
A:Molecule type: DNA  
A:Residues: 1-461 <FOS1>  
A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334  
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
A:Title: Evolution and organization of the human protein C gene.  
A:Reference number: A25426; MUID:86120978; PMID:3511471

A:Accession: A25426  
A:Molecule type: DNA  
A:Residues: 1-445; 'L', 446-461 <PLU>  
A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
R:Forster, D.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
A:Title: Characterization of a cDNA coding for human protein C.  
A:Reference number: A21781; MUID:84272714; PMID:6589623  
A:Accession: A21781  
A:Molecule type: mRNA  
A:Residues: 'Q', 107-461 <FOS2>  
A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323  
R:Beckmann, R.U.; Schmidt, R.U.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
Nucleic Acids Res. 13, 5233-5247, 1985  
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and 1  
A:Reference number: A23789; MUID:85269639; PMID:2991859  
A:Accession: A23789  
A:Molecule type: mRNA  
A:Residues: 1-461 <BEC>  
A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120  
R:Meierlich, J.P.; Broze Jr., G.J.  
J. Biol. Chem. 265, 11397-11404, 1990  
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m  
A:Reference number: A44605; MUID:90293094; PMID:1694179  
A:Contents: annotation; carboxylate binding sites; activation peptide  
A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
R:Harrie, R.J.; Long, V.T.; Spellman, M.W.  
J. Biol. Chem. 267, 5102-5107, 1992  
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor  
A:Reference number: A44606; MUID:92184750; PMID:11544894  
A:Contents: annotation; beta-hydroxyaspartic acid  
C:Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
C:Comment: protein C is strongly enhanced by complexing with protein S. Protein C also f  
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
C:Genetics:  
A:Gene: GDB:PROC  
A:Cross-references: GDB:120317; OMIM:176860  
A:Map position: 2q13-2q21  
A:Insertions: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:27-86/Domain: Gla domain homology <GLA>  
F:33-42/Domain: propeptide #status predicted <PRO>  
F:43-197/Product: protein C light chain #status predicted <LCH>  
F:92-131/Domain: EGF homology <EG1>  
F:140-175/Domain: EGF homology <EG2>  
F:200-461/Product: activation peptide #status experimental <APR>  
F:200-211/Domain: activation peptide #status experimental <APR>  
F:212-445/Domain: trypsin homology <TRY>  
F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,338-354,373-387,398-426/D  
F:106-111/Disulfide bonds: #status predicted  
F:110/Binding site: carboxylate (Thr) (covalent) #status absent  
F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:119,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
F:251,259,402/Active site: His, Asp, Ser #status predicted  
F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 46.1%; Score 88; DB 1; Length 461;  
Best Local Similarity 46.3%; Pred. No. 1.4e-07;  
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

1 ANGFLLXLRDGLXRCXKXLCSPFXAFPIFNXXRTQFW 41  
43 ANSFLEBRHSSLRRECEBETCDPEBAKEIRQNVDDTLAFW 83

RESULT 10

EXBO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Ping, M.R.; Campbell, R.M.; MacGillivray, T.A.  
 A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; PMID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FUN>  
 A:Cross-references: GB:X00673; NID:9192; PIDN:CA25286.1; PID:9193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; PMID:80130563; PMID:6666735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, 'N', '104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; PMID:83308813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; PMID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T  
 A>Note: carboxylate binding sites and disulfide bonds were determined  
 R:Person, E.; Selander, M.; Linde, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; PMID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A>Note: beta-hydroxyaspartic acid site  
 R:Imoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; PMID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196,199-209,216-233 <INO>  
 A>Note: carboxylate binding sites  
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D  
 Biochemistry 11, 4899-4903, 1972  
 A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammal  
 A:Reference number: A12453; PMID:73053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to  
 A:Contents: annotation; activation  
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic  
 A:Reference number: A38024; PMID:84185716; PMID:6546930  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; PMID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of tw  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-499/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <AP>  
 F:234-499/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F:234-461/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s  
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:200/Binding site: sulfite (Tyr) (covalent) #status experimental  
 F:208-485/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #statu  
 F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental  
 F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 45.5% Score 87; DB 1; Length 492;  
 Best Local Similarity 36.4% Pred. No. 2.3e-07;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRDGLXRXCRXXLCSFYXAFYFRNXXRTQPFVWSY 44  
 Db 41 NSFLEFVKGQNLRECRLEACSLERAREVFEDAEQTFEFWKY 84

RESULT 11  
 KFHU  
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
 N:Alternate names: antihemophilic factor B; Christmas factor  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 15-Sep-2000  
 C:Accession: A00922; A37570; A30511; A22989; A22673; A21337; A37546; A30623; A60486; A20  
 R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.  
 Biochemistry 24, 3736-3750, 1985  
 A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).  
 A:Reference number: A00922; PMID:8600558; PMID:2994716  
 A:Accession: A00922  
 A:Molecule type: DNA  
 A:Residues: 1-461 <YOS>  
 A:Cross-references: GB:K02402; NID:9182612; PIDN:AA59620.1; PID:9182613  
 R:Ranson, D.S.; Choc, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro  
 EMBO J. 3, 1053-1060, 1984  
 A>Title: The gene structure of human anti-haemophilic factor IX.  
 A:Reference number: A37570; PMID:84236100; PMID:6329734  
 A:Accession: A37570  
 A:Molecule type: DNA  
 A:Residues: 1-461 <ANS>  
 A:Cross-references: GB:K02048  
 R:Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
 Blood 72, 1074-1076, 1988  
 A>Title: The putative factor IX gene promoter in hemophilia B Leyden.  
 A:Reference number: A30511; PMID:88327116; PMID:3416069  
 A:Accession: A30511  
 A:Molecule type: DNA  
 A:Residues: 8-24 <REI>  
 A:Cross-references: EMBL:X55008; NID:9311288; PIDN:CAB36245.2; PID:94469253  
 R:Rocheberl, D.D.; Bottema, C.D.K.; Buertede, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor  
 A:Reference number: A32989; PMID:89371752; PMID:2773937  
 A:Accession: A32989

A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 30-92 <KOE>  
 R:McGraw, R.A.; Davies, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985  
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat  
 A:Reference number: A22673; PMID:85190593; PMID:3857619  
 A:Accession: A22673  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', 195-461 <MCG>  
 A:Cross-references: GB:M1309; NID:G180552; PIDN:AAA52023.1; PID:G180553  
 A:Note: the authors translated the codon ACA for residue 29 as Tyr  
 R:Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstosh  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-bp  
 A:Reference number: A21337; PMID:83220788; PMID:6687940  
 A:Accession: A21337  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', 195-461 <JAY>  
 A:Cross-references: GB:J00137; NID:G182610; PIDN:AAA52763.1; PID:G182611  
 R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I  
 A:Reference number: A37546; PMID:84300526; PMID:6089357  
 A:Accession: A37546  
 A:Molecule type: mRNA  
 A:Residues: 38-193, 'T', 195-326 <JAG>  
 A:Cross-references: GB:M35672  
 R:Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
 A:Title: Isolation and characterization of a cDNA coding for human factor IX.  
 A:Reference number: A30623; PMID:83065193; PMID:6959130  
 A:Accession: A30623  
 A:Molecule type: mRNA  
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',  
 A:Cross-references: GB:J00136; NID:G182608; PIDN:AAA98726.1; PID:G182609  
 A:Experimental source: liver  
 R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
 Vox Sang. 58, 21-29, 1990  
 A:Title: Development of an immunoaffinity process for factor IX purification.  
 A:Reference number: A60486; PMID:90194857; PMID:2316207  
 A:Accession: A60486  
 A:Molecule type: protein  
 A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; PMID:83308813; PMID:6688526  
 A:Accession: A20274  
 A:Molecule type: protein  
 A:Residues: 105-109, 'X', 111-115 <MCM>  
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall  
 Eur. J. Biochem. 172, 565-572, 1988  
 A:Title: Characterisation of two differently processed forms of human recombinant factor  
 A:Reference number: S02527; PMID:88166735; PMID:3280312  
 A:Accession: S02527  
 A:Molecule type: protein  
 A:Residues: 29-63 <BAL>  
 A:Note: processed forms expressed in recombinant system  
 R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meullen,  
 EMBO J. 9, 3295-3301, 1990  
 A:Title: Characterization of recombinant human factor IX expressed in transgenic mice ar  
 A:Reference number: S12058; PMID:91006024; PMID:2205546  
 A:Accession: S12058  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-68 <JAL>  
 A:Note: processed forms expressed in recombinant system  
 R:Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe  
 EMBO J. 9, 475-480, 1990  
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium  
 A:Reference number: S12377; PMID:90151623; PMID:2406129  
 A:Accession: S12377  
 A:Molecule type: protein

A:Residues: 92-130 <HAN>  
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system  
 R:de la Salle, C.; Charmanfrier, J.L.; Baas, M.U.; Schwartz, A.; Wiesel, M.L.; Grunbaum,  
 Thromb. Haemost. 70, 370-371, 1993  
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsib  
 A:Reference number: 159612; PMID:94054330; PMID:8236150  
 A:Accession: 159612  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 444-461 <RES>  
 A:Cross-references: GB:S66752; NID:G439773; PIDN:AA26588.1; PID:G439774  
 R:Stoffet, E.S.; Koebert, D.D.; Sarkar, G.; Sommer, S.S.  
 Science 239, 491-494, 1988  
 A:Title: Genetic amplification with transcript sequencing.  
 A:Reference number: 159529; PMID:88127096; PMID:3340835  
 A:Accession: 159529  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 290-359 <RE2>  
 A:Cross-references: GB:M19063; NID:G182622; PIDN:AAA52456.1; PID:G182623  
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.; Iw  
 Biochemistry 33, 5167-5171, 1994  
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin  
 A:Reference number: A54255; PMID:94227047; PMID:8172892  
 A:Accession: A54255  
 A:Molecule type: protein  
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>  
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrat  
 R:Di Scipio, R.G.; Kurachi, K.; Davie, E.W.  
 J. Clin. Invest. 61, 1528-1538, 1978  
 A:Title: Activation of human factor IX (Christmas factor).  
 A:Reference number: A18483; PMID:78194509; PMID:659613  
 A:Contents: annotation; activation; active site; carbohydrate binding  
 R:McGraw, R.A.; Davies, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
 Am. Soc. Hematol. Abstr. 64(Suppl. 1), 262a, 1984  
 A:Reference number: A37569  
 A:Contents: annotation  
 A:Note: 194-Thr was also found  
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
 J. Biol. Chem. 259, 5698-5704, 1984  
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
 A:Reference number: A37543; PMID:84185715; PMID:6425296  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
 J. Biol. Chem. 260, 2583, 1985  
 A:Reference number: A37544  
 A:Contents: annotation; calcium binding; correction  
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
 Cell 45, 343-348, 1986  
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation  
 A:Reference number: A37545; PMID:86189947; PMID:3009023  
 A:Contents: annotation; signal sequence cleavage site  
 R:Shuhito, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,  
 J. Biol. Chem. 264, 21257-21265, 1989  
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan  
 A:Reference number: A30622; PMID:90078229; PMID:2592373  
 A:Contents: annotation; sequence of mutant B(M) Nagoya  
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Handford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle  
 submitted to the Brookhaven Protein Data Bank, November 1991  
 A:Reference number: A51252; PDB:1IXA  
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
 A:Note: recombinant form expressed in yeast  
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
 C:Genetics:  
 A:Gene: GDB:1F9  
 A:Cross-references: GDB:119900; OMIM:306900  
 A:Map position: Xq27.1-Xq27.2  
 A:Map position: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese



A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic  
 F:1-28/Domain: signal sequence #status experimental <PPT>  
 F:29-46/Domain: propeptide #status experimental <PPT>  
 F:31-91/Domain: Gla domain homology <Gla>  
 F:47-191/Product: coagulation factor IXa 11ght chain #status experimental <ALC>  
 F:97-128/Domain: EGF homology <EG1>  
 F:134-170/Domain: EGF homology <EG2>  
 F:1227-226/Domain: activation peptide #status experimental <ACT>  
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:227-454/Domain: trypsin homology <TRY>  
 F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxylglutamic acid (Glu) #S  
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D  
 F:99/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:191-199/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental  
 F:203-213/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:205-215/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 44.5% Score 85; DB 1; Length 461;  
 Best Local Similarity 39.5%; Pred. NO. 4.9e-07;  
 Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

Qy 2 NGFLXXLRDGSIXRCXKXLCFFXAXFXIFRNXXRTQFWWSY 44  
 Db 49 SGKLEBFVQGNLERECMEKCSFEAREVENTERTTEFKQY 91

## RESULT 12

thrombin (EC 3.4.21.5) precursor [validated] - human  
 N:Alternate names: coagulation factor II

C:Species: Homo sapiens (man)  
 C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000  
 C:Accession: A29351; A00914; A37549; A37550; I51952  
 R:Degeen, S.U.F.; Davie, E.W.  
 Biochemistry 26, 6165-6177, 1987  
 A:Title: Nucleotide sequence of the gene for human prothrombin.  
 A:Reference number: A29351; MUID:88077877; PMID:2825773  
 A:Accession: A29351

A:Molecule type: DNA  
 A:Residues: 1-622 <DE>  
 A:Cross-references: GB:M3262; GB:M33691; NID:9558069; PIDN:AC63054.1; PID:9339641  
 R:Degeen, S.U.F.; MacGillivray, R.T.A.; Davie, E.W.  
 Biochemistry 22, 2087-2097, 1983  
 A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for  
 A:Reference number: A00914; MUID:83231469; PMID:6305407  
 A:Accession: A00914

A:Molecule type: mRNA  
 A:Residues: 8-163, 'N', 165-622 <DE2>  
 A:Cross-references: GB:V00593; GB:J00307; NID:937128; PIDN:CAA23842.1; PID:91335344  
 A:Accession: B00914  
 A:Molecule type: DNA  
 A:Residues: 188-311 <DE3>  
 R:Walt, D.A.; Hewett-Ewmett, D.; Seeger, W.H.  
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977  
 A:Reference number: A37549; MUID:77193964; PMID:266717  
 A:Accession: A37549

A:Molecule type: protein  
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,  
 R:Butkowski, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.  
 J. Biol. Chem. 252, 4942-4957, 1977  
 A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.  
 A:Reference number: A37550; MUID:77207112; PMID:873923  
 A:Accession: A37550

A:Molecule type: protein  
 A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-  
 R:Rabiet, M.J.; Blachet, A.; Fritie, B.; Fritie, B.C.  
 J. Biol. Chem. 261, 13210-13215, 1986  
 A:Reference number: A37551; MUID:87008532; PMID:3759958

A:Contents: annotation; activation cleavages  
 R:MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.  
 Ann. N. Y. Acad. Sci. 485, 73-79, 1986  
 A:Title: Recombinant genetic approaches to functional mapping of thrombin.  
 A:Reference number: I51952; MUID:87182874; PMID:3471151  
 A:Accession: I51952

A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2, 'R', 5-100 <RES>  
 A:Cross-references: GB:M33031; NID:9190723; PIDN:AAA60220.1; PID:9190724  
 C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C:Comment: Prothrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.  
 C:Comment: The gamma-carboxylglutamic acid residues bind calcium ions, result from the carboxy-  
 ent interaction with the negatively charged phospholipid membrane surface.  
 C:Comment: The prothrombin precursor is synthesized in the liver.

A:Gene: GDB:F2  
 A:Cross-references: GDB:119894; OMIM:176930  
 A:Map position: 11p11-11q12  
 A:Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/2

C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxylglutamic acid; dupli  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-43/Domain: propeptide #status predicted <PRO>  
 F:28-87/Domain: Gla domain homology <Gla>  
 F:44-622/Product: prothrombin #status experimental <MAT>  
 F:44-327/Domain: activation peptide #status experimental <APT>  
 F:108-186/Domain: kringle homology <KR1>  
 F:213-291/Domain: kringle homology <KR2>  
 F:328-363/Product: thrombin light chain #status experimental <LCH>  
 F:364-622/Product: thrombin heavy chain #status experimental <HCH>  
 F:364-613/Domain: trypsin homology <TRY>  
 F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxylglutamic acid (Glu) #status  
 F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status  
 F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:326-482,536-550,564-594/Disulfide bonds: #status predicted  
 F:391-407/Disulfide bonds: #status experimental  
 F:406-462/Active site: His, Asp #status predicted  
 F:416/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:568/Active site: Ser #status experimental

Query Match 44.5% Score 85; DB 1; Length 622;  
 Best Local Similarity 38.6%; Pred. NO. 6.5e-07;  
 Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRDGSIXRCXKXLCFFXAXFXIFRNXXRTQFWWSY 44  
 Db 44 ANTFLEVRKGNLERECVETCSYEAFALSSSTATDVFMAYK 87

## RESULT 13

KFE0  
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
 N:Alternate names: Christmas factor

C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999  
 C:Accession: A14757; B20274; I45891; A00923  
 R:Katayama, K.; Ericsson, L.H.; Entfeld, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
 A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac  
 A:Reference number: A14757; MUID:80056119; PMID:291916  
 A:Accession: A14757

A:Molecule type: protein  
 A:Residues: 1-63, 'T', 65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coag  
 A:Reference number: A20274; MUID:83308813; PMID:6686526  
 A:Accession: B20274  
 A:Molecule type: protein





Search completed: March 19, 2003, 15:01:01  
Job time : 30.125 secs

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)  
328.082 Million cell updates/sec

Title: 10ASP28PHE\_4  
Perfect score: 191  
Sequence: 1 ANGFLXXLRGSLKRCRX.....XXAFXIPRNXXRTQFWVSY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description          |
|------------|-------|-------------|--------|------------|----------------------|
| 1          | 148   | 77.5        | 407    | FA7_BOVIN  | P22457 bos taurus    |
| 2          | 128   | 67.0        | 444    | FA7_RABIT  | P98139 oryctolagus   |
| 3          | 120   | 62.8        | 466    | FA7_HUMAN  | P08709 homo sapien   |
| 4          | 105   | 55.0        | 218    | TWGI_HUMAN | O14668 homo sapien   |
| 5          | 104   | 54.5        | 461    | PRTC_MOUSE | P33587 mus musculu   |
| 6          | 103   | 53.9        | 446    | FA7_MOUSE  | P70375 mus musculu   |
| 7          | 102   | 53.4        | 461    | FA7_RAT    | P31394 rattus norv   |
| 8          | 99    | 51.8        | 459    | PRTC_PIG   | O951P2 sus scrofa    |
| 9          | 98    | 51.3        | 231    | TWGI_HUMAN | O9Bzd7 homo sapien   |
| 10         | 95    | 49.7        | 490    | FA10_RABIT | O19045 oryctolagus   |
| 11         | 94    | 49.2        | 456    | PRTC_BOVIN | P00745 bos taurus    |
| 12         | 91    | 47.6        | 488    | FA10_HUMAN | P00742 homo sapien   |
| 13         | 88    | 46.1        | 461    | PRTC_HUMAN | P04070 homo sapien   |
| 14         | 87    | 45.5        | 492    | FA10_BOVIN | P00743 bos taurus    |
| 15         | 85    | 44.5        | 461    | FA9_HUMAN  | P00740 homo sapien   |
| 16         | 85    | 44.5        | 622    | THRB_HUMAN | P00734 homo sapien   |
| 17         | 83    | 43.5        | 416    | FA9_BOVIN  | P00741 bos taurus    |
| 18         | 82    | 42.9        | 458    | PRTC_RABIT | O28661 oryctolagus   |
| 19         | 82    | 42.9        | 617    | THRB_RAT   | P18292 rattus norv   |
| 20         | 82    | 42.9        | 618    | THRB_MOUSE | P19221 mus musculu   |
| 21         | 79    | 41.4        | 475    | FA10_CHICK | P23155 gallus gall   |
| 22         | 78    | 40.8        | 452    | FA9_CANFA  | P19540 canis famli   |
| 23         | 78    | 40.8        | 455    | FA9_MOUSE  | P16294 mus musculu   |
| 24         | 76    | 39.8        | 625    | THRB_BOVIN | P00735 bos taurus    |
| 25         | 68    | 35.6        | 202    | TWGI_HUMAN | O14669 homo sapien   |
| 26         | 67    | 35.1        | 226    | TWGI_HUMAN | O292d6 homo sapien   |
| 27         | 67    | 35.1        | 649    | PRTS_MACVU | O28520 macaca mula   |
| 28         | 67    | 35.1        | 675    | PRTS_BOVIN | P07224 bos taurus    |
| 29         | 67    | 35.1        | 676    | PRTS_HUMAN | P07225 homo sapien   |
| 30         | 66    | 34.6        | 376    | FA10_TROCA | P81428 tropicidichis |
| 31         | 66    | 34.6        | 400    | PRTZ_HUMAN | P22891 homo sapien   |
| 32         | 66    | 34.6        | 646    | PRTS_RABIT | P98118 oryctolagus   |
| 33         | 64    | 33.5        | 675    | PRTS_RAT   | P55813 rattus norv   |

|    |      |      |      |   |            |                    |
|----|------|------|------|---|------------|--------------------|
| 34 | 62   | 32.5 | 396  | 1 | PRTZ_BOVIN | P00744 bos taurus  |
| 35 | 57   | 29.8 | 675  | 1 | PRTS_MOUSE | O08761 mus musculu |
| 36 | 52   | 27.2 | 604  | 1 | VE1_BPv2   | P11298 bovine papi |
| 37 | 52   | 27.2 | 605  | 1 | VE1_BPv1   | P03116 bovine papi |
| 38 | 48   | 25.1 | 413  | 1 | NCAP_IHNV  | P19691 infectious  |
| 39 | 45.5 | 23.8 | 2133 | 1 | FA8_PIG    | P12263 sus scrofa  |
| 40 | 42.5 | 22.3 | 105  | 1 | UL03_HCMVA | P16775 human cytom |
| 41 | 42   | 22.0 | 320  | 1 | GSHE_BUCAI | P57612 buchnera ap |
| 42 | 42   | 22.0 | 3061 | 1 | POLG_PVYHU | O02963 p genome po |
| 43 | 41   | 21.5 | 97   | 1 | VCRB_MYCCA | P45619 mycoplasma  |
| 44 | 41   | 21.5 | 371  | 1 | LST_NEIMA  | O9Juv5 neisseria m |
| 45 | 41   | 21.5 | 371  | 1 | LST_NEIMB  | P72097 neisseria m |

## ALIGNMENTS

| RESULT 1 | FA7_BOVIN   | STANDARD; | PRT; | 407 AA. |
|----------|---|-----------|------|---------|
| ID       | FA7_BOVIN   |           |      |         |
| AC       | P22457:   |           |      |         |
| DT       | 01-AUG-1991 (Rel. 19, Created)  |           |      |         |
| DT       | 01-AUG-1991 (Rel. 19, Last sequence update)                                       |           |      |         |
| DT       | 15-JUN-2002 (Rel. 41, Last annotation update)                                     |           |      |         |
| DE       | Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator). |           |      |         |
| DE       | accelerator).   |           |      |         |
| CN       | F7.   |           |      |         |
| OS       | Bos taurus (Bovine).  |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                 |           |      |         |
| OC       | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;                 |           |      |         |
| OC       | Bovidae; Bovinae; Bos.  |           |      |         |
| OX       | NCBI_TaxID=9913;  |           |      |         |
| RN       | [1]   |           |      |         |
| RP       | SEQUENCE.   |           |      |         |
| RX       | MEDLINE=89008362; PubMed=3049594;   |           |      |         |
| RA       | Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,                     |           |      |         |
| RA       | Iwanaga S.;   |           |      |         |
| RT       | "Bovine factor VII. Its purification and complete amino acid                      |           |      |         |
| RT       | sequence.";   |           |      |         |
| RL       | J. Biol. Chem. 263:14868-14877(1988).   |           |      |         |
| RN       | [2]   |           |      |         |
| RP       | STRUCTURE OF CARBOHYDRATE ON SER-52.  |           |      |         |
| RX       | MEDLINE=89213999; PubMed=3149637;   |           |      |         |
| RA       | Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,                       |           |      |         |
| RA       | Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;                       |           |      |         |
| RT       | "A new trisaccharide sugar chain linked to a serine residue in bovine             |           |      |         |
| RT       | blood coagulation factors VII and IX.";   |           |      |         |
| RL       | J. Biochem. 104:867-868(1988).  |           |      |         |
| RN       | [3]   |           |      |         |
| RP       | STRUCTURE OF CARBOHYDRATE ON SER-52.  |           |      |         |
| RX       | MEDLINE=91344709; PubMed=2129367.   |           |      |         |
| RA       | Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;           |           |      |         |
| RT       | "A new trisaccharide sugar chain linked to a serine residue in the                |           |      |         |
| RT       | first EGF-like domain of clotting factors VII and IX and protein Z.";             |           |      |         |
| RL       | Adv. Exp. Med. Biol. 281:121-131(1990).   |           |      |         |
| CC       | -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS             |           |      |         |
| CC       | CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR                 |           |      |         |
| CC       | THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR                   |           |      |         |
| CC       | AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa                 |           |      |         |
| CC       | BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO                |           |      |         |
| CC       | FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.                          |           |      |         |
| CC       | -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to              |           |      |         |
| CC       | form factor Xa.   |           |      |         |
| CC       | -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED                |           |      |         |
| CC       | BY A DISULFIDE BOND.  |           |      |         |
| CC       | -I- TISSUE SPECIFICITY: PLASMA.   |           |      |         |
| CC       | -I- PMV: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME                  |           |      |         |
| CC       | GUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND                         |           |      |         |
| CC       | CALCIUM.  |           |      |         |
| CC       | -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.                                   |           |      |         |
| CC       | -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.                                      |           |      |         |
| DR       | PIR; A31979; A31979.  |           |      |         |
| DR       | HSSP; P08709; 1BP9.   |           |      |         |

```

DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_blood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00063; GLA; 1.
DR SMART; SM00020; Tryp_Spec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 358
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT MOD_RES 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
SQ SEQUENCE 407 AA; 44431 NM; 70381PF0636FP710 CRC64;

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Query Match      77.5%; Score 148; DB 1; Length 407;
Best Local Similarity 68.2%; Pred No. 6,9e-19;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Oy 1 ANGFLKXKLRDGLKRCXKXLCSPFXAXFIIPNXXKRTROFWWSY 44
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 ANGFLLELLPGSLIERECREELCSFEERAHIEFNNEERTROFWWSY 44

RESULT 2
FA7_RABIT
ID FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCB1_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93190306; PubMed=8383365;
RA Brochers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -!- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; U77477; AB37326.1; -.
DR HSRF; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPE; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01166; EGF\_2; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 21  
 FT PROPEP 22 39  
 FT CHAIN 40 191  
 FT CHAIN 192 444  
 FT DOMAIN 45 74  
 FT DOMAIN 85 121  
 FT DOMAIN 126 167  
 FT DOMAIN 192 444  
 FT SITE 191 192  
 FT ACT\_SITE 232 232  
 FT ACT\_SITE 281 281  
 FT ACT\_SITE 383 383  
 FT BINDING 377 377  
 FT BINDING 377 61  
 FT DISULFID 89 100  
 FT DISULFID 94 109  
 FT DISULFID 111 120  
 FT DISULFID 130 141  
 FT DISULFID 137 151  
 FT DISULFID 153 166  
 FT DISULFID 174 301  
 FT DISULFID 198 203  
 FT DISULFID 217 233  
 FT DISULFID 349 368  
 FT DISULFID 379 407  
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 FT MOD\_RES 46 46  
 FT MOD\_RES 53 53  
 FT MOD\_RES 55 55  
 FT MOD\_RES 58 58  
 FT MOD\_RES 59 59  
 FT MOD\_RES 64 64  
 FT MOD\_RES 65 65  
 FT MOD\_RES 68 68  
 FT MOD\_RES 74 74  
 FT MOD\_RES 102 102  
 FT MOD\_RES 211 211  
 FT CARBOHYD 242 242  
 FT CARBOHYD 306 306  
 SQ SEQUENCE 444 AA; 49011 MW; 0481IABCFE54278B CRC64;

Query March 67.0%; Score 128; DB 1; Length 444;  
 Best Local Similarity 52.3%; Pred. No. 2.9e-15;  
 Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

1 ANGFLXKLIDGSLKRXCRXKLCSPFXAFIFRNXXRTQFWVSY 44  
 40 ANSFLELRPGSLRECKEELCSFEAREVFOSTERTKQFWITY 83

RESULT 3  
 FA7 HUMAN STANDARD; PRT; 466 AA.  
 AC P08709; Q14339;  
 DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 DE conversion accelerator) (Eptacog alfa).  
 GN F7.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=66205965; PubMed=3486420;  
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,  
 RA Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor VII.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260948; PubMed=3037537;  
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
 RA Hagen F.S., Murray M.U.;  
 RT "Nucleotide sequence of the gene coding for human factor VII, a  
 RT vitamin K-dependent protein participating in blood coagulation.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.  
 RA Rieder W.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=89088153; PubMed=3264725;  
 RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
 RA Pedersen A.H., Hedner U.;  
 RT "Amino acid sequence and posttranslational modifications of human  
 RT factor VIIa from plasma and transfected baby hamster kidney cells.";  
 RT Biochemistry 27:7785-7793(1988).  
 RN [5]  
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
 RX MEDLINE=91250411; PubMed=1904059;  
 RA Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,  
 RA Komiyama Y., Pedersen A.H., Kistiel W.;  
 RT "Human plasma and recombinant factor VII. Characterization of O-  
 RT glycosylations at serine residues 52 and 60 and effects of site-  
 RT directed mutagenesis of serine 52 to alanine.";  
 RT J. Biol. Chem. 266:11051-11057(1991).  
 RN [6]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=9062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RT J. Biol. Chem. 264:20320-20325(1989).  
 RN [7]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RT Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=8598903;  
 RA Bannet D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RT Nature 380:41-46(1996).

[9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=9925787;  
 RA Zhang B., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPT mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=96367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gippert G.P., Forren S., Stenflo J.,  
 RT Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.W., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys->Tyr) and two neutral polymorphisms  
 RT (115His and 333Ser) in the human coagulation factor VII gene.";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamiya O., Kembell-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RX MEDLINE=94264305; PubMed=8204879;  
 RA Chang S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294Ala->Val) and X (334Ser->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohnishi K., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA "Factor VII Mie: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).  
 [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr159Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 [19]  
 RP VARIANTS W-263; K-325; V-358; Q-364; E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,  
 RA Zaitov R., Seligsohn U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 [21]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerif C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).  
 [22]  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -1- PHARMACEUTICAL: Available under the names Niasate or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in  
 CC Query Match 62.8%; Score 120; DB 1; Length 466;  
 CC Best Local Similarity 52.3%; Pred No. 8.3e-14;  
 CC Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANGFLXXLRDGLRXCRXXLCSFYXAFYIFRNXXRTQFWVS 44  
 Db 61 ANAFLEELRPGSLERCKEKGCSFEERAREIFKDARITKLFWSY 104  
 RESULT 4  
 TMG1\_HUMAN  
 ID TMG1\_HUMAN STANDARD; PRT; 218 AA.  
 AC 014668;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-  
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein  
 DE 1).  
 GN FRKG1 OR TMG1 OR PRGP1.  
 OS Homo sapiens (Human).



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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Glycoprotein; Serine protease;
KM Gamma-carboxylglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL; 1 33
FT PROPEP; 34 41
FT CHAIN; 42 196
FT CHAIN; 199 461
FT PEPTIDE; 199 212
FT SITE; 212 213
FT DOMAIN; 96 131
FT DOMAIN; 135 175
FT DOMAIN; 213 461
FT MOD_RES; 47 47
FT MOD_RES; 48 48
FT MOD_RES; 55 55
FT MOD_RES; 57 57
FT MOD_RES; 60 60
FT MOD_RES; 61 61
FT MOD_RES; 66 66
FT MOD_RES; 67 67
FT MOD_RES; 70 70
FT MOD_RES; 112 112
FT ACT_SITE; 253 253
FT ACT_SITE; 299 299
FT ACT_SITE; 402 402
FT ACT_SITE; 58 63
FT DISULFID; 91 110
FT DISULFID; 100 105
FT DISULFID; 104 119
FT DISULFID; 121 130
FT DISULFID; 139 150
FT DISULFID; 146 159
FT DISULFID; 161 174
FT DISULFID; 182 319
FT DISULFID; 238 254
FT DISULFID; 373 387
FT DISULFID; 398 426
FT CARBOHYD; 214 214
FT CARBOHYD; 220 220
FT CARBOHYD; 335 335
FT CARBOHYD; 355 355
FT CONFLICT; 333 333
FT CONFLICT; 393 393
SQ SEQUENCE 461 AA; 51945 MW; 53FAAD85B194D6E CRC64;

Query Match 54.5%; Score 104; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 6; 1e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-UN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP MEDLINE=97127167; PubMed=8972017;
RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964 (1996).
CC -! FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -! CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -! SUBUNIT: HETEROIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -! TISSUE SPECIFICITY: PLASMA.
CC -! PTM: THE VITAMIN K-DEPENDENT, ENZYMTIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -! SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U66079; AAC33796.1; -.
DR HSP; P08709; IBE9.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR001052; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001811; EGF Ca.
DR InterPro; IPR001283; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxylglutamic acid;

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KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 193  
 FT CHAIN 194 446  
 FT DOMAIN 47 76  
 FT DOMAIN 87 123  
 FT DOMAIN 128 169  
 FT DOMAIN 193 446  
 FT SITE 194 194  
 FT ACT\_SITE 234 234  
 FT ACT\_SITE 283 283  
 FT ACT\_SITE 385 385  
 FT BINDING 379 379  
 FT DISULFID 91 102  
 FT DISULFID 96 111  
 FT DISULFID 113 122  
 FT DISULFID 132 143  
 FT DISULFID 139 153  
 FT DISULFID 155 168  
 FT DISULFID 176 303  
 FT DISULFID 200 205  
 FT DISULFID 219 235  
 FT DISULFID 351 370  
 FT DISULFID 381 409  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 76 76  
 FT MOD\_RES 104 104  
 FT CARBOHYD 186 186  
 FT CARBOHYD 244 244  
 SQ SEQUENCE 446 AA; 50276 MW; 251284445CB96E CRC64;  
 Query Match 53.9%; Score 103; DB 1; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 8-11;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRDGLRXPXCRXXLCFFXXAFIFNNXXRTQFWVS 44  
 DB 42 ANSLLEELMPGSLRECNBEGCSFEAREIFKSPERTQFWIV 85  
 RESULT 7  
 PRTC RAT STANDARD; PRT; 461 AA.  
 AC P31394;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Anticlotting protein C) (Anticoagulant protein C) (Blood coagulation factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistat; TISSUE=Liver;  
 RX MEDLINE=9232550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C";  
 RL Biochim. Biophys. Acta 1131:329-332(1992).

CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL; X64336; CAA45617.1; -.  
 CC PIR; S18994; S18994.  
 CC PIR; S24312; S24312.  
 CC HSSP; P04070; IPCU.  
 CC MEROPS; S01.218; -.  
 CC InterPro; IPR000152; Aex\_hydroxyl.  
 CC InterPro; IPR001314; Chymotrypsin.  
 CC InterPro; IPR000561; EGF-like.  
 CC InterPro; IPR001881; EGF Ca.  
 CC InterPro; IPR002383; GLA\_blood.  
 CC InterPro; IPR001254; Ser\_protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00008; EGF; 2.  
 CC Pfam; PF00089; trypsin.1.  
 CC Pfam; PF00594; Gla; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00001; GLABLOOD.  
 CC SMART; SM00179; EGF\_CA; 1.  
 CC SMART; SM00001; EGF\_like; 1.  
 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; TRYPSIN\_SPC; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 2.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 CC PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC Blood coagulation; Glycoprotein; Serine protease;  
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 CC KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 CC FT SIGNAL 1 32  
 CC FT PROPEP 33 41  
 CC FT CHAIN 42 196  
 CC FT CHAIN 199 461  
 CC FT PEPTIDE 199 212  
 CC FT SITE 212 213  
 CC FT DOMAIN 96 131  
 CC FT DOMAIN 135 175  
 CC FT DOMAIN 213 461  
 CC FT MOD\_RES 47 47  
 CC MOD\_RES 48 48  
 CC MOD\_RES 48 48  
 CC PROTEIN C LIGHT CHAIN (BY SIMILARITY).  
 CC PROTEIN C HEAVY CHAIN (BY SIMILARITY).  
 CC ACTIVATION PEPTIDE (BY SIMILARITY).  
 CC CLEAVAGE (BY THROMBIN) (BY SIMILARITY).  
 CC EGF-LIKE 1.  
 CC EGF-LIKE 2.  
 CC SERINE PROTEASE.  
 CC GAMMA-CARBOXYGLUTAMIC ACID  
 CC (BY SIMILARITY).  
 CC GAMMA-CARBOXYGLUTAMIC ACID



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FT  MOD_RES  55  55  GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES  57  57  SIMILARITY).
FT  MOD_RES  60  60  GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES  61  61  SIMILARITY).
FT  MOD_RES  61  61  GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES  66  66  SIMILARITY).
FT  MOD_RES  67  67  GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES  70  70  SIMILARITY).
FT  MOD_RES  70  70  GAMMA-CARBOXYGLUTAMIC ACID (BY
FT  MOD_RES  112  112  SIMILARITY).
FT  ACT_SITE  255  255  CHARGE RELAY SYSTEM.
FT  ACT_SITE  301  301  CHARGE RELAY SYSTEM.
FT  ACT_SITE  400  400  CHARGE RELAY SYSTEM.
FT  DISULFID  58  63  BY SIMILARITY.
FT  DISULFID  91  110  BY SIMILARITY.
FT  DISULFID  100  105  BY SIMILARITY.
FT  DISULFID  104  119  BY SIMILARITY.
FT  DISULFID  121  130  BY SIMILARITY.
FT  DISULFID  139  150  BY SIMILARITY.
FT  DISULFID  146  159  BY SIMILARITY.
FT  DISULFID  161  174  BY SIMILARITY.
FT  DISULFID  182  321  INTERCHAIN (BY SIMILARITY).
FT  DISULFID  240  256  BY SIMILARITY.
FT  DISULFID  371  385  BY SIMILARITY.
FT  DISULFID  396  424  BY SIMILARITY.
FT  CARBOHYD  138  138  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD  292  292  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD  353  353  N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE  459 AA; 51866 MW; 8541AAC14C16D09 CRC64;

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Query Match 51.8%; Score 99; DB 1; Length 459;
Best Local Similarity 45.5%; Pred. No. 4.7e-10;
Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

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Oy 1 ANGFLXLRDGLKXCRXXLCSPXAFYIPNXXRTQFWVSY 44
Db 42 ANSFLELRPSSLERCKETCDPEAREIFONTENTMAFWSKY 85

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RESULT 9
ID TMG3 HUMAN STANDARD; PRT; 231 AA.
AC Q9B2D7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN NCB1;
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RX MEDLINE=21117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
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CC -----
DR EMBL; AF326350; AAK0955.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 78 PROTEIN 3.
FT TRANSMEM 79 101 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 102 231 POTENTIAL.
FT DOMAIN 23 60 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 231 AA; 25848 MW; 8A373B4848490D81 CRC64;

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Query Match 51.3%; Score 98; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.6e-10;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

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Oy 1 ANGFLXLRDGLKXCRXXLCSPXAFYIPNXXRTQFWVSY 44
Db 20 ANSFLELRQGTIERECMEICSYEKEVEFENKEKTFWFGY 63

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RESULT 10
ID FA10 RABIT STANDARD; PRT; 490 AA.
AC O19045;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN F10.
OS Eucyrtolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN NCB1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; PubMed=9101642;
RA Pendurthi U.R., Anderson K.D., James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X.";
RL Thromb. Res. 85:503-514(1997).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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DR EMBL/AF003200; AAB62542.1; -  
 DR HSSP; P00742; 1HC.  
 DR MEROPS; S01.216; -  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
 FT PROPEP 21 40  
 FT CHAIN 41 180  
 FT CHAIN 184 490  
 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT DOMAIN 86 122  
 FT DOMAIN 125 165  
 FT DOMAIN 233 490  
 FT MOD\_RES 46 46  
 FT MOD\_RES 47 47  
 FT MOD\_RES 54 54  
 FT MOD\_RES 56 56  
 FT MOD\_RES 59 59  
 FT MOD\_RES 60 60  
 FT MOD\_RES 65 65  
 FT MOD\_RES 66 66  
 FT MOD\_RES 69 69  
 FT MOD\_RES 72 72  
 FT MOD\_RES 75 75  
 FT MOD\_RES 79 79  
 FT MOD\_RES 103 103  
 FT ACT\_SITE 274 274

FT ACT\_SITE 320 320 CHANGE RELAY SYSTEM.  
 FT ACT\_SITE 417 417 CHARGE RELAY SYSTEM.  
 FT DISULFID 90 101 BY SIMILARITY.  
 FT DISULFID 95 110 BY SIMILARITY.  
 FT DISULFID 112 121 BY SIMILARITY.  
 FT DISULFID 129 140 BY SIMILARITY.  
 FT DISULFID 136 149 BY SIMILARITY.  
 FT DISULFID 151 164 BY SIMILARITY.  
 FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 239 244 BY SIMILARITY.  
 FT DISULFID 259 275 BY SIMILARITY.  
 FT DISULFID 388 402 BY SIMILARITY.  
 FT DISULFID 413 441 BY SIMILARITY.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CMC64;

Query Match 49.7%; Score 95; DB 1; Length 490;  
 Best Local Similarity 38.6%; Pred. No. 2.6e-09;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGLXRXCRXXLCSPXXAFXPNNXXRTQFWYSY 44  
 DB 41 ANSFLEELKGNLRECEMCENCSYEBALFVFEDEKXNEFMNXY 84

RESULT 11  
 ID\_PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN [2]  
 RP SEQUENCE OF 40-194.  
 RX MEDLINE=83007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.;  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RT J. Biol. Chem. 257:12170-12179(1982).  
 RN [3]  
 RP REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RT Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN [4]  
 RP SEQUENCE OF 197-456.  
 RX MEDLINE=83007326; PubMed=6896877;  
 RA Stenflo J., Fernlund P.;  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RT J. Biol. Chem. 257:12180-12190(1982).  
 RN [5]  
 RP PROCESSING AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213513; PubMed=6304092;  
 RA Eamon N.L., Debault L.E., Eamon C.T.;  
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
 RT domainless protein C";

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RL J. Biol. Chem. 258:5548-5553(1983).
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid."
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and villia.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TERTRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE. BEYOND THE GLA DOMAIN, THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; K02435; AAA30685.1; -.
DR PIR; A00928; KXBO.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylacton;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 1
FT PROPEP 29
FT CHAIN 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
SERINE PROTEASE.

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[illegible]

RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595 (1985).  
 RN [4]  
 RN SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA";  
 RL Gene 41:311-314 (1986).  
 RN [5]  
 RN SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMillen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid";  
 RL Biochemistry 22:2875-2884 (1983).  
 RN [6]  
 RN SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=8422026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702 (1984).  
 RN [7]  
 RN SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X";  
 RL Eur. J. Biochem. 218:153-163 (1993).  
 RN [8]  
 RN SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=9012829; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hameshushan K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X";  
 RL Gene 84:517-519 (1989).  
 RN [9]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279; Tulinsky A., Park C.H., Bode W.,  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution";  
 RL J. Mol. Biol. 232:947-966 (1993).  
 RN [10]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoro H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635 (1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL, K03194; AA52490.1; -;  
 CC EMBL, M57285; AA52421.1; -;  
 CC EMBL, L29433; AA52764.1; -;  
 CC EMBL, L00390; AA52764.1; JOINED.  
 CC EMBL, L00391; AA52764.1; JOINED.  
 CC EMBL, L00392; AA52764.1; JOINED.  
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 CC EMBL, L00394; AA52764.1; JOINED.  
 CC EMBL, L00395; AA52764.1; JOINED.  
 CC EMBL, L00396; AA52764.1; JOINED.  
 CC EMBL, M22613; AA51984.1; -;  
 CC EMBL, K01886; AA52486.1; -;  
 CC EMBL, M3297; AA52636.1; -;  
 CC PIR, A00924; EXHU.  
 CC PIR, A25853; A25853.  
 CC PIR, A24478; A24478.  
 CC PDB, 1HCG; 08-MAY-95.  
 CC PDB, 1PAX; 29-OCT-97.  
 CC PDB, 1EXY; 17-JUN-98.  
 CC PDB, 1KXB; 23-MAR-99.  
 CC MEROPS, S01.216; -;  
 CC GlycosultDB: P00742; -;  
 CC Genew: HGNC:3528; F10.  
 CC MIM, 134530; -;  
 CC MIM, 227600; -;  
 CC InterPro: IPR000152; Asx\_hydroxyl.  
 CC InterPro: IPR001314; Chymotrypsin.  
 CC InterPro: IPR000561; EGF-like.  
 CC InterPro: IPR000742; EGF 2.  
 CC InterPro: IPR001881; EGF\_Ca.  
 CC InterPro: IPR002383; GLA\_blood.  
 CC InterPro: IPR001254; Ser\_protease\_Try.  
 CC InterPro: IPR000294; VitK\_dep\_GLA.  
 CC Pfam: PF00008; EGF\_2.  
 CC Pfam: PF00089; trypsin\_1.  
 CC Pfam: PF00594; gla\_1.  
 CC PRINTS: PR00722; CHYMOTRYPSIN.  
 CC PRINTS: PR00001; GLABLOOD.  
 CC SMART: SM00179; EGF\_CA; 1.  
 CC SMART: SM00001; EGF\_like; 1.  
 CC SMART: SM00069; GLA; 1.  
 CC SMART: SM00020; Tryp\_Spec; 1.  
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 CC PROSITE: PS00022; EGF\_1; 1.  
 CC PROSITE: PS0186; EGF\_2; 2.  
 CC PROSITE: PS01187; EGF\_CA; 1.  
 CC PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 CC PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 CC PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE: PS00135; TRYPSIN\_SER; 1.  
 CC KEGG: Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 CC Signal; Zymogen; EGF-like domain; Repeat; 3d-structure.  
 CC KEGG: Signal; 31  
 CC FT PROPEP 32 40  
 CC FT CHAIN 41 179  
 CC FT CHAIN 183 488  
 CC FT PROPEP 183 234  
 CC FT CHAIN 235 488  
 CC FT DOMAIN 86 122  
 CC FACTOR X LIGHT CHAIN.  
 CC FACTOR X HEAVY CHAIN.  
 CC ACTIVATION PEPTIDE.  
 CC ACTIVATED FACTOR XA, HEAVY CHAIN.  
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 125 165 EGF-LIKE 2.
FT MOD_RES 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 O-LINKED (GLA)NAC.
FT MOD_RES 103 103 O-LINKED (GLA)NAC.
FT CARBOHYD 211 211 N-LINKED (GLC)NAC.
FT CARBOHYD 221 221 /FTID=CAR 000012.
FT CARBOHYD 231 231 /FTID=CAR 000013.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

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Query Match 47.6%; Score 91; DB 1; Length 488;  
 Best Local Similarity 36.4%; Pred. No. 1.4e-08;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGLPLXLRDGLXKRCXKXLCSPFXKXAFIPFNXKRTQFWSY 44  
 Db 41 ANSFLKMKKGLHREKMEETCSYEAREVEFDSDKTNEFMWY 84

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RESULT 13
PRTC HUMAN STANDARD, PRT: 461 AA.
AC P04070; Q16001; Q15190; Q15189;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)
DE (Anticoproteomycin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85270390; PubMed=2991887;
RA Foster D.C., Yoshitake S., Davie E.W.;
RT "The nucleotide sequence of the gene for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85269639; PubMed=2991859;
RA Beckmann R.J., Schmidt R.J., Sauter R.F., Plutsky J., Crabtree G.R.,
RA Long G.L.;
RT "The structure and evolution of a 461 amino acid human protein C
RT precursor and its messenger RNA, based upon the DNA sequence of
RL cloned human liver cDNAs.";
RN [3]
RP Nucleic Acids Res. 13:5233-5247(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120978; PubMed=3511471;
RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;
RT "Evolution and organization of the human protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).

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RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 106-461 FROM N.A.
RX MEDLINE=84272714; PubMed=6589623;
RA Foster D.C., Davie E.W.;
RT "Characterization of a cDNA coding for human protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE ASN-371.
RX MEDLINE=90293094; PubMed=1694179;
RA Miletich J.P., Broze G.J. Jr.;
RT "Beta protein C is not glycosylated at asparagine 329. The rate of
RT translation may influence the frequency of usage at asparagine-X-
RT cysteine sites.";
RL J. Biol. Chem. 265:11397-11404(1990).
RN [7]
RP HYDROXYLATION.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [8]
RP 3D-STRUCTURE MODELING OF 175-450.
RX MEDLINE=94272342; PubMed=8003977;
RA Fisher C.L., Greengard J.S., Griffin J.H.;
RT "Models of the serine protease domain of the human antithrombotic
RT plasma factor activated protein C and its zymogen.";
RL Protein Sci. 3:588-599(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
RX MEDLINE=97157472; PubMed=9003757;
RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Bamon C.,
RA Bode W.;
RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
RL EMBO J. 15:6822-6831(1996).
RN [10]
RP REVIEW ON PROC VARIANTS.
RX MEDLINE=93190290; PubMed=8446940;
RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
RA Sala N., Cooper D.N.;
RT "Protein C deficiency: a database of mutations. For the Protein C & S
RT Subcommittee of the Scientific and Standardization Committee of the
RT International Society on Thrombosis and Haemostasis.";
RL Thromb. Haemost. 69:77-84(1993).
RN [11]
RP VARIANT CYS-444.
RX MEDLINE=87204221; PubMed=2437584;
RA Romeo G., Haasan H.J., Staemfili S., Roncuazi L., Cianetti L.,
RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
RA Cortese R.;
RT "Hereditary thrombophilia: identification of nonsense and missense
RT mutations in the protein C gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
RN [12]
RP VARIANT TRP-211 (LONDON-1).
RX MEDLINE=90098906; PubMed=2602169;
RA Grundy C.B., Chitolie A., Talbot S., Bevan D., Kakkar V.V.,
RA Cooper D.N.;
RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
RT the protein C gene causing thrombosis.";
RL Nucleic Acids Res. 17:10513-10513(1989).
RN [13]
RP VARIANT CYS-272.
RX MEDLINE=91329836; PubMed=1866249;
RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
RT "The spectrum of genetic defects in a panel of 40 Dutch families with
RT symptomatic protein C deficiency type I: heterogeneity and founder
RT effects.";

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RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).  
 RN [5]  
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 RA Neurath H., Davie E.W.;  
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 RL Biochemistry 11:4899-4903(1972).  
 RN [7]  
 RP PROCESSING.  
 RX MEDLINE=76053121; PubMed=1059122;  
 RA Fujikawa K., Titani K., Davie E.W.;  
 RT "Activation of bovine factor X (Stuart factor): conversion of factor  
 RT Xa-alpha to factor Xa-beta.";  
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 RN [8]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185716; PubMed=6546930;  
 RA Sugo T., Bjoerck I., Holmgren A., Stenflo J.;  
 RT "Calcium-binding properties of bovine factor X lacking the gamma-  
 RT carboxyglutamic acid-containing region.";  
 RL J. Biol. Chem. 259:5705-5710(1984).  
 RN [9]  
 RP SULFATION.  
 RX MEDLINE=86140210; PubMed=3949800;  
 RA Morita T., Jackson C.M.;  
 RT "Localization of the structural difference between bovine blood  
 RT coagulation factors XI and X2 to tyrosine 18 in the activation  
 RT peptide.";  
 RL J. Biol. Chem. 261:4008-4014(1986).  
 RN [10]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=91084483; PubMed=2261466;  
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;  
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of  
 RT the amino-terminal epidermal growth factor like domain in coagulation  
 RT factor X.";  
 RL Biochemistry 29:8111-8118(1990).  
 RN [11]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=92329412; PubMed=1627540;  
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,  
 RA Telemann O.;  
 RT "Three-dimensional structure of the apo form of the N-terminal  
 RT EGF-like module of blood coagulation factor X as determined by NMR  
 RT spectroscopy and simulated folding.";  
 RL Biochemistry 31:5974-5983(1992).  
 RN [12]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=92406922; PubMed=1527084;  
 RA Selander M., Ullner M., Persson E., Telemann O.,  
 RA Stenflo J., Drakenberg T.;  
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High  
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-  
 RT like domain in coagulation factor X.";  
 RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sunnehaugen M., Olah G.A., Stenflo J., Foren S., Drakenberg T.,  
 RA Trewheella J.;  
 RT "The relative orientation of Gla and EGF domains in coagulation  
 RT factor X is altered by Ca2+ binding to the first EGF domain. A  
 RT combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL, X00673; CA25286.1; --  
 CC PIR, A00925; EXBO.  
 CC PDB, IAP0, 31-JAN-94.  
 CC PDB, ICF, 31-MAY-94.  
 CC PDB, 1WHE, 15-MAY-97.  
 CC PDB, 1WHE, 15-MAY-97.  
 CC MEROPS, S01.216; --  
 CC Glycosylated; P00743; --  
 CC InterPro: IPR000152; Asx\_hydroxyl.  
 CC InterPro: IPR001314; Chymotrypsin.  
 CC InterPro: IPR000561; EGF-like.  
 CC InterPro: IPR000742; EGF\_2.  
 CC InterPro: IPR001881; EGF\_Ca.  
 CC InterPro: IPR002383; GLA\_Blood.  
 CC InterPro: IPR001254; Ser\_protease\_Try.  
 CC InterPro: IPR000294; VitK\_dep\_GLA.  
 CC Pfam, PR00008; EGF\_2.  
 CC Pfam, PR00089; trypsin\_1.  
 CC Pfam, PR00594; gla\_1.  
 CC PRINTS, PR00722; CHYMOTRYPSIN.  
 CC PRINTS, PR00001; GLABLOOD.  
 CC SMART, SM00017; EGF\_CA\_1.  
 CC SMART, SM00001; EGF\_like\_1.  
 CC SMART, SM00069; GLA\_1.  
 CC SMART, SM00020; TRYPSIN\_1.  
 CC PROSITE, PS00010; ASX\_HYDROXYL, 1.  
 CC PROSITE, PS00022; EGF\_1, 1.  
 CC PROSITE, PS01186; EGF\_2, 2.  
 CC PROSITE, PS01187; EGF\_CA\_1.  
 CC PROSITE, PS00011; GLU\_CARBOXYLATION, 1.  
 CC PROSITE, PS50240; TRYPSIN\_DOM, 1.  
 CC PROSITE, PS00134; TRYPSIN\_HIS, 1.  
 CC PROSITE, PS00135; TRYPSIN\_SER, 1.  
 CC Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 CC Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.  
 CC SIGNAL 1 23  
 CC PROPEP 24 40  
 CC CHAIN 41 180  
 CC CHAIN 183 492  
 CC PROPEP 183 233  
 CC CHAIN 234 492  
 CC PROPEP 476 492  
 CC DOMAIN 86 122  
 CC FACTOR X LIGHT CHAIN.  
 CC FACTOR X HEAVY CHAIN.  
 CC ACTIVATION PEPTIDE.  
 CC ACTIVATED FACTOR XA, HEAVY CHAIN.  
 CC MAY BE REMOVED BUT IS NOT NECESSARY FOR  
 CC ACTIVATION.  
 CC EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 125 165 BGF-LIKE 2.  
 FT DOMAIN 234 492 SERINE PROTEASE.  
 FT ACT SITE 275 425 CHARGE RELAY SYSTEM.  
 FT ACT SITE 321 418 CHARGE RELAY SYSTEM.  
 FT ACT SITE 418 418 CHARGE RELAY SYSTEM.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.  
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 FT MOD\_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.

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CY 1 ANGFLXLRDGLXRCXKXLCFFXAFIFRNXXRTQPTWY 44  
 DB 41 ANSFLEEVKGNLERECLEBACSLBEAREVFEDAEQIDFERWXY 84

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 AC P00740;  
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 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).  
 GN F9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86000558; PubMed=2994716;  
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;  
 RT "Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).";  
 RL Biochemistry 24:3736-3750(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85190593; PubMed=3857619;  
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,  
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 RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84336100; PubMed=6329734;  
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 RX MEDLINE=8320788; PubMed=6667940;  
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 RP SEQUENCE OF 36-326 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=84300526; PubMed=6089357;  
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 RP SEQUENCE OF 290-359 FROM N.A.  
 RX MEDLINE=88127096; PubMed=3340835;  
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 RT "Genomic amplification with transcript sequencing.";  
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 RP SEQUENCE OF 444-461 FROM N.A.  
 RX MEDLINE=94054330; PubMed=8236150;  
 RA de la Salle C., Charmanier J.L., Baas M.J., Schwartz A.,  
 RT "A deletion located in the 3' non translated part of the factor IX gene responsible for mild haemophilia B.";  
 RL Thromb. Haemost. 70:370-371(1993).  
 RN [8]  
 RP SEQUENCE OF 47-461 (VARIANT NAGOVA).  
 RX MEDLINE=90078229; PubMed=2592373;  
 RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by tryptophan and its activation by alpha-chymotrypsin and rat mast cell chymase.";  
 RL J. Biol. Chem. 264:21257-21265(1989).  
 RN [9]  
 RP HYDROXYLATION OF ASP-110.  
 RX MEDLINE=83308813; PubMed=6688526;  
 RA McMullen B.A., Fujikawa K., Kistiel W.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation zymogens.";  
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
 RN [10]  
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=78194509; PubMed=659613;  
 RA di Scipio R.G., Kurachi K., Davie E.W.;  
 RT "Activation of human factor IX (Christmas factor).";  
 RL J. Clin. Invest. 61:1528-1538(1978).  
 RN [11]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185715; PubMed=6425296;  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RT "Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site that lacks gamma-carboxyglutamic acid.";  
 RL J. Biol. Chem. 259:5698-5704(1984).  
 RN [12]  
 RP ERRATUM.  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RL J. Biol. Chem. 260:2583-2583(1985).  
 RN [13]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE.  
 RX MEDLINE=86189947; PubMed=3009023;  
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
 RT "Defective propeptide processing of blood clotting factor IX caused by mutation of arginine to glutamine at position -4.";  
 RL Cell 45:343-348(1986).  
 RN [14]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20323(1989).  
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 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the first BGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).

RP [16] STRUCTURE OF CARBOHYDRATE ON SER-107.  
RX MEDLINE=92386094; PubMed=1517205;.  
RA Nishimura H., Takao T., Hase S., Shimomishi Y., Iwanaga S.;  
RT "human factor IX has a tetrascacharide O-glycosidically linked to  
RT serine 61 through the fucose residue."  
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RP PHOSPHORYLATION OF SER-114.  
RA Harris R.J., Papac D.I., Truong L., Smith K.J.;  
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX."  
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RL structure analysis, pp.50-50, Anney (1996).  
RN [18]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=20575397; PubMed=1113752;  
RA Arruda V.R., Hagstrom J.N., Delich J., Heiman-Patterson T.,  
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
RA Larson P.J., High K.A.;  
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RT human factor IX."  
RL Blood 97:130-138(2001).  
RN [19]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=95229607; PubMed=7713897;  
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
RT binding region of factor IX by two-dimensional NMR spectroscopy."  
RL J. Biol. Chem. 270:7980-7987(1995).  
RN [20]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=96032604; PubMed=7547952;  
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
RT domain of factor IX."  
RL Biochemistry 34:12126-12137(1995).  
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RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=96279169; PubMed=8663165;  
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
RA Furie B.;  
RT "Identification of the phospholipid binding site in the vitamin K-  
RT dependent blood coagulation protein factor IX."  
RL J. Biol. Chem. 271:16227-16236(1996).  
RN [22]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=97199336; PubMed=9047312;  
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RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
RT molecular dynamics simulation with initial Ca2+ positions determined  
RT by a genetic algorithm."  
RL Biochemistry 36:2132-2138(1997).  
RN [23]  
RP STRUCTURE BY NMR OF 91-133.  
RX MEDLINE=91308127; PubMed=1854745;  
RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney M.V.;  
RT "Sequence-specific 1H NMR assignments, secondary structure, and  
RT location of the calcium binding site in the first epidermal growth  
RT factor like domain of blood coagulation factor IX."  
RL Biochemistry 30:7402-7409(1991).  
RN [24]  
RP STRUCTURE BY NMR OF 92-130.  
RX MEDLINE=93264090; PubMed=1304885;  
RA Baton M., Notman D.G., Harvey T.S., Handford P.A., Mayhew M.,  
RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;  
RT "The three-dimensional structure of the first EGF-like module of  
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RL Protein Sci. 1:81-90(1992).  
RN [25]  
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
RX MEDLINE=95330802; PubMed=7606779;

RA Rao Z, Handford P, Mayhew M, Knott V, Brownlee G.G., Stuart D.  
RT "The structure of a Ca(2+)-binding epidermal growth factor-like  
RT domain: its role in protein-protein interactions." *J*  
RL *Cell* 82:131-141(1995).  
RN [26]  
RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

|                       |                 |                    |           |             |
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| Matches 17;           | Conservative 4; | Mismatches 22;     | Indels 0; | Gaps 0;     |

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RA  Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
RT  "The structure of a Ca(2+)-binding epidermal growth factor-like
RL  domain: its role in protein-protein interactions.";
RN  Cell 82:131-141(1995).
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GenCore version 5.1.4 p5 4578  
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OW protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(without alignments)  
196.288 Million cell updates/sec

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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL\_21:\*
- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4          | 98    | 51.3        | 460       | 11 | Q99PC6      |
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| 6          | 91    | 47.6        | 482       | 11 | Q63207      |
| 7          | 88    | 46.1        | 481       | 11 | Q54740      |
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| 9          | 88    | 46.1        | 481       | 11 | Q88947      |
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| 15         | 84    | 44.0        | 469       | 6  | Q9GMD9      |
| 16         | 83    | 43.5        | 49        | 6  | Q95ME8      |

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| 18 | 77   | 40.3 | 433  | 13 | Q90YK1 | Q90YK1 brachydanio  |
| 19 | 73   | 38.2 | 607  | 13 | Q91001 | Q91001 gallus gall  |
| 20 | 72   | 37.7 | 648  | 6  | Q29094 | Q29094 sus scrofa   |
| 21 | 71   | 37.2 | 399  | 11 | Q9CQW3 | Q9CQW3 mus musculus |
| 22 | 68.5 | 35.9 | 542  | 5  | Q8T613 | Q8T613 halocynthia  |
| 23 | 68   | 35.6 | 179  | 4  | Q8TAS3 | Q8TAS3 homo sapien  |
| 24 | 68   | 35.6 | 198  | 11 | Q8RI82 | Q8RI82 mus musculus |
| 25 | 67   | 35.1 | 650  | 4  | Q9NSD0 | Q9NSD0 homo sapien  |
| 26 | 67   | 35.1 | 650  | 4  | Q16519 | Q16519 homo sapien  |
| 27 | 56   | 29.3 | 25   | 11 | Q9QVH6 | Q9QVH6 rattus sp.   |
| 28 | 56   | 29.3 | 678  | 4  | Q14393 | Q14393 homo sapien  |
| 29 | 55   | 28.8 | 673  | 11 | Q61592 | Q61592 mus musculus |
| 30 | 55   | 28.8 | 674  | 11 | Q99K57 | Q99K57 mus musculus |
| 31 | 54   | 28.3 | 98   | 13 | P82807 | P82807 notechis sc  |
| 32 | 53   | 27.7 | 674  | 11 | Q63772 | Q63772 rattus sp.   |
| 33 | 51   | 26.7 | 130  | 12 | Q9DUB8 | Q9DUB8 tt virus. o  |
| 34 | 50   | 26.2 | 184  | 10 | Q9LVE1 | Q9LVE1 arabidopsis  |
| 35 | 49   | 25.7 | 1159 | 13 | Q9YIA6 | Q9YIA6 cyprinus ca  |
| 36 | 47.5 | 24.9 | 575  | 10 | Q94B17 | Q94B17 oryza sativ  |
| 37 | 47.5 | 24.9 | 608  | 10 | Q9XK36 | Q9XK36 medicago sa  |
| 38 | 47   | 24.6 | 249  | 5  | Q9VYS0 | Q9VYS0 drosophila   |
| 39 | 46.5 | 24.3 | 196  | 10 | Q04284 | Q04284 selaginella  |
| 40 | 46.5 | 24.3 | 567  | 10 | Q8W4J2 | Q8W4J2 arabidopsis  |
| 41 | 46.5 | 24.3 | 603  | 10 | Q9LPG7 | Q9LPG7 arabidopsis  |
| 42 | 46.5 | 24.3 | 606  | 10 | Q9SUG9 | Q9SUG9 arabidopsis  |
| 43 | 46.5 | 24.3 | 651  | 10 | Q8S218 | Q8S218 oryza sativ  |
| 44 | 46   | 24.1 | 204  | 17 | Q9HSQ0 | Q9HSQ0 halobacteri  |
| 45 | 45.5 | 23.8 | 431  | 10 | Q94EY5 | Q94EY5 arabidopsis  |

ALIGNMENTS

RESULT 1

| ID | Q96PQ8   | PRELIMINARY; | PRT; | 701 AA. |
|----|--|--------------|------|---------|
| AC | Q96PQ8:  |              |      |         |
| DT | 01-DEC-2001 (TRENBLREL. 19, Created)                                   |              |      |         |
| DT | 01-DEC-2001 (TRENBLREL. 19, Last sequence update)                      |              |      |         |
| DT | 01-MAR-2002 (TRENBLREL. 20, Last annotation update)                    |              |      |         |
| DE | Factor VII active site mutant immunocongulate.                         |              |      |         |
| OS | Homo sapiens (Human).  |              |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |              |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.            |              |      |         |
| NC | NCBI_TaxID=9606;   |              |      |         |
| RN | [1]  |              |      |         |
| RP | SEQUENCE FROM N.A.   |              |      |         |
| RX | MEDLINE=21477448; PubMed=11593034;                                     |              |      |         |
| RA | Hu Z., Garen A.;   |              |      |         |
| RT | "Targeting tissue factor on tumor vascular endothelial cells and tumor |              |      |         |
| RT | cells for immunotherapy in mouse models of prostatic cancer.";         |              |      |         |
| RL | Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).                   |              |      |         |
| DR | EMBL; AF272774; AAKS8686.1; -  |              |      |         |
| DR | InterPro: IPR000152; Aex hydroxyl.                                     |              |      |         |
| DR | InterPro: IPR000561; BGF-like.   |              |      |         |
| DR | InterPro: IPR007742; BGF_2.  |              |      |         |
| DR | InterPro: IPR003061; IG_MHC.   |              |      |         |
| DR | InterPro: IPR001254; Ser protease_Try.                                 |              |      |         |
| DR | InterPro: IPR000294; VitK_dep_GLA.                                     |              |      |         |
| DR | Pfam; PF00008; EGF_2.  |              |      |         |
| DR | Pfam; PF00594; Gla_1.  |              |      |         |
| DR | Pfam; PF00047; Ig_2.   |              |      |         |
| DR | Pfam; PF00089; trypsin_1.  |              |      |         |
| DR | SMART; SM00181; EGF_2.   |              |      |         |
| DR | PROSITE; PS00022; ASX_HYDROXYL; UNKNOWN_1.                             |              |      |         |
| DR | PROSITE; PS00020; EGF_1; UNKNOWN_1.                                    |              |      |         |
| DR | PROSITE; PS01186; EGF_2; UNKNOWN_1.                                    |              |      |         |
| DR | PROSITE; PS01187; EGF_CA; UNKNOWN_1.                                   |              |      |         |
| DR | PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.                        |              |      |         |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN_1.                                   |              |      |         |
| DR | PROSITE; PS00240; TRYPSIN_DOM; 1.                                      |              |      |         |

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 62.8%; Score 120; DB 4; Length 701;  
 Best Local Similarity 52.3%; Pred. No. 1.8e-13;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXKXLCSEFXAXFIFRXNXXRTQFWVSY 44  
 DB 61 ANAFLEELRPGSLERECQCSFEERAREIFKDAERTKLFWISY 104

## RESULT 2

ID 091WN8 PRELIMINARY; PRT; 460 AA.  
 AC 091WN8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Similar to protein C.  
 GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013896; AAH13896.1; -  
 DR MGI; MGI:97771; Proc.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; GLA; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
 DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SQ SEQUENCE 460 AA; 51818 MW; 011F26568FCC274 CRC64;

Query Match 54.5%; Score 104; DB 11; Length 460;  
 Best Local Similarity 45.5%; Pred. No. 1.1e-10;  
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXKXLCSEFXAXFIFRXNXXRTQFWVSY 44  
 DB 42 ANSFLLEMPGSLERECQCSFEERAREIFKQVNEDTLAWIKY 85

## RESULT 3

ID 061109 PRELIMINARY; PRT; 446 AA.  
 AC 061109;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Coagulation factor VII.  
 GN F7 OR FVII.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=96276538; PubMed=8701412;  
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";

CC Thromb. Haemost. 75:481-487(1996).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL; U44795; AAC52570.1; -  
 DR HSSP; P08709; 1FAK.  
 DR MEROPS; S01.215; -  
 DR MGI; MGI:109325; F7.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001064; Crystallin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; GLA; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.

DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;  
 KW Serine protease.  
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BBEDA6870 CRC64;

Query Match 53.9%; Score 103; DB 11; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 1.6e-10;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXKXLCSEFXAXFIFRXNXXRTQFWVSY 44  
 DB 42 ANSLEELMPGSLERECQCSFEERAREIFKSPKTKQFWIVY 85

## RESULT 4

ID 099PC6 PRELIMINARY; PRT; 460 AA.  
 AC 099PC6;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Anticoagulant protein C.  
 GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/  
 RA Korf I.;



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DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 47.6%; Score 91; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 2.9e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGLRXCRXXLCSFXAXAFIFRNXXRTROFWWSY 44
DB 41 ANSFEEFKGNLERECVEICSEFEAREVFEEDNEKTFEWMKY 84

RESULT 7
ID 054740 PRELIMINARY; PRT; 481 AA.
AC 054740;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F10.
OS Mus musculus (Mouse).
OC Plasmid pJ1uescripC.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=98454993; PubMed=9783672;
RA Heidtmann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RT Thromb. Res. 92:33-41(1998).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAAL0933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

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DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481
SQ SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D97AE CRC64;

Query Match 46.1%; Score 88; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1e-07;
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGLRXCRXXLCSFXAXAFIFRNXXRTROFWWSY 44
DB 41 ANSFEEFKGNLERECVEICSEFEAREVFEEDNEKTFEWMKY 84

RESULT 8
ID 099L32 PRELIMINARY; PRT; 481 AA.
AC 099L32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RA Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; GLABLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.

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DR PROSITE, PS01187; EGF\_CA; 1.  
DR PROSITE, PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE, PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE, PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE, PS00135; TRYPSIN\_SER; 1.  
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;  
KW Serine protease.  
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;  
Query Match 46.1%; Score 88; DB 11; Length 481;  
Best Local Similarity 31.8%; Pred. No. 1e-07;  
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 ANGFLXLRDGLKRXCRXXLCSPFXAFXIFRNXXRTQFWVS 44  
Db 41 ANSFEEFRKGNLERECMEICSYEEVREIFEDDEKTEKWTKY 84  
RESULT 9  
ID 088947 PRELIMINARY; PRT; 481 AA.  
AC 088947;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Coagulation factor X precursor.  
GN F10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;  
RX MEDLINE=98347933; PubMed=9684791;  
RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,  
RA Castellino F.J., Rosen E.D.;  
RT "Cloning and characterization of a cDNA encoding murine coagulation  
RT factor X";  
RL Thromb. Haemost. 80:87-91(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129S1;  
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;  
RT "Cloning and Characterization of the Murine Factor X Gene";  
RL Thromb. Haemost. 0:0-0(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
CC EMBL; AF087644; AAC36345.1; -;  
DR EMBL; AF211347; AAF22980.1; -;  
DR HSSP; P00742; 1XKA.  
DR MEROPS; S01.216; -;  
DR MGD; MGI:103107; F10.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF-2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SMO0179; EGF\_CA; 1.  
DR SMART; SMO0001; EGF\_like; 1.  
DR SMART; SMO0068; GLA; 1.  
DR SMART; SMO0020; Tryp\_Spc; 1.  
DR PROSITE, PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE, PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE, PS01186; EGF\_2; 2.

DR PROSITE, PS01187; EGF\_CA; 1.  
DR PROSITE, PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE, PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE, PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE, PS00135; TRYPSIN\_SER; 1.  
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;  
KW Serine protease; Signal.  
FT SIGNAL 1 40  
FT CHAIN 41 481  
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E5F9D271E CRC64;  
Query Match 46.1%; Score 88; DB 11; Length 481;  
Best Local Similarity 31.8%; Pred. No. 1e-07;  
Matches 14; Conservative 9; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 ANGFLXLRDGLKRXCRXXLCSPFXAFXIFRNXXRTQFWVS 44  
Db 41 ANSFEEFRKGNLERECMEICSYEEVREIFEDDEKTEKWTKY 84  
RESULT 10  
ID 015253 PRELIMINARY; PRT; 100 AA.  
AC 015253;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Thrombin precursor (Fragment).  
GN F2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87182874; PubMed=3471151;  
RA McGillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;  
RT "Recombinant genetic approaches to functional mapping of thrombin";  
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).  
DR EMBL; M33031; AAA60220.1; -;  
DR HSSP; P00733; 2EP1.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SMO0069; GLA; 1.  
DR PROSITE, PS00011; GLU\_CARBOXYLATION; 1.  
KW Signal.  
FT SIGNAL 1 43  
FT CHAIN 44 >100  
FT NON\_TER 100 100  
SQ SEQUENCE 100 AA; 11302 MW; FDESD0174E1F6FE CRC64;  
Query Match 44.5%; Score 85; DB 4; Length 100;  
Best Local Similarity 38.6%; Pred. No. 7.3e-08;  
Matches 17; Conservative 4; Mismatches 23; Indels 0; Gaps 0;  
Qy 1 ANGFLXLRDGLKRXCRXXLCSPFXAFXIFRNXXRTQFWVS 44  
Db 44 ANTFLEEVKGNLERECVEETCSYEAFEALESSTATDVFWAKY 87  
RESULT 11  
ID 014316 PRELIMINARY; PRT; 456 AA.  
AC 014316;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1999 (TRENBLrel. 11, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas  
DE disease, HAEMOPHILIA B) (Factor IX)).  
GN F9 OR FACTOR IX.  
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RN Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Bricet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SBR; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 44.5%; Score 85; DB 4; Length 456;
Best Local Similarity 39.5%; Pred. No. 3.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY 2 NGFLXXLRDGLKRCXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 44 SGTLSEFVGQNLRECEMEKCSFEAREVFEVNTERTTEFWKQY 86

RESULT 12
O95ND7 PRELIMINARY; PRT; 461 AA.
AC O95ND7;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxId=9598;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SBR; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 44.5%; Score 85; DB 6; Length 461;
Best Local Similarity 39.5%; Pred. No. 3.5e-07;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

OY 2 NGFLXXLRDGLKRCXXLCSPFXAXFIFRNXXRTROFWVS 44
DB 49 SGTLSEFVGQNLRECEMEKCSFEAREVFEVNTERTTEFWKQY 91

RESULT 13
O95ND6 PRELIMINARY; PRT; 461 AA.
AC O95ND6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=505;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.

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DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; gla\_1.  
DR Pfam: PF00089; trypsin\_1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE: PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KM Hydrolase; Serine protease.  
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 44.5%; Score 85; DB 6; Length 461;  
Best Local Similarity 39.5%; Pred. No. 3.5e-07;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

2 NGFLXLRDGLKRXCRXXLCSPXXAFIFRNXXRTROFWVS 44  
Db 49 SGKLEEFVQGNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 14  
ID Q9PTW7 PRELIMINARY; PRT; 608 AA.  
AC Q9PTW7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created).  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Prothrombin.  
GN OSEP.  
OS Struthio camelus (Ostrich).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;  
OC Struthio.  
OX NCBI\_TaxID=8801;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20579470; PubMed=1137455;  
RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;  
RT "Purification and characterization of ostrich prothrombin.";  
RL Int. J. Biochem. Cell Biol. 32:1151-1153(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
DR EMBL: AB028871; BAA89046.1; -.  
DR HSSP: P00734; IUVS.  
DR MEROPS: S01.217; -.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR000001; Kringie.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00594; gla\_1.  
DR Pfam: PF00051; kringie\_2.  
DR Pfam: PF00089; trypsin\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR PRINTS: PR00018; KRINGLE.  
DR ProDom: PD000395; Kringie\_2.  
DR SMART: SM00069; GLA\_1.  
DR SMART: SM00130; KR\_2.  
DR SMART: SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS00021; KRINGLE\_1; 2.  
DR PROSITE: PS50070; KRINGLE\_2; 2.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.

SQ SEQUENCE 608 AA; 69392 MW; 11B974B9A8E54EA2 CRC64;  
Query Match 44.5%; Score 85; DB 13; Length 608;  
Best Local Similarity 35.7%; Pred. No. 4.7e-07;  
Matches 15; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

3 GFLXLRDGLKRXCRXXLCSPXXAFIFRNXXRTROFWVS 44  
Db 47 GFLEMLKGNLERECLEETCIYEAFALSTARTTEFWMSKY 88

RESULT 15  
ID Q9GMD9 PRELIMINARY; PRT; 469 AA.  
AC Q9GMD9;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Coagulation factor X.  
OS Ornithorhynchus anatinus (Duckbill platypus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.  
OX NCBI\_TaxID=9258;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21015017; PubMed=1132153;  
RA Poorafshar M., Aveakogh M., Munday B., Hellman L.;  
RT "Identification and structural analysis of four serine proteases in a monotreme, the platypus, Ornithorhynchus anatinus.";  
RL Immunogenetics 52:19-28(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
DR EMBL: AF275654; AAC00453.1; -.  
DR HSSP: P00742; IXKB.  
DR MEROPS: S01.216; -.  
DR InterPro: IPR000152; Asx\_hydroxyL.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF\_Like.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_CA.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; gla\_1.  
DR Pfam: PF00089; trypsin\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00179; EGF\_CA; 1.  
DR SMART: SM00001; EGF\_Like; 2.  
DR SMART: SM00069; GLA\_1.  
DR SMART: SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_CA; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 44.0%; Score 84; DB 6; Length 469;  
Best Local Similarity 34.1%; Pred. No. 5.5e-07;  
Matches 15; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

1 ANGFLXLRDGLKRXCRXXLCSPXXAFIFRNXXRTROFWVS 44  
Db 41 ANSLFEELKGNLERECMEETCSYEAREVEFDTKNEFWNIY 84

Search completed: March 19, 2003, 15:13:41  
Job time : 47.3125 secs

GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10ASP28PHE\_4  
Sequence: 1 ANGFLXLRDGSILKRCXCRXX.....XXAFXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
|------------|-------|-------------|--------|----|------------------|
| 1          | 155   | 81.2        | 44     | 3  | US-08-955-636-4  |
| 2          | 129   | 67.5        | 44     | 3  | US-08-955-636-28 |
| 3          | 127   | 66.5        | 44     | 3  | US-08-955-636-27 |
| 4          | 123   | 64.4        | 44     | 3  | US-08-955-636-26 |
| 5          | 120   | 62.8        | 44     | 3  | US-08-955-636-3  |
| 6          | 120   | 62.8        | 406    | 1  | US-08-293-778-24 |
| 7          | 120   | 62.8        | 406    | 1  | US-08-295-411-5  |
| 8          | 120   | 62.8        | 406    | 1  | US-08-955-471-5  |
| 9          | 120   | 62.8        | 406    | 5  | PCT-US92-10242-5 |
| 10         | 120   | 62.8        | 444    | 1  | US-08-475-845-2  |
| 11         | 120   | 62.8        | 444    | 2  | US-08-327-690-2  |
| 12         | 120   | 62.8        | 444    | 2  | US-08-660-289-2  |
| 13         | 120   | 62.8        | 444    | 2  | US-08-537-807-2  |
| 14         | 120   | 62.8        | 444    | 2  | US-08-871-003-2  |
| 15         | 120   | 62.8        | 444    | 3  | US-08-464-233-2  |
| 16         | 120   | 62.8        | 444    | 4  | US-09-189-607-2  |
| 17         | 120   | 62.8        | 444    | 4  | US-09-378-907-2  |
| 18         | 120   | 62.8        | 444    | 5  | PCT-US94-05779-2 |
| 19         | 120   | 62.8        | 466    | 1  | US-07-882-202A-4 |
| 20         | 120   | 62.8        | 466    | 1  | US-08-021-615A-4 |
| 21         | 120   | 62.8        | 466    | 1  | US-08-321-777-4  |
| 22         | 120   | 62.8        | 466    | 4  | US-09-009-217-14 |
| 23         | 120   | 62.8        | 466    | 4  | US-09-009-656-14 |
| 24         | 120   | 62.8        | 466    | 5  | PCT-US93-04493-4 |
| 25         | 119   | 62.3        | 44     | 3  | US-08-955-636-30 |
| 26         | 116   | 60.7        | 44     | 3  | US-08-955-636-29 |
| 27         | 106   | 55.5        | 41     | 1  | US-08-229-280-4  |

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|----|----|------|-----|---|------------------|--------------------|
| 28 | 96 | 50.3 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appli  |
| 29 | 96 | 50.3 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appli  |
| 30 | 96 | 50.3 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appli  |
| 31 | 96 | 50.3 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appli  |
| 32 | 96 | 50.3 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appli  |
| 33 | 96 | 50.3 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appli  |
| 34 | 96 | 50.3 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appli  |
| 35 | 94 | 49.2 | 44  | 3 | US-08-955-636-23 | Sequence 23, Appli |
| 36 | 94 | 49.2 | 44  | 3 | US-08-955-636-25 | Sequence 25, Appli |
| 37 | 91 | 47.6 | 44  | 3 | US-08-955-636-35 | Sequence 35, Appli |
| 38 | 91 | 47.6 | 44  | 3 | US-08-295-411-3  | Sequence 3, Appli  |
| 39 | 91 | 47.6 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appli  |
| 40 | 91 | 47.6 | 448 | 2 | PCT-US92-10068-1 | Sequence 1, Appli  |
| 41 | 91 | 47.6 | 448 | 5 | PCT-US92-10242-3 | Sequence 33, Appli |
| 42 | 91 | 47.6 | 448 | 5 | US-08-955-636-13 | Sequence 22, Appli |
| 43 | 90 | 47.1 | 44  | 3 | US-08-955-636-22 | Sequence 24, Appli |
| 44 | 89 | 46.6 | 44  | 3 | US-08-955-636-24 |                    |
| 45 | 89 | 46.6 | 44  | 3 | US-08-955-636-24 |                    |

## ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      81.2%; Score 155; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 9e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1 ANGFLXLRDGSILKRCXCRXXLCSPFXAXIFRNXXRTQFWVSY 44
Db      1 ANGFLXLRDGSILKRCXCRXXLCSPFXAXIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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/ NAME/KEY: MOD\_RES  
/ LOCATION: (0)...(0)  
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-28

Query Match 67.5%; Score 129; DB 3; Length 44;  
Best Local Similarity 77.3%; Pred. No. 2, 6e-15;  
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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DB 1 ANAFLLXLRGSLRXKCKXXQCSFXAXIFKDXAKRTKLFWISY 44

RESULT 3  
US-08-955-636-27  
/ Sequence 27, Application US/08955636A  
/ Patent No. 6017882  
/ GENERAL INFORMATION:  
/ APPLICANT: Neissestuen, Gary  
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
/ FILE REFERENCE: 09531/002001  
/ CURRENT APPLICATION NUMBER: US/08/955,636A  
/ CURRENT FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 35  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 27  
/ LENGTH: 44  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (0)...(0)  
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-27

Query Match 66.5%; Score 127; DB 3; Length 44;  
Best Local Similarity 77.3%; Pred. No. 5, 7e-15;  
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 ANGLXXLRDGLRXXCRXXLCSPXXAFXIFRNXXRTROFWISY 44  
DB 1 ANAFLLXLRDGLRXXKCKXXQCSFXAXIFKDXAKRTKLFWISY 44

RESULT 4  
US-08-955-636-26  
/ Sequence 26, Application US/08955636A  
/ Patent No. 6017882  
/ GENERAL INFORMATION:  
/ APPLICANT: Neissestuen, Gary  
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
/ FILE REFERENCE: 09531/002001  
/ CURRENT APPLICATION NUMBER: US/08/955,636A  
/ CURRENT FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 35  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 26  
/ LENGTH: 44  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (0)...(0)  
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-26

Query Match 64.4%; Score 123; DB 3; Length 44;  
Best Local Similarity 75.0%; Pred. No. 2, 8e-14;  
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 ANGLXXLRDGLRXXCRXXLCSPXXAFXIFRNXXRTROFWISY 44  
DB 1 ANAFLLXLRGSLRXKCKXXQCSFXAXIFKDXAKRTKLFWISY 44

RESULT 5  
US-08-955-636-3  
/ Sequence 3, Application US/08955636A  
/ Patent No. 6017882  
/ GENERAL INFORMATION:  
/ APPLICANT: Neissestuen, Gary  
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
/ FILE REFERENCE: 09531/002001  
/ CURRENT APPLICATION NUMBER: US/08/955,636A  
/ CURRENT FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 35  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 3  
/ LENGTH: 44  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (0)...(0)  
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-3

Query Match 62.8%; Score 120; DB 3; Length 44;  
Best Local Similarity 75.0%; Pred. No. 9e-14;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGLXXLRDGLRXXCRXXLCSPXXAFXIFRNXXRTROFWISY 44  
DB 1 ANAFLLXLRGSLRXKCKXXQCSFXAXIFKDXAKRTKLFWISY 44

RESULT 6  
US-08-293-778-24  
/ Sequence 24, Application US/08293778  
/ Patent No. 5580560  
/ GENERAL INFORMATION:  
/ APPLICANT: Nicolsen, Else M.  
/ APPLICANT: Bjorn, Soren E.  
/ APPLICANT: Wiberg, Finn C.  
/ APPLICANT: Woodbury, Richard  
/ TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa  
/ NUMBER OF SEQUENCES: 26  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560ch America, Inc.  
/ STREET: 405 Lexington Avenue, 62nd Floor  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: United States of America  
/ ZIP: 10174-6201  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/293,778  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/104,509  
/ FILING DATE:  
/ APPLICATION NUMBER: DK 3235/87  
/ FILING DATE: 25-JUN-1987  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/434,149  
/ FILING DATE: 13-NOV-1989  
/ PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129,224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 62.8%; Score 120; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 9,2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRDGLXRXCRXXLCSPXXAFYIPNXXRTQFWVS 44  
Db 1 ANAFILYLRPGSLRYCKYQCSFYARIFPDARTKLFWISY 44

RESULT 7  
US-08-295-411-5  
Sequence 5, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263,0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note="Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note="Factor VII Heavy Chain"  
US-08-295-411-5

Query Match 62.8%; Score 120; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 9,2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRDGLXRXCRXXLCSPXXAFYIPNXXRTQFWVS 44  
Db 1 ANAFLEBLRPGSLERECKEQQCSFEAREIFPDARTKLFWISY 44

RESULT 8  
US-08-955-471-5  
Sequence 5, Application US/0895471  
Patent No. 5968751  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,471  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/295,411  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263,0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153...406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-955-471-5

Query Match 62.8%; Score 120; DB 2; Length 406;  
Best Local Similarity 52.3%; Pred. No. 9.2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXRLCSFXXAFXFRNXXRTQFWWSY 44  
DB 1 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 9  
PCT-US92-10242-5  
Sequence 5, Application PC/TUS9210242

GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Meesters, Rolf  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: For Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 North Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10242  
FILING DATE: 19921118

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRO472P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"

FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
PCT-US92-10242-5

Query Match 62.8%; Score 120; DB 5; Length 406;  
Best Local Similarity 52.3%; Pred. No. 9.2e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ANGFLXXLRDGSIXRCXRLCSFXXAFXFRNXXRTQFWWSY 44  
DB 1 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 10  
US-08-475-845-2  
Sequence 2, Application US/08475845  
Patent No. 5788965

GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stuart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,845  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,690  
FILING DATE: 24-OCT-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Palmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-475-845-2

Query Match 62.8%; Score 120; DB 1; Length 444;  
Best Local Similarity 52.3%; Pred. No. 1e-12;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXRLCSFXXAFXFRNXXRTQFWWSY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 11  
US-08-327-690-2



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; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match          62.8%; Score 120; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 1e-12;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match          62.8%; Score 120; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 1e-12;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 62.8%; Score 120, DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 1e-12;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXXLCSPXXAFIFRNXXRTROFWVS 44  
DB 39 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTKLFWIS 82

RESULT 14  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5997864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 62.8%; Score 120, DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 1e-12;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXXLCSPXXAFIFRNXXRTROFWVS 44  
DB 39 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTKLFWIS 82

RESULT 15  
US-08-464-233-2  
Sequence 2, Application US/08464233  
Patent No. 6039944  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,233  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-233-2

Query Match 62.8%; Score 120, DB 3; Length 444;  
Best Local Similarity 52.3%; Pred. No. 1e-12;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRDGSIXRCXXLCSPXXAFIFRNXXRTROFWVS 44  
DB 39 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTKLFWIS 82

Search completed: March 19, 2003, 15:16:21  
Job time: 10.75 secs

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds  
(without alignments)  
280.876 Million cell updates/sec

Title: 10ASP28PHE\_4  
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Sequence: 1 ANGLFLXXLRDGLXRCXCRXX.....XXAFXIFRNXXRTQFWVSY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

## Database :

Published Applications\_AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PC7\_NEM\_PUB pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEM\_PUB pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEM\_PUB pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
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| 1          | 120   | 62.8        | 406    | 9  | US-10-109-498-1    |
| 2          | 89    | 46.6        | 419    | 9  | US-10-182-263-6    |
| 3          | 88    | 46.1        | 419    | 9  | US-10-182-263-1    |
| 4          | 88    | 46.1        | 419    | 9  | US-10-182-263-3    |
| 5          | 88    | 46.1        | 419    | 9  | US-10-182-263-4    |
| 6          | 88    | 46.1        | 419    | 9  | US-10-182-263-5    |
| 7          | 88    | 46.1        | 419    | 9  | US-09-978-917A-4   |
| 8          | 88    | 46.1        | 461    | 9  | US-10-182-263-2    |
| 9          | 88    | 46.1        | 461    | 9  | US-09-978-917A-2   |
| 10         | 85    | 44.5        | 415    | 10 | US-09-118-748-2    |
| 11         | 85    | 44.5        | 461    | 10 | US-10-132-829-5    |
| 12         | 85    | 44.5        | 461    | 10 | US-09-884-901-3    |
| 13         | 67    | 35.1        | 96     | 9  | US-09-759-130B-313 |
| 14         | 67    | 35.1        | 209    | 9  | US-09-759-130B-310 |
| 15         | 67    | 35.1        | 226    | 9  | US-09-759-130B-310 |
| 16         | 50    | 26.2        | 98     | 9  | US-09-759-130B-356 |
| 17         | 50    | 26.2        | 208    | 9  | US-09-759-130B-355 |
| 18         | 50    | 26.2        | 225    | 9  | US-09-759-130B-353 |
| 19         | 41    | 21.5        | 125    | 10 | US-09-925-301-1491 |

|    |    |      |      |    |                    |                    |
|----|----|------|------|----|--------------------|--------------------|
| 20 | 41 | 21.5 | 1438 | 12 | US-10-006-091-1    | Sequence 1, Appli  |
| 21 | 41 | 21.5 | 1438 | 12 | US-10-047-257-1    | Sequence 1, Appli  |
| 22 | 41 | 21.5 | 1471 | 12 | US-10-095-718-2    | Sequence 2, Appli  |
| 23 | 41 | 21.5 | 1663 | 10 | US-09-875-519A-22  | Sequence 22, Appli |
| 24 | 41 | 21.5 | 2332 | 9  | US-09-957-641-2    | Sequence 2, Appli  |
| 25 | 41 | 21.5 | 2351 | 9  | US-10-132-829-4    | Sequence 4, Appli  |
| 26 | 40 | 20.9 | 484  | 10 | US-09-801-368-334  | Sequence 334, App  |
| 27 | 39 | 20.4 | 197  | 9  | US-10-076-622-516  | Sequence 516, App  |
| 28 | 39 | 20.4 | 197  | 12 | US-10-007-805-516  | Sequence 516, App  |
| 29 | 39 | 20.4 | 232  | 9  | US-10-076-622-517  | Sequence 517, App  |
| 30 | 39 | 20.4 | 232  | 12 | US-10-007-805-517  | Sequence 517, App  |
| 31 | 39 | 20.4 | 233  | 10 | US-09-867-550-1024 | Sequence 1024, Ap  |
| 32 | 39 | 20.4 | 243  | 9  | US-09-938-418-7    | Sequence 7, Appli  |
| 33 | 39 | 20.4 | 243  | 9  | US-10-045-992-4    | Sequence 4, Appli  |
| 34 | 39 | 20.4 | 243  | 9  | US-10-063-547-122  | Sequence 122, App  |
| 35 | 39 | 20.4 | 243  | 9  | US-10-174-590-366  | Sequence 366, App  |
| 36 | 39 | 20.4 | 243  | 9  | US-10-176-758-366  | Sequence 366, App  |
| 37 | 39 | 20.4 | 243  | 9  | US-10-063-616-122  | Sequence 122, App  |
| 38 | 39 | 20.4 | 243  | 9  | US-10-175-737-366  | Sequence 366, App  |
| 39 | 39 | 20.4 | 243  | 9  | US-10-063-502-122  | Sequence 122, App  |
| 40 | 39 | 20.4 | 243  | 9  | US-10-076-622-514  | Sequence 514, App  |
| 41 | 39 | 20.4 | 243  | 9  | US-10-173-706-366  | Sequence 366, App  |
| 42 | 39 | 20.4 | 243  | 9  | US-10-175-738-366  | Sequence 366, App  |
| 43 | 39 | 20.4 | 243  | 9  | US-10-175-752-366  | Sequence 366, App  |
| 44 | 39 | 20.4 | 243  | 9  | US-10-176-482-366  | Sequence 366, App  |
| 45 | 39 | 20.4 | 243  | 9  | US-10-176-757-366  | Sequence 366, App  |

## ALIGNMENTS

```
RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908a1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      62.8% Score 120, DB 9; Length 406;
Best Local Similarity 75.0%; Pred. No. 5.2e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Cy 1 ANGLFLXXLRDGLXRCXCRXXLCSPFXAXIFRNXXRTQFWVSY 44
Db 1 ANGLFLXXLRDGLXRCXCRXXLCSPFXAXIFRNXXRTQFWVSY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030023354a1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
```

```
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          46.1%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY      1 ANGFLXXLRDGLRXCRXXLCSPFXAFXIFRNXXRTROFW 41
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANSFLELRHGSLERECIEICDFEEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          46.1%; Score 88; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY      1 ANGFLXXLRDGLRXCRXXLCSPFXAFXIFRNXXRTROFW 41
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANSFLELRHGSLERECIEICDFEEAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          46.1%; Score 88; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY      1 ANGFLXXLRDGLRXCRXXLCSPFXAFXIFRNXXRTROFW 41
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANSFLELRHGSLERECIEICDFEEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          46.1%; Score 88; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY      1 ANGFLXXLRDGLRXCRXXLCSPFXAFXIFRNXXRTROFW 41
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANSFLELRHGSLERECIEICDFEEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-182-263-5

Query Match 46.1%; Score 88; DB 9; Length 419;  
Best Local Similarity 46.3%; Pred. No. 1.9e-07;  
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRDGLRXCRXXLCSPXXAFIFRNXXRTQFW 41  
DB 1 ANSFLELRHSSLRECEIEICDFEAKEIFQVDDTLAFW 41

RESULT 7

US-09-978-917A-4  
Sequence 4, Application US/09978917A  
Publication No. US20030027299A1  
GENERAL INFORMATION:

APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219us310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978,917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-917A-4

Query Match 46.1%; Score 88; DB 9; Length 419;  
Best Local Similarity 46.3%; Pred. No. 1.9e-07;  
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRDGLRXCRXXLCSPXXAFIFRNXXRTQFW 41  
DB 1 ANSFLELRHSSLRECEIEICDFEAKEIFQVDDTLAFW 41

RESULT 8

US-10-182-263-2  
Sequence 2, Application US/10182263  
Publication No. US20030022354A1  
GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E  
APPLICANT: Jones, Bryan E  
APPLICANT: Ginnell, Brian W  
TITLE OF INVENTION: PROTEIN C DERIVATIVES  
FILE REFERENCE: X-13611  
CURRENT APPLICATION NUMBER: US/10/182,263  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: 60/181948  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: 60/189199  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-182-263-2

Query Match 46.1%; Score 88; DB 9; Length 461;  
Best Local Similarity 46.3%; Pred. No. 2.1e-07;  
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRDGLRXCRXXLCSPXXAFIFRNXXRTQFW 41  
DB 43 ANSFLELRHSSLRECEIEICDFEAKEIFQVDDTLAFW 83

RESULT 9

US-09-978-917A-2  
Sequence 2, Application US/09978917A  
Publication No. US20030027299A1  
GENERAL INFORMATION:

APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219us310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978,917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens

NAME/KEY: SIGNAL  
LOCATION: (1)...(42)  
FEATURE:  
NAME/KEY: CHAIN  
LOCATION: (43)...(461)  
US-09-978-917A-2

Query Match 46.1%; Score 88; DB 9; Length 461;  
Best Local Similarity 46.3%; Pred. No. 2.1e-07;  
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRDGLRXCRXXLCSPXXAFIFRNXXRTQFW 41  
DB 43 ANSFLELRHSSLRECEIEICDFEAKEIFQVDDTLAFW 83

RESULT 10

US-09-118-748-2  
Sequence 2, Application US/09118748A  
Patent No. US20020031799A1  
GENERAL INFORMATION:

APPLICANT: Chang, Jinli  
APPLICANT: Stafford, Darrel W.  
TITLE OF INVENTION: Factor IX Antithrombotic Factor with Increased Clotting  
TITLE OF INVENTION: Activily  
FILE REFERENCE: 5470-183  
CURRENT APPLICATION NUMBER: US/09/118,748A  
CURRENT FILING DATE: 1998-07-17  
EARLIER APPLICATION NUMBER: 60/053,571  
EARLIER FILING DATE: 1997-07-21  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-118-748-2

Query Match 44.5%; Score 85; DB 10; Length 415;  
Best Local Similarity 39.5%; Pred. No. 6.3e-07;  
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXLRDGLRXCRXXLCSPXXAFIFRNXXRTQFW 44  
DB 3 SGKLEFPVQGNLERCEMEKCSFEARREVENTERTEFWQY 45

RESULT 11

US-10-132-829-5  
Sequence 5, Application US/10132829  
Publication No. US20030044982A1  
GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R  
APPLICANT: Hoshijima, Masahiko  
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII  
FILE REFERENCE: 6627-P41170

```

CURRENT APPLICATION NUMBER: US/10/132,829
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,314
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-132-829-5

Query Match
Best Local Similarity 44.5%; Score 85; DB 9; Length 461;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXXLRDGSILRXCRXXLCSEFXAXFIRNXXRTQFWWSY 44
Db 49 SGLKEEFVQGNLERECMEKCSFEAREVFEENTERTEFFWQY 91

RESULT 12
Sequence 3, Application US/09884901
Patent No. US2002076798A1
GENERAL INFORMATION:
APPLICANT: Miao, Carol
APPLICANT: Kay, Mark
TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
FILE REFERENCE: US09-1-17396
CURRENT APPLICATION NUMBER: US/09/884,901
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/212,902
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 461
TYPE: PRT
ORGANISM: Homosapien
US-09-884-901-3

Query Match
Best Local Similarity 44.5%; Score 85; DB 10; Length 461;
Matches 17; Conservative 4; Mismatches 22; Indels 0; Gaps 0;

QY 2 NGFLXXLRDGSILRXCRXXLCSEFXAXFIRNXXRTQFWWSY 44
Db 49 SGLKEEFVQGNLERECMEKCSFEAREVFEENTERTEFFWQY 91

RESULT 13
US-09-759-130B-313
Sequence 313, Application US/09759130B
Publication No. US2003002279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Frazer, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirt, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: US5.
FILE REFERENCE: MP100-5350NMIM
CURRENT APPLICATION NUMBER: US/09/759,130B

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CURRENT FILING DATE: 2002-09-16
PRIORITY APPLICATION NUMBER: US 09/479,249
PRIORITY FILING DATE: 2000-01-07
PRIORITY APPLICATION NUMBER: US 09/559,497
PRIORITY FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: US 09/578,063
PRIORITY FILING DATE: 2000-05-24
PRIORITY APPLICATION NUMBER: US 09/333,159
PRIORITY FILING DATE: 1999-06-14
PRIORITY APPLICATION NUMBER: US 09/596,194
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 09/342,364
PRIORITY FILING DATE: 1999-06-29

Query Match          35.1%; Score 67; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 0.0002;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY      11  GSLKRXCRXXLCSFFXAFIFRNXXRTQFVSVY 44
          |||:|||||:|:|:|
DB       46  GNLERECNELCNVEAREIFVDEDKTIAFQGEY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: MP100-535ONMIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIORITY APPLICATION NUMBER: US 09/479,249
PRIORITY FILING DATE: 2000-01-07
PRIORITY APPLICATION NUMBER: US 09/559,497
PRIORITY FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: US 09/578,063
PRIORITY FILING DATE: 2000-05-24
PRIORITY APPLICATION NUMBER: US 09/333,159
PRIORITY FILING DATE: 1999-06-14
PRIORITY APPLICATION NUMBER: US 09/596,194
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 09/342,364
PRIORITY FILING DATE: 1999-06-29

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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-130B-312

Query Match      35.1%; Score 67; DB 9; Length 209;
Best Local Similarity 38.2%; Pred. No. 0.00043;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      11 GSIKXCRXXLCSFYXAFIFRNXXRTROFWVS 44
Db      46 GNLRECNBELCNYEAREIFVDEDKTIAFWQY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-5350AM1H
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
; US-09-759-130B-310

Query Match      35.1%; Score 67; DB 9; Length 226;
Best Local Similarity 38.2%; Pred. No. 0.00046;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      11 GSIKXCRXXLCSFYXAFIFRNXXRTROFWVS 44
Db      63 GNLRECNBELCNYEAREIFVDEDKTIAFWQY 96
```

Search completed: March 20, 2003, 13:30:19  
Job time : 8.375 secs

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds  
(without alignments)  
186.869 Million cell updates/sec

Title: 10Gln28Glu\_4  
Perfect score: 189  
Sequence: 1 ANGFLXLRQGSILXRRCRX.....XXAEXIFRNXXRTQFWVSY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A\_Geneseq\_101002:\*  
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 156   | 82.5        | 44     | 20    | AAV18306    |
| 2          | 156   | 82.5        | 44     | 22    | AAV18306    |
| 3          | 127   | 67.2        | 44     | 20    | AAV18302    |
| 4          | 126   | 66.7        | 44     | 20    | AAV18310    |
| 5          | 124   | 65.6        | 44     | 20    | AAV18311    |
| 6          | 123   | 65.1        | 44     | 20    | AAV18305    |
| 7          | 123   | 65.1        | 44     | 22    | AAV18395    |
| 8          | 123   | 65.1        | 401    | 22    | AAV18470    |
| 9          | 123   | 65.1        | 401    | 22    | AAV18471    |
| 10         | 123   | 65.1        | 406    | 14    | AAV18574    |

|    |     |      |     |    |          |                    |
|----|-----|------|-----|----|----------|--------------------|
| 11 | 123 | 65.1 | 406 | 18 | AAV14509 | Modified blood coa |
| 12 | 123 | 65.1 | 406 | 18 | AAV14510 | Modified blood coa |
| 13 | 123 | 65.1 | 406 | 22 | AAV77745 | Human factor VIIa  |
| 14 | 123 | 65.1 | 406 | 22 | AAV52171 | Human FVII SEQ ID  |
| 15 | 123 | 65.1 | 406 | 22 | AAV52172 | Mammalian expresse |
| 16 | 123 | 65.1 | 406 | 22 | AAV52181 | Human FVII mutant  |
| 17 | 123 | 65.1 | 406 | 22 | AAV52182 | Human FVII mutant  |
| 18 | 123 | 65.1 | 406 | 22 | AAV52183 | Human FVII mutant  |
| 19 | 123 | 65.1 | 406 | 22 | AAV52184 | Human FVII mutant  |
| 20 | 123 | 65.1 | 406 | 22 | AAV52185 | Human FVII mutant  |
| 21 | 123 | 65.1 | 406 | 22 | AAV52186 | Human FVII mutant  |
| 22 | 123 | 65.1 | 406 | 22 | AAV52187 | Human FVII mutant  |
| 23 | 123 | 65.1 | 406 | 22 | AAV52188 | Wild-type human bl |
| 24 | 123 | 65.1 | 406 | 22 | AAV52189 | Mutant blood coagu |
| 25 | 123 | 65.1 | 406 | 22 | AAV52190 | Mutant blood coagu |
| 26 | 123 | 65.1 | 406 | 22 | AAV52191 | Mutant blood coagu |
| 27 | 123 | 65.1 | 406 | 22 | AAV52192 | Mutant blood coagu |
| 28 | 123 | 65.1 | 406 | 23 | AAV52193 | Human coagulation  |
| 29 | 123 | 65.1 | 406 | 23 | AAV52194 | Human coagulation  |
| 30 | 123 | 65.1 | 406 | 23 | AAV52195 | Human coagulation  |
| 31 | 123 | 65.1 | 406 | 23 | AAV52196 | Human coagulation  |
| 32 | 123 | 65.1 | 406 | 23 | AAV52197 | Human coagulation  |
| 33 | 123 | 65.1 | 406 | 23 | AAV52198 | Human coagulation  |
| 34 | 123 | 65.1 | 406 | 23 | AAV52199 | Human coagulation  |
| 35 | 123 | 65.1 | 406 | 23 | AAV52200 | Human coagulation  |
| 36 | 123 | 65.1 | 406 | 23 | AAV52201 | Human coagulation  |
| 37 | 123 | 65.1 | 406 | 23 | AAV52202 | Human coagulation  |
| 38 | 123 | 65.1 | 406 | 23 | AAV52203 | Human coagulation  |
| 39 | 123 | 65.1 | 406 | 23 | AAV52204 | Human coagulation  |
| 40 | 123 | 65.1 | 406 | 23 | AAV52205 | Human coagulation  |
| 41 | 123 | 65.1 | 406 | 23 | AAV52206 | Human coagulation  |
| 42 | 123 | 65.1 | 406 | 23 | AAV52207 | Human coagulation  |
| 43 | 123 | 65.1 | 406 | 23 | AAV52208 | Human coagulation  |
| 44 | 123 | 65.1 | 406 | 23 | AAV52209 | Human coagulation  |
| 45 | 123 | 65.1 | 406 | 23 | AAV52210 | Human coagulation  |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| AAV18306 | AAV18306 standard; peptide; 44 AA.                          |
| XX       | XX  |
| AC       | AAV18306;   |
| XX       | XX  |
| DT       | 17-AUG-1999 (first entry)                                   |
| XX       | XX  |
| DE       | Bovine factor VII GLA domain.                               |
| XX       | XX  |
| KW       | GLA domain; vitamin K-dependent protein; clotting disorder; |
| KM       | therapy.  |
| XX       | XX  |
| OS       | Bos taurus.   |
| XX       | XX  |
| PH       | Key   |
| FT       | Misc-difference 1..44 Location/Qualifiers                   |
| FT       | note="Xaa= gamma-carboxyglutamic acid, or glutamic acid"    |
| PD       | W09920767-A1.   |
| PD       | 29-APR-1999.  |
| PF       | 20-OCT-1998; 98WO-US22152.                                  |
| PR       | 23-OCT-1997; 97US-0955636.                                  |
| PA       | (MINU) UNIV MINNESOTA.                                      |
| XX       | XX  |
| PI       | Neisestuen GL;  |
| XX       | XX  |
| DR       | WPI, 1999-288309/24.  |

XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
PS Disclosure: Page 15; 86pp; English.  
XX  
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
  
Query Match 82.5%; Score 156; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 1.7e-18;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ANGFLXXLRQGSIXRCRXXLCSPXXAEXIFRNXXRTROPFWSY 44  
Db 1 ANGFLXXLRPGSLXRCRXXLCSPXXAHXIFRNXXRTROPFWSY 44  
  
RESULT 2  
ID AAB36396 standard; peptide; 44 AA.  
AC AAB36396;  
XX  
DT 27-FEB-2001 (first entry)  
XX  
DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.  
XX  
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;  
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;  
KW factor X; prothrombin; enhanced membrane binding affinity;  
KW clot formation; thrombolytic; haemostatic; bleeding disorder;  
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;  
KW liver disease.  
XX  
OS Bos taurus.  
XX  
PN WO200066753-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US11416.  
XX  
PR 29-APR-1999; 99US-0302239.  
XX  
PA (MINU) UNIV MINNESOTA.  
XX  
PI Nelsestuen GL;  
XX  
PS MPI; 2001-007226/01.  
XX  
DR Novel vitamin K-dependent polypeptide useful for treating clotting  
PT disorders such as thrombosis and hemophilia, comprises modified  
PT gamma-carboxy glutamic acid domain that enhances membrane binding  
PT affinity -  
XX  
PS Disclosure: Page 12; 81pp; English.  
XX  
CC The present invention describes a vitamin K-dependent polypeptide (I)  
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having  
CC at least one amino acid substitution, that enhances membrane binding  
CC affinity and the activity of the polypeptide relative to a corresponding  
CC native vitamin K-dependent polypeptide and inhibits clot formation.  
CC (I) can have thrombolytic and haemostatic activities, and can be used  
CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified  
CC GLA domain is useful for increasing clot formation and for treating a  
CC bleeding disorder, including thrombosis and clotting disorders such as  
CC haemophilia A, haemophilia B and liver disease. The present sequence  
CC represents a wild type bovine factor VII GLA domain sequence, given in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 44 AA;  
  
Query Match 82.5%; Score 156; DB 22; Length 44;  
Best Local Similarity 95.5%; Pred. No. 1.7e-18;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ANGFLXXLRQGSIXRCRXXLCSPXXAEXIFRNXXRTROPFWSY 44  
Db 1 ANGFLXXLRPGSLXRCRXXLCSPXXAHXIFRNXXRTROPFWSY 44  
  
RESULT 3  
ID AAY18302 standard; peptide; 44 AA.  
AC AAY18302;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..44  
FT "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
XX  
PN WO920767-A1.  
XX  
PD 29-APR-1999.  
XX  
PF 20-OCT-1998; 98WO-US22152.  
XX  
PR 23-OCT-1997; 97US-0955636.  
XX  
PA (MINU) UNIV MINNESOTA.  
XX  
PI Nelsestuen GL;  
XX  
PS MPI; 1999-288309/24.  
XX  
DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
PS Claim 11; Page 81; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
  
Query Match 67.2%; Score 127; DB 20; Length 44;  
Best Local Similarity 77.3%; Pred. No. 1.1e-13;  
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;



|    |  |
|----|--|
| XX | 29-APR-1999.   |
| PD |  |
| XX |  |
| XX | 20-OCT-1998; 98WO-US22152.   |
| PF |  |
| XX |  |
| PR | 23-OCT-1997; 97US-0955636.   |
| XX |  |
| XX | (MINU ) UNIV MINNESOTA.  |
| PA |  |
| XX |  |
| XX | Nelsetuen GL;  |
| PI |  |
| XX | WPI; 1999-288309/24.   |
| DR |  |
| XX |  |
| XX | Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic      |
| PT | acid domain, useful for treating clotting disorders                      |
| XX |  |
| XX |  |
| XX | Disclosure; Page 15; 86pp; English.                                      |
| PS |  |
| XX |  |
| CC | This sequence is the factor VII GUA (gamma-carboxyglutamic acid)         |
| CC | domain. The invention relates to a vitamin K-dependent polypeptide       |
| CC | comprising a modified GUA domain containing an amino acid substitution   |
| CC | which enhances membrane binding of the modified polypeptide as compared  |
| CC | to the native polypeptide. The polypeptide is used to treat a clotting   |
| CC | disorder by decreasing or increasing clot formation. Modification of the |
| CC | GUA domain results in a protein which has enhanced membrane binding      |
| CC | affinity as compared to the native protein.                              |
| XX |  |
| XX |  |
| XX | Sequence 44 AA;  |
| XQ |  |

|                       |                |                 |          |           |
|-----------------------|----------------|-----------------|----------|-----------|
| Query Match           | 65.1%          | Score 123       | DB 20    | Length 44 |
| Best Local Similarity | 75.0%          | Pred. No. 5e-13 |          |           |
| Matches 33            | Conservative 5 | Mismatches 6    | Indels 0 | Gaps 0    |

```
QY      1 ANGFLXXLRQGSLXRXCRXXLCSFXXAEXI FRNXXRTRQFWVSY 44
        |||||:::||:::||::||
Db       1 ANAFLLXLRPGSLXRXCKKXQCFSFXAXRI FKDAAXRTKLFWISY 44
```

RESULT 7  
AAB36395  
ID AAB36395 standard; peptide; 44 AA.

|    |                           |
|----|---------------------------|
| AC | AAB36395;                 |
| XX |                           |
| DT | 27-FEB-2001 (first entry) |

Human factor VII gamma-carboxylutamic acid domain SEQ ID NO:3.

KM Vitamin K-dependent protein; factor VII; protein C; GIIa domain;  
KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;  
KM factor X; prothrombin; enhanced membrane binding affinity;  
KM clot formation; thrombolytic; haemostatic; bleeding disorder;  
KM thrombosis; clotting disorder; haemophilia A; haemophilia B;  
KM liver disease.

OS Homo sapiens.

PN WO200066753-A2

PD 09-NOV-2000

PF 28-APR-2000; 2000WO-US12416.

PR 29-APR-1999; 99US-0302239.

PA (MINU ) UNIV MINNESOTA.

PI Nelsestuen GL;

DR WPI; 2001-007226/01.

Novel vitamin K-dependent polypeptide useful for treating clotting disorders such as thrombosis and hemophilia, comprises modified

PT gamma-carboxy glutamic acid domain that enhances membrane binding  
PT affinity -  
XX  
PS Disclosure, Page 12, 81pp, English.

CC The present invention describes a vitamin K-dependent polypeptide (I)  
CC comprising a modified gamma-carboxy glutamic acid (Gla) domain having  
CC at least one amino acid substitution, that enhances membrane binding  
CC affinity and the activity of the polypeptide relative to a corresponding  
CC native vitamin K-dependent polypeptide and inhibits clot formation.  
CC (I) can have thrombolytic and haemostatic activities, and can be used  
CC as an inhibitor of clot formation. (I) is useful for decreasing clot  
CC formation in a mammal, a factor VII or factor IX containing a modified  
CC Gla domain is useful for increasing clot formation and for treating a  
CC bleeding disorder, including thrombosis and clotting disorders such as  
CC haemophilia A, haemophilia B and liver disease. The present sequence  
CC represents a wild type human factor VII Gla domain sequence, given in  
CC the exemplification of the present invention.

SQ Sequence 44 AA;

|                       |                 |                  |           |            |
|-----------------------|-----------------|------------------|-----------|------------|
| Query Match           | 65.1%           | Score 123;       | DB 22;    | Length 44; |
| Best Local Similarity | 75.0%           | Pred. No. 5e-13; |           |            |
| Matches 33;           | Conservative 5; | Mismatches 6;    | Indels 0; | Gaps 0;    |

```
Oy      1 ANGFLXXLRQGS�XRXCRRXLCSFXXAEXIFRNXRXTRQFWVSY    44  
         ||||| :||| :||| :||| :||| :||| :||| :|||  
Db      1 ANAFLLXLRPGSLXRXCCKXQCFFXXARXIFKDAAXRTKLFWISY   44
```

|          |                                     |
|----------|-------------------------------------|
| RESULT 8 |                                     |
| AAB84870 |                                     |
| ID       | AAB84870 standard; Protein; 401 AA. |

AC AAB84870;

|    |             |               |
|----|-------------|---------------|
| DT | 31-JUL-2001 | (first entry) |
|----|-------------|---------------|

DE Mutant blood coagulant factor VII (FVII-31).

KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;

XX

Synthetic.

| FH | key | Location/Qualifiers |
|----|-----|---------------------|
|    |     |                     |

FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp  
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33

XX

PT the treatment of hemophilia -

PS Claim 14; Page 20-21; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII

CC sequence is one such mutant FVII: VII-11. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.

```
XX Sequence 401 AA;
SQ
Query Match 65.1%; Score 123; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 4.1e-12;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGLKRXCRXXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 1 ANAFLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 9
AAB84871
ID AAB84871 standard; Protein; 401 AA.
XX
AC AAB84871;
XX
DT 31-JUL-2001 (first entry)
XX
DE Mutant blood coagulant factor VII (FVII-39).
XX
KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
mutant; mutcin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 235..239
FT /note= "Wild-type Val-Pro-Gly-Thr substituted by
FT Asp-Arg-Lys-Thr-Leu"
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
FT
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 65.1%; Score 123; DB 22; Length 401;
Best Local Similarity 52.3%; Pred. No. 4.1e-12;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGLKRXCRXXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 1 ANAFLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 10
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX
AC AAR35764;
XX
XX 24-SEP-1993 (first entry)
XX
DT Factor VII (VII).
XX
DE PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KM Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
exosite; catalytic activity.
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FH Region 1..152
FH /note= "Factor VII light chain"
FH Region 153..406
FH /note= "Factor VII heavy chain"
FH Peptide 374..388
FH /note= "exosite 1"
FH Peptide 290..310
FH /note= "exosite 2"
FH Peptide 290..310
FH /note= "pref. PC polypeptide; claim 2, page 136"
FH Peptide 374..388
FH /note= "pref. PC polypeptide; claim 2, page 136"
FH Peptide 289..304
FH /note= "pref. PC polypeptide; claim 4, page 137"
FH Peptide 290..304
FH /note= "pref. PC polypeptide; claim 4, page 137"
FH Peptide 245..266
FH /note= "claim 9, page 138-139 describes an antibody
that reacts with Factor VII; fragments
289-304, 290-304, 290-310, 374-388 and
400-414 but not with fragment 245-266"
XX
XX WO9309804-A.
XX
XX 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US10242.
XX
XX 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Griffiin JH, Masters RM;
XX
XX WPI; 1993-182244/22.
XX
XX Serine protease derived-polypeptide(s) and anti-peptide
PT antibodies - for inhibiting coagulation and assaying for the
PT presence of serine protease in fluid samples
XX
XX Disclosure; Page 133-135; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit
CC coagulation (they prevent binding of serine protease to natural
CC substrates), esp. when admin. to give an intravascular blood
CC concn. of 0.1-100 (pref. 0.5-10) microm.
CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
CC in the specification but have not yet been added to the SEQUENCE
CC LISTING.
XX
XX Sequence 406 AA;
SQ
Query Match 65.1%; Score 123; DB 14; Length 406;
Best Local Similarity 52.3%; Pred. No. 4.2e-12;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGLKRXCRXXLCSPFXAEXIFRNXXRTQFWVSY 44
Db 1 ANAFLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
```





KW Factor VIIa; human; shock heat treatment; protein stability;  
 KW protein manufacture; protein conformation; mutant; mutein.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT Active-site 193  
 FT Active-site /note= "Member of the factor VIIa catalytic triad"  
 FT Active-site 242  
 FT Active-site /note= "Member of the factor VIIa catalytic triad"  
 FT Active-site 344  
 FT Active-site /note= "Member of the factor VIIa catalytic triad"  
 FT Misc-difference 344  
 FT /label= Gly, Met, Thr  
 FT /note= "Preferably Ala. Wild type Ser"  
 XX  
 XX  
 PN WO200177141-A1.  
 PD 18-OCT-2001.  
 XX  
 XX  
 PF 06-APR-2001; 2001WO-DK00234.  
 XX  
 PR 06-APR-2000; 2000DK-0000573.  
 PR 17-APR-2000; 2000US-197650P.  
 XX  
 XX (NOVO ) NOVO NORDISK AS.  
 PA  
 PI Matchiesen F;  
 DR WPI; 2001-657162/75.  
 XX  
 XX  
 PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition  
 PT involves a shock heat treatment -  
 XX  
 XX  
 PS Disclosure; Page -; 22pp; English.  
 CC The invention describes a method of stabilising a polypeptide involving  
 CC shock heat treatment of the polypeptide. The method is useful in a  
 CC pharmaceutical composition, in the industrial or large scale method of  
 CC manufacturing a polypeptide, also as a unit operation during preparation,  
 CC purification, recovery and/or formulation of polypeptides. The shock heat  
 CC treatment improves the protein stability without substantial loss of  
 CC biological activity. The method can be applied to change polypeptide  
 CC conformation in a very fast and non-invasive manner. The polypeptide  
 CC formed is stable. The method is also useful for decreasing the  
 CC association of the polypeptide. This sequence represents a modified  
 CC human factor VIIa protein, mutated at the catalytic site, described  
 CC in the invention.  
 CC Note: This sequence does not appear in the specification but has  
 CC been obtained using information given in the invention.  
 CC  
 SQ Sequence 406 AA;  
 Query Match 65.1%; Score 123; DB 22; Length 406;  
 Best Local Similarity 52.3%; Pred. No. 4.2e-12;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANGELXLLRQGSIXRXCRLXLSFXXAEXIFRXXXRTQFVWSY 44  
 DB 1 AANAFLERLPGSLRCKEQQCFEERAREIFKDAERTKLFWISY 44  
 RESULT 14  
 AAM52171  
 ID AAM52171 standard; Protein; 406 AA.  
 XX  
 AC AAM52171;  
 XX  
 DT 07-FEB-2002 (first entry)  
 XX  
 DE Human FVII SEQ ID NO 1.  
 XX

KW Factor VII; FVII. Factor VIIa; FVIIa; haemostatic; thrombolytic;  
 KW cardiatic; hepatocytic; cerebroprotective; haemophilia; liver disease;  
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT Misc-difference 6  
 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 7  
 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 14  
 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 16  
 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
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 FT /label= Glu, OTHER  
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 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 29  
 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 35  
 FT /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 52  
 FT /note= "O-glycosylated"  
 FT Modified-site 60  
 FT /note= "O-glycosylated"  
 FT Modified-site 145  
 FT /note= "N-glycosylated"  
 FT Cleavage-site 152..153  
 FT /note= "proteolytic cleavage site converting FVII zymogen  
 FT to an activated form, comprising two chains  
 FT linked by a single disulphide bridge"  
 FT Modified-site 322  
 FT /note= "N-glycosylated"  
 XX  
 XX  
 PN WO200158935-A2.  
 PD 16-AUG-2001.  
 XX  
 XX  
 PF 12-FEB-2001; 2001WO-DK00094.  
 XX  
 PR 11-FEB-2000; 2000DK-0000218.  
 PR 18-OCT-2000; 2000DK-0001558.  
 XX  
 XX (MAXY-) MAXYGEN APS.  
 PA  
 PI Andersen KV, Pedersen AH, Bornaes C;  
 DR WPI; 2001-581807/65.  
 DR N-PSDB; AA199982.  
 XX  
 PT New conjugate, useful for treating Factor VIIa related diseases or  
 PT disorders such as haemophilia, liver disease, myocardial infarction and  
 PT deep-vein thrombosis, comprises non-polypeptide group covalently  
 PT attached to polypeptide group -  
 XX  
 XX  
 XX Claim 1; Page 81-83; 89pp; English.  
 XX



CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group,  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.

**SQ**      **Sequence**      **406 AA;**

|                       |        |              |      |            |     |        |      |
|-----------------------|--------|--------------|------|------------|-----|--------|------|
| Query Match           | 123;   | Score        | 123; | DB         | 22; | length | 406; |
| Best Local Similarity | 75.0%; | Pred.        | No.  | 4.2e-12;   |     |        |      |
| Matches               | 33;    | Conservative | 5;   | Mismatches | 6;  | Indels | 0;   |
|                       |        |              |      |            |     | Gaps   | 0;   |

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QY      1  ANGFLXXLRQGS.LXRRCXXLCSFXXAEXI.FRNXXRTPQFWISY 44
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Db      1  ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRRTLFWISY 44

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RESULT 15  
AAM52172

| ID  | AA  | 52172 | standard; Protein; 406 AA. |
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| 4   | 4   | 4     | 4                          |
| 5   | 5   | 5     | 5                          |
| 6   | 6   | 6     | 6                          |
| 7   | 7   | 7     | 7                          |
| 8   | 8   | 8     | 8                          |
| 9   | 9   | 9     | 9                          |
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| 38  | 38  | 38    | 38                         |
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| 43  | 43  | 43    | 43                         |
| 44  | 44  | 44    | 44                         |
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| 46  | 46  | 46    | 46                         |
| 47  | 47  | 47    | 47                         |
| 48  | 48  | 48    | 48                         |
| 49  | 49  | 49    | 49                         |
| 50  | 50  | 50    | 50                         |
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| 79  | 79  | 79    | 79                         |
| 80  | 80  | 80    | 80                         |
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| 87  | 87  | 87    | 87                         |
| 88  | 88  | 88    | 88                         |
| 89  | 89  | 89    | 89                         |
| 90  | 90  | 90    | 90                         |
| 91  | 91  | 91    | 91                         |
| 92  | 92  | 92    | 92                         |
| 93  | 93  | 93    | 93                         |
| 94  | 94  | 94    | 94                         |
| 95  | 95  | 95    | 95                         |
| 96  | 96  | 96    | 96                         |
| 97  | 97  | 97    | 97                         |
| 98  | 98  | 98    | 98                         |
| 99  | 99  | 99    | 99                         |
| 100 | 100 | 100   | 100                        |

AC AAM52172;

DT 07-FEB-2002. (first entry)

**Mammalian expressed human FVII SEQ ID NO 3.**

KW Factor VII; FVII, Factor VIIa; FVIIa, haemostatic; thrombolytic;  
 KW cardiatic; hepatotrophic; cerebroprotective; haemophilia; liver disease  
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.

OS . Homo sapiens.

| FH | Key    | Location/Qualifiers |
|----|--------|---------------------|
| FM | 346133 | 315                 |

/note= "O-glycosylated"

FT /note= "O-glycosylated"

/note= "N-glycosylated"

FT /note= "proteolytic cleavage site converting FVII zymogen

FT 1000

Et

PN WO200158935-A2.

PD 16-AUG-2001.

PF 12-FEB-2001; 2001WO-DK00094.

PR 11-FEB-2000; 2000DK-0000218.

XX  
XX

XXXXX XXXXXX

2 XX

2000

DR N-PSDB; AAI99983.

PT New conjugate, useful for treating Factor VIIa related diseases or  
PT disorders such as haemophilia, liver disease, myocardial infarction and  
PT deep-vein thrombosis, comprises non-polypeptide group covalently  
PT attached to polypeptide group -

PS Disclosure; Page 85-86; 89pp; English

CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional *in vivo* half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.

**SQ Sequence 406 AA;**

|                       |              |                   |                |             |
|-----------------------|--------------|-------------------|----------------|-------------|
| Query Match           | 65.1%        | Score 123;        | DB 22;         | Length 406; |
| Best Local Similarity | 52.3%        | Pred. NC 4.2e-12; |                |             |
| Matches 23;           | Conservative | 5;                | Mismatches 16; | Indels 0;   |
|                       |              |                   |                | Gaps 0;     |

```

OY      1  ANGFLXLRQGSILXRXKRRXXLCSFXXAEIYFRNXKXRTQFWISY 44
      |||||  :  |||  ::  ||  ::||
DB      1  ANAFLEELRPGSLEREKEEQCSFPEARLIFKQERTYLFWISY 44

```

Search completed: March 19, 2003, 14:51:12  
Job time : 31.4375 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10GLN28GLU\_4  
Perfect score: 189  
Sequence: 1 ANGFLXXLRQSLKRCRCRX.....XXAEXIFRNXXRTQFMVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 149   | 78.8        | 407    | 1 KPB07  | coagulation factor |
| 2          | 131   | 69.3        | 443    | 2 I46932 | coagulation factor |
| 3          | 123   | 65.1        | 466    | 1 KFHU7  | coagulation factor |
| 4          | 109   | 57.7        | 461    | 1 JX0210 | protein C (activat |
| 5          | 108   | 57.1        | 461    | 1 S18994 | protein C (activat |
| 6          | 97    | 51.3        | 456    | 1 KXBO   | protein C (activat |
| 7          | 96    | 50.8        | 482    | 1 EXRT   | coagulation factor |
| 8          | 96    | 50.8        | 488    | 1 EXHU   | coagulation factor |
| 9          | 95    | 50.3        | 492    | 1 EXBO   | coagulation factor |
| 10         | 93    | 49.2        | 461    | 1 KFHU   | coagulation factor |
| 11         | 93    | 49.2        | 461    | 1 KXHU   | protein C (activat |
| 12         | 89    | 47.1        | 416    | 1 KPB0   | coagulation factor |
| 13         | 87    | 46.0        | 475    | 1 EXCH   | coagulation factor |
| 14         | 84    | 44.4        | 452    | 1 A30351 | coagulation factor |
| 15         | 84    | 44.4        | 459    | 2 JQ0419 | coagulation factor |
| 16         | 84    | 42.3        | 642    | 2 S53433 | plasma protein S p |
| 17         | 78    | 41.3        | 622    | 1 TBHU   | thrombin (EC 3.4.2 |
| 18         | 75    | 39.7        | 617    | 2 S10511 | thrombin (EC 3.4.2 |
| 19         | 75    | 39.7        | 618    | 2 A35827 | thrombin (EC 3.4.2 |
| 20         | 75    | 39.7        | 642    | 2 S53434 | plasma protein S p |
| 21         | 75    | 39.7        | 676    | 1 KXHUS  | plasma protein S p |
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| 23         | 71    | 37.6        | 646    | 2 S38819 | plasma protein S p |
| 24         | 69    | 36.5        | 422    | 1 KXHUZ  | plasma protein S p |
| 25         | 69    | 36.5        | 625    | 1 TBBO   | thrombin (EC 3.4.2 |
| 26         | 69    | 36.5        | 675    | 1 KXRTS  | plasma protein S p |
| 27         | 65    | 34.4        | 396    | 1 KXB0Z  | plasma protein S p |
| 28         | 64    | 33.9        | 678    | 2 B48089 | growth arrest-spec |
| 29         | 63    | 33.3        | 673    | 2 A48089 | growth arrest-spec |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 62   | 32.8 | 675  | 1 KXMS   | plasma protein S p  |
| 31 | 61   | 32.3 | 674  | 2 I55476 | growth potential in |
| 32 | 56   | 29.6 | 413  | 1 VHVNH  | nucleoprotein - in  |
| 33 | 53   | 28.0 | 605  | 1 M1WLB  | E1 protein - bovin  |
| 34 | 53   | 28.0 | 620  | 1 M1WLB2 | E1 protein - bovin  |
| 35 | 49.5 | 26.2 | 594  | 2 D84859 | probable MAP kinase |
| 36 | 49.5 | 26.2 | 603  | 2 C96575 | probable MAP kinase |
| 37 | 48.5 | 25.7 | 576  | 2 G96763 | probable DNA topoi  |
| 38 | 45   | 23.8 | 687  | 2 T08528 | hypothetical prote  |
| 39 | 45   | 22.8 | 619  | 2 AE2449 | conserved hypotet   |
| 40 | 43   | 22.8 | 371  | 2 T08759 | protein kinase SLT  |
| 41 | 43   | 22.8 | 484  | 2 S43737 | hypothetical prote  |
| 42 | 43   | 22.8 | 1101 | 2 T26919 | hypothetical prote  |
| 43 | 43   | 22.8 | 1217 | 2 T21403 | unknown protein [i  |
| 44 | 42.5 | 22.5 | 706  | 2 D86441 | hypothetical prote  |
| 45 | 42.5 | 22.5 | 907  | 2 T15792 | hypothetical prote  |

## ALIGNMENTS

## RESULT 1

KPB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; MUID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TRK>

R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co.

A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCN>

A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; MUID:89213999; PMID:3149637

A:Contents: annotation

A:Note: structure and location of covalently bound carbohydrate

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; Bgf homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F.1-152/Product: coagulation factor VIIa light chain #status experimental <MA>

F.1-44/Domain: Gla domain homology (fragment) <GLA>

F.50-81/Domain: Bgf homology <BGF>

F.91-127/Domain: Bgf homology <BGF>

F.153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F.153-387/Domain: trypsin homology <TRY>

F.67-114,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F.17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F.152/Binding site: carbohydrate (Ser) (covalent) #status experimental

F.145-203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F.145-153/Cleavage site: Arg-11e (coagulation factor XIra) #status experimental

F.193-242,344/active site: His, Asp, Ser #status predicted

F.1290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match 78.8%; Score 149; DB 1; Length 407;

Best Local Similarity 68.2%; Pred. No. 3.8e-18;

Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy 1 ANGFLXXLRQGLRXCRXXLCSPFXAEXIFRNXXRTQRFWSY 44
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Db 1 ANGFLEELRPGSLERCKEELCSFEAREVFQSTERTKQFWISY 44

RESULT 2
coagulation factor VII - rabbit
146932
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #ext_change 12-Feb-1999
A:Accession: 146932
R:Brothers, A.B.; Clarke, B.U.; Sheffield, W.P.; Blajchman, M.A.
  Thromb. Res. 69, 231-238, 1993
A>Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: 146932; PMID:93190306; PMID:8383365
A:Accession: 146932
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:S56300; NID:g266294; PID:g266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <GLA>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match 69.3%; Score 131; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 5, 8e-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQGLRXCRXXLCSPFXAEXIFRNXXRTQRFWSY 44
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 40 ANGFLEELRPGSLERCKEELCSFEAREVFQSTERTKQFWISY 83

RESULT 3
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
KHU7
C:Species: Homo sapiens (man)
C>Date: 19-May-1989 #sequence_revision 19-May-1994 #ext_change 08-Dec-2000
A:Accession: A28322; A23819; A31186; B31186; S63554
R:O'Hara, P.U.; Grant, F.U.; Haldeman, B.A.; Gray, C.L.; Inley, M.Y.; Hagen, F.S.; Wirtz
  Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A>Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; PMID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OHA>
A:Cross-references: GB:J02933; NID:g180333; PIDN:AAAS1983.1; PID:g180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.U.; Saari, G.C.; Woodbury, R.G.; Hart, C
  Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A>Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; PMID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M13322; NID:g182799; PIDN:AA88040.1; PID:g182801
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
  Biochemistry 27, 7785-7793, 1988
A>Title: Amino acid sequence and posttranslational modifications of human factor VII-a
A:Reference number: A90539; PMID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
  J. Biol. Chem. 266, 11051-11057, 1991
A>Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations
A:Reference number: A40529; PMID:91250411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Pedersen, E.; Petersen, L.C.

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Eur. J. Biochem. 234, 293-300, 1995
A>Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A:Reference number: S63524; PMID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Intron: 22/1, 44/1, 97/3, 106/1, 144/1, 191/1, 227/3, 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
coagulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:61-104/Domain: Gla domain homology <GLA>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA>
F:110-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66,67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F:112,120/Binding site: carboxylate (Ser) (covalent) #status experimental
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-Ile (coagulation factor X1a) #status experimental
F:253,302,404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 65.1%; Score 123; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 1, 5e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQGLRXCRXXLCSPFXAEXIFRNXXRTQRFWSY 44
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 ANGFLEELRPGSLERCKEELCSFEAREVFQSTERTKQFWISY 104

RESULT 4
protein C (activated) (EC 3.4.21.69) precursor - mouse
JX0210
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 16-Jun-2000
A:Accession: JX0210
R:Tade, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
  J. Biochem. 111, 491-495, 1992
A>Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; PMID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
s.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <GLA>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <RC>
F:91-130/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VTR>

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F:212-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
 F:214,220,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:253,259,402/Active site: His, Asp, Ser #status predicted

Query Match 57.7%; Score 109; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 6,4e-11;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGSILXRXCRXXLCSPYXAEIIFNNXXRTROFWVS 44  
 Db 42 ANSFLEENRPGSLERECMEICDFEAAQEIFQVEDTLAFWIKY 85

RESULT 5  
 S18994  
 protein C (activated) (EC 3.4.21.69) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
 C:Accession: S18994; S24312  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 A:Description: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S18994  
 A:Accession: S18994  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OK>

A:Cross-references: EMBL:X64336; NID:G56962; PIDD:CAA5617.1; PID:G56963  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 Biochim. Biophys. Acta 1131, 329-332, 1992  
 A:Title: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S24312; MUID:92329550; PMID:1627650  
 A:Accession: S24312  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OK>

A:Cross-references: EMBL:X64336; NID:G56962; PIDD:CAA5617.1; PID:G56963  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:127-85/Domain: Gla domain homology <GLA>  
 F:133-42/Domain: propeptide #status predicted <PRO>  
 F:43-461/Product: protein C #status predicted <PRC>  
 F:91-130/Domain: EGF homology <EG1>  
 F:133-174/Domain: EGF homology <EG2>  
 F:213-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-320,239-253,373-387,398-426/Disulfide bonds: #stat  
 F:215,221,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 57.1%; Score 108; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 6,4e-11;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGSILXRXCRXXLCSPYXAEIIFNNXXRTROFWVS 44  
 Db 42 ANSFLEENRPGSLERECMEICDFEAAQEIFQVEDTLAFWIKY 85

RESULT 6  
 KXBO  
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)  
 M:Alternate names: autoprothrombin IIA; plasma protein C  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Nov-1980 #sequence\_revision 17-Mar-1997 #text\_change 16-Jul-1999  
 C:Accession: A26250; A18385; A18386; A00928  
 R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100

A:Accession: A26250

A:Molecule type: mRNA

A:Residues: 1-456 <LON>

R:Stenflo, J.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982

A:Title: Amino acid sequence of the light chain of bovine protein C.

A:Reference number: A18385; MUID:83007325; PMID:6896876

A:Accession: A18385

A:Molecule type: protein

A:Residues: 40-194 <PER>

A:Note: 82-Lys was also found

R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.

A:Reference number: A19316; MUID:83169769; PMID:6572939

A:Contents: annotation; revision to residue 110

R:Stenflo, J.; Fernlund, P.

J. Biol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine protein C.

A:Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386

A:Molecule type: protein

A:Residues: 197-454, 'PV' <STE>

R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.

J. Biol. Chem. 258, 5548-5553, 1983

A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless p

A:Reference number: A37541; MUID:8521513; PMID:6304092

A:Contents: annotation; activation; calcium binding

R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.

J. Biol. Chem. 258, 5554-5560, 1983

A:Title: Structural changes required for activation of protein C are induced by Ca2+ bind

A:Reference number: A37542; MUID:8521514; PMID:6406503

A:Contents: annotation; activation; calcium binding

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re-

B. C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c-

bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti-

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro-

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>

F:124-83/Domain: Gla domain homology <GLA>

F:30-39/Domain: propeptide #status predicted <PRO>

F:40-194/Product: protein C light chain #status experimental <LCH>

F:98-128/Domain: EGF homology <EG1>

F:137-172/Domain: EGF homology <EG2>

F:197-456/Product: protein C heavy chain #status experimental <HCH>

F:197-210/Domain: activation peptide #status experimental <AP>

F:211-440/Domain: trypsin homology <TRY>

F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #statu

F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #statu

F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:252,258,337/Active site: His, Asp, Ser #status predicted

F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.3%; Score 97; DB 1; Length 456;  
 Best Local Similarity 43.2%; Pred. No. 5,4e-09;  
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGSILXRXCRXXLCSPYXAEIIFNNXXRTROFWVS 44  
 Db 40 ANSFLEENRPGSLERECMEICDFEAAQEIFQVEDTLAFWFSFY 83

RESULT 7  
 EXRT  
 coagulation factor Xa (EC 3.4.21.6) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #exec\_change 08-Dec-2000  
 C/Accession: S49075; J04670; PS0191; PS0190; 162745  
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 Thromb. Res. 80, 63-73, 1995  
 A>Title: Evidence for competition between vitamin K-dependent clotting factors for intra  
 A/Reference number: A58498; MUID:96093366; PMID:8578533  
 A/Accession: S49075  
 A/Molecule type: mRNA  
 A/Residues: 1-482 <STA1>  
 A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
 A/Note: submitted to the EMBL Data Library, June 1994  
 A/Note: neither the complete nucleic acid sequence nor the complete translation are show  
 R/Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
 Gene 169, 269-273, 1996  
 A>Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
 A/Reference number: J04670; MUID:96194815; PMID:8647460  
 A/Accession: J04670  
 A/Molecule type: mRNA  
 A/Residues: 1-482 <STA2>  
 A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
 A/Experimental source: Cos-1 cell  
 R/Enjyoji, K.; Miyazaki, K.; Kato, H.  
 U. Biochem. 109, 890-898, 1991  
 A>Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
 A/Reference number: PS0190; MUID:92041742; PMID:1718949  
 A/Accession: PS0191  
 A/Molecule type: protein  
 A/Residues: 41-58 'X', 60-65 <ENU1>  
 A/Accession: PS0190  
 A/Molecule type: protein  
 A/Residues: 183-186, 'X', 188-207 <ENU2>  
 R/Murkawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A>Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
 A/Reference number: I46196; MUID:94222160; PMID:8168596  
 A/Accession: I62745  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 295-383, 'G', 385-455 <MUR>  
 A/Cross-references: GB:D1215; NID:G415309; PIDN:BA04756.1; PID:G455396  
 C/Function: A:descriptions: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A/pathway: blood coagulation  
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:124-80/Domain: propeptide #status predicted <PRO>  
 F:125-84/Domain: Gla domain homology <Gla>  
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F:90-121/Domain: EGF homology <EGF>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:183-231/Domain: activation peptide #status predicted <APT>  
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F:232-460/Domain: trypsin homology <TRY>  
 F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
 F:57-82, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 338-243, 259-275, 388-402, 41  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:187/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F:218/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:231-232/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:274, 320, 417/Active site: His, Asp, Ser #status predicted

Query Match 50.8%; Score 96; DB 1; Length 482;  
 Best Local Similarity 36.4%; Pred. No. 8.5e-09;  
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGELXXLRQSGSLRXCRXXLCGFFXAXEXIFRNXXRTROFVWS 44  
 DB 41 ANSFPEIRKGNLERECVERICSEFEAREVFEDEKTEFMNKT 84

RESULT 8  
EXNU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human  
 N/Alternate names: Stuart factor  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
 C/Accession: A24478; J00917; A44485; A25853; A22208; A21284; A20362; S39415; I54051; A00  
 R/Leytus, S.P.; Foeter, D.C.; Kurachi, K.; Davie, E.W.  
 Biochemistry 25, 5098-5102, 1986  
 A>Title: Gene for human Factor X: a blood coagulation factor whose gene organization is  
 A/Reference number: A24478; MUID:87026600; PMID:3768336  
 A/Accession: A24478  
 A/Molecule type: DNA  
 A/Residues: 1-488 <LEY>  
 A/Cross-references: GB:I29433; GB:M14327; NID:G459809; PIDN:AAA52764.1; PID:G182831  
 R/Meslier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.  
 Gene 99, 291-294, 1991  
 A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag  
 A/Reference number: J00917; MUID:91216473; PMID:1902434  
 A/Accession: J00917  
 A/Molecule type: mRNA  
 A/Residues: 1-488 <MES>  
 A/Cross-references: GB:M57285; NID:G182389; PIDN:AAA52421.1; PID:G182390  
 R/Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.  
 J. Biol. Chem. 267, 7395-7401, 1992  
 A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagul  
 A/Reference number: A42485; MUID:92218390; PMID:1313796  
 A/Accession: A42485  
 A/Molecule type: DNA  
 A/Residues: 1-15 <MIA>  
 A/Experimental source: liver  
 A/Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)  
 R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
 Gene 41, 311-314, 1986  
 A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
 A/Reference number: A25853; MUID:86221713; PMID:3011603  
 A/Accession: A25853  
 A/Molecule type: mRNA  
 A/Residues: 19-284, 'E', 289-488 <KAU>  
 A/Cross-references: GB:M2613; NID:G180335; PIDN:AAA51984.1; PID:G180336  
 R/Pung, M.R.; Hay, C.W.; MacCullliver, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
 A>Title: Characterization of an almost full-length cDNA coding for human blood coagulati  
 A/Reference number: A22208; MUID:85216545; PMID:3582420  
 A/Accession: A22208  
 A/Molecule type: mRNA  
 A/Residues: 13-441, 'S', 443-488 <FUN>  
 A/Cross-references: GB:K03194; NID:G182840; PIDN:AAA52490.1; PID:G182841  
 R/Leytus, S.P.; Chung, D.W.; Kistel, W.; Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
 A>Title: Characterization of a cDNA coding for human factor X.  
 A/Reference number: A21284; MUID:84222026; PMID:6587384  
 A/Accession: A21284  
 A/Molecule type: mRNA  
 A/Residues: 13-284, 'E', 289-488 <LE2>  
 A/Cross-references: GB:K01886  
 R/McMullen, B.A.; Fujikawa, K.; Kistel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss  
 Biochemistry 22, 2875-2884, 1983  
 A>Title: Complete amino acid sequence of the light chain of human blood coagulation fact  
 A/Reference number: A20362; MUID:8357207; PMID:6871167  
 A/Accession: A20362  
 A/Molecule type: protein  
 A/Residues: 41-179 <MCW>  
 R/Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A/Reference number: S39414; MUID:94062825; PMID:8234461  
 A/Accession: S39415  
 A/Molecule type: protein  
 A/Residues: 183-234 <INO>  
 A/Note: glycosylation sites  
 A/Note: identification and characterization of beta-hydroxyaspartic acid  
 R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamaabushanam, K.; Lyman, G.

Gene 84, 517-519, 1989  
 A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
 A:Reference number: 154051; MUID:90128299; PMID:2612918  
 A:Accession: 154051  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-23 <RES>  
 A:Cross-references: GB:M33297; NID:G183860; PIDN:AAA52636.1; PID:G553330  
 J:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bl  
 J. Mol. Biol. 232, 947-966, 1993  
 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A49458; MUID:93360277; PMID:8355279  
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 C:Genetics:  
 A:Gene: GDB:F10  
 A:Cross-references: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A>Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG2>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:235-488/Product: activation peptide #status experimental <AP>  
 F:235-462/Domain: trypsin homology <TRY>  
 F:46-47; 54; 56; 59; 60; 65; 66; 69; 72; 79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:57-62/Disulfide bonds: #status predicted  
 F:90-101; 95-110; 112-121; 129-140; 136-149; 151-164; 172-342; 241-246; 261-277; 390-404; 415-443/  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:199; 211/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:221; 231/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:276; 322; 419/Active site: His, Asp, Ser #status experimental

Query Match 50.8%; Score 96; DB 1; Length 488;  
 Best Local Similarity 36.4%; Pred. No. 8.6e-09;  
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

1 ANGFLXLRQSLRXRCXLCSPFXAEXIFPNXXRTROFVSY 44  
 41 ANSFLBKKKGLHRECHMEETCYEAREVFEEDSDKTFEFMKY 84

RESULT 9  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; MUID:8424715; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FNU>  
 A:Cross-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochemistry 19, 659-667, 1980  
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735

A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102; 'N', 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-292; 294-295; 'GPE', 299-334; 336-348; 'AE', 351-354; 356-441; 'GKEG', 446-492 <T  
 A>Note: carbohydrate binding sites and disulfide bonds were determined  
 R:Petersen, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; MUID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A>Note: beta-hydroxyaspartic acid site  
 R:Linoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196; 199-209; 216-233 <INO>  
 A>Note: carbohydrate binding sites  
 R:Titani, K.; Hemmerson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D  
 Biochemistry 11, 4899-4903, 1972  
 A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
 A:Reference number: A12453; MUID:79053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic  
 A:Reference number: A38024; MUID:84185716; PMID:6546930  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of tw  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
 C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG2>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <AP>

F/234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F/234-461/Domains: trypsin homology <TR>  
 F/46/47/54/56/59/60/65/66/69/72/75/79/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F/57-62/90-101/110-112/120-121/122-123/136-149/151-164/172-241/Disulfide bonds: #status F  
 F/103/Modified site: ethyl-2-beta-hydroxyaspartic acid (Asp) #status experimental  
 F/200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F/208/485/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F/218/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F/233-234/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat  
 F/240-245/260-276/389-403/414-442/Disulfide bonds: #status experimental  
 F/275/321/418/Active site: His, Asp, Ser #status predicted

Query Match 50.3%; Score 95; DB 1; Length 492;  
 Best Local Similarity 38.6%; Pred. No. 1.3e-08;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSIXRCXKXLLGSPXXAEXFRXXRTROFWAY 44  
 Db 41 ANSFLERVXKGNLERECLEACSLERAEVFEADQOTDFWSKY 84

RESULT 10  
 KFHU  
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
 N/Alternate names: antihemophilic factor B; Christmae factor  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #ext, change 15-Sep-2000  
 A/Cross-references: A00922; A37570; A30511; A32673; A21337; A37546; A30623; A60486; A20  
 R/Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.  
 Biochemistry 24, 3736-3750, 1985  
 A/Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).  
 A/Reference number: A00922; PMID:8600558; PMID:2594716  
 A/Accession: A00922  
 A/Molecule type: DNA  
 A/Residues: 1-461 <YOS>  
 A/Cross-references: GB:K02402; NID:g182612; PIDN:AA59620.1; PID:g182613  
 R/Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Ghanelli, F.; Gould, K.; Huddleston, J.A.; Bro  
 EMO 0.3, 1053-1060, 1984  
 A/Title: The gene structure of human anti-haemophilic factor IX.  
 A/Reference number: A37570; PMID:8423610; PMID:6329734  
 A/Accession: A37570  
 A/Molecule type: DNA  
 A/Residues: 1-461 <YOS>  
 A/Cross-references: GB:K02048  
 R/Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
 Blood 72, 1074-1076, 1988  
 A/Title: The putative factor IX gene promoter in hemophilia B Leyden.  
 A/Reference number: A30511; PMID:88327116; PMID:3416069  
 A/Accession: A30511  
 A/Molecule type: DNA  
 A/Residues: 8-24 <REI>  
 A/Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253  
 R/Koberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A/Title: Functionally important regions of the factor IX gene have a low rate of polymor  
 A/Reference number: A32989; PMID:89371752; PMID:2773937  
 A/Accession: A32989  
 A/Status: not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 30-92 <KOE>  
 R/McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985  
 A/Title: Evidence for a prevalent polymorphism in the activation peptide of human coagulat  
 A/Reference number: A22673; PMID:85190593; PMID:3857619  
 A/Accession: A22673  
 A/Molecule type: mRNA  
 A/Residues: 1-193, 'T', 195-461 <MCG>  
 A/Cross-references: GB:M13109; NID:g180552; PIDN:AA52023.1; PID:g180553  
 A/Note: the authors translated the codon ACA for residue 29 as Tyr  
 R/Jay, M.; de la Salle, H.; Schamber, F.; Baland, A.; Kohl, V.; Finkel, A.; Tolstosh  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A/Title: Isolation of a human anti-hemophilic factor IX cDNA clone using a unique 52-bp  
 A/Reference number: A21337; PMID:83220788; PMID:6687940

A/Accession: A21337  
 A/Molecule type: mRNA  
 A/Residues: 1-193, 'T', 195-461 <JAY>  
 A/Cross-references: GB:J00136; NID:g182610; PIDN:AA52763.1; PID:g182611  
 R/Jagdeeswaran, P.; Javelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A/Title: Isolation and characterization of human factor IX cDNA: identification of Tag I  
 A/Reference number: A37546; PMID:84300526; PMID:6089357  
 A/Accession: A37546  
 A/Molecule type: mRNA  
 A/Residues: 38-193, 'T', 195-326 <JAG>  
 A/Cross-references: GB:M35672  
 R/Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
 A/Title: Isolation and characterization of a cDNA coding for human factor IX.  
 A/Reference number: A30623; PMID:83065193; PMID:6959130  
 A/Accession: A30623  
 A/Molecule type: mRNA  
 A/Residues: 1-12, 'S', '14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',  
 A/Cross-references: GB:J00136; NID:g182608; PIDN:AA598726.1; PID:g182609  
 A/Experimental source: liver  
 R/Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
 Vox Sang. 58, 21-29, 1990  
 A/Title: Development of an immunocaffinity process for factor IX purification.  
 A/Reference number: A60486; PMID:90194857; PMID:2316207  
 A/Accession: A60486  
 A/Molecule type: protein  
 A/Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>  
 R/McMullen, B.A.; Fujikawa, K.; Kistel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A/Reference number: A20274; PMID:83508813; PMID:6688526  
 A/Accession: A20274  
 A/Molecule type: protein  
 A/Residues: 105-109, 'X', 111-115 <MCW>  
 R/Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall  
 Eur. J. Biochem. 172, 565-572, 1988  
 A/Title: Characterization of two differently processed forms of human recombinant factor  
 A/Reference number: S02527; PMID:8816735; PMID:3280312  
 A/Accession: S02527  
 A/Molecule type: protein  
 A/Residues: 29-63 <BAL>  
 A/Note: processed forms expressed in recombinant system  
 R/Pallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,  
 EMO 0.9, 3295-3301, 1990  
 A/Title: Characterization of recombinant human factor IX expressed in transgenic mice an  
 A/Reference number: S12058; PMID:91006024; PMID:2209546  
 A/Accession: S12058  
 A/Molecule type: mRNA; protein  
 A/Residues: 1-68 <DAL>  
 A/Note: processed forms expressed in recombinant system  
 R/Hanford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campe  
 EMO 0.9, 475-480, 1990  
 A/Title: The first EGF-like domain from human factor IX contains a high-affinity calcium  
 A/Reference number: S12377; PMID:90151623; PMID:2406129  
 A/Accession: S12377  
 A/Molecule type: protein  
 A/Residues: 92-130 <HAN>  
 A/Note: NMR detection of calcium binding by domain expressed in recombinant system  
 R/de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,  
 Thromb. Haemost. 70, 370-371, 1993  
 A/Title: A deletion located in the 3' non translated part of the factor IX gene responsi  
 A/Reference number: S159612; PMID:94054330; PMID:8236150  
 A/Accession: S159612  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 444-461 <RES>  
 A/Cross-references: GB:S66752; NID:g439773; PIDN:AA628588.1; PID:g439774  
 R/Stoffet, E.S.; Koberl, D.D.; Sarkar, G.; Sommer, S.S.  
 Science 229, 491-494, 1988  
 A/Title: Genomic amplification with transcript sequencing.  
 A/Reference number: S15929; PMID:88127096; PMID:3340835  
 A/Accession: S15929



A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 290-359 <R2>  
A:Cross-references: GB:M19063; NID:G182623; PIDN:AAA52456.1; PID:G182623  
R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murate, H.; Shimonishi, Y.; Nishimura, H.; In  
Biochemistry 33, 5167-5171, 1994  
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin  
A:Reference number: A54255; MUID:94227047; PMID:8172892  
A:Accession: A54255  
A:Molecule type: protein  
A:Residues: 'D',204,'X',206-211,'212','D',214,'X',216-221,'D',<AGA>  
A:Note: The residues designated 'X' were determined to be threonine bound to carbohydrate  
R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.  
J. Clin. Invest. 61, 1528-1538, 1978  
A:Title: Activation of human factor IX (Christmas factor).  
A:Reference number: A18483; MUID:78194509; PMID:659613  
A:Contents: annotation; activation; active site; carbohydrate binding  
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984  
A:Reference number: A37569  
A:Contents: annotation  
A:Note: 194-Thr was also found  
R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
J. Biol. Chem. 259, 5698-5704, 1984  
A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
A:Reference number: A37543; MUID:84185715; PMID:6425296  
A:Contents: annotation; calcium binding  
R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
J. Biol. Chem. 260, 2583, 1985  
A:Reference number: A37544  
A:Contents: annotation; calcium binding, correction  
R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
Cell 45, 343-348, 1986  
A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation  
A:Reference number: A37545; MUID:8618947; PMID:3005023  
R:Sehito, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J.  
J. Biol. Chem. 264, 21257-21265, 1989  
A:Title: Blood clotting factor IX (B) Nagoya: substitution of arginine 180 by tryptophan  
A:Reference number: A30622; MUID:90078229; PMID:2592373  
A:Contents: annotation; sequence of mutant B(M) Nagoya  
R:Bayon, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle  
submitted to the Brookhaven Protein Data Bank, November 1991  
A:Reference number: A51252; PDB:1IXA  
A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
A:Note: recombinant form expressed in yeast  
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr  
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc  
C:GeneticS:  
A:Gene: GDB:F9  
A:Cross-references: GDB:119900; OMIM:306900  
A:Map position: Xq27.1-Xq27.2  
A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
A:Pathway: blood coagulation intrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-46/Domain: propeptide #status experimental <PP>  
F:31-91/Domain: Gla domain homology <Gla>  
F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>  
F:97-128/Domain: EGF homology <EG1>  
F:134-170/Domain: EGF homology <EG2>  
F:129-226/Domain: activation peptide #status experimental <ACT>  
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F:227-464/Domain: trypsin homology <TRY>  
F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #  
F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D  
F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental  
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental  
F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental  
Query Match 49.2%; Score 93; DB 1; Length 461;  
Best Local Similarity 41.9%; Pred. No. 2,76-08;  
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
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Db 49 SGKLEEFVQNLNERCMEKCSFEAREVFENTERFTFWMQY 91  
RESULT 11  
KCHU  
protein C (activated) (EC 3.4.21.69) precursor - human  
N:Alternate names: autoprothrombin IIA; plasma protein C  
C:Species: Homo sapiens (man)  
C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
R:Poster, D.C.; Yoshitake, S.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
A:Title: The nucleotide sequence of the gene for human protein C.  
A:Reference number: A22331; MUID:85270390; PMID:2991887  
A:Accession: A22331  
A:Molecule type: DNA  
A:Residues: 1-461 <F081>  
A:Cross-references: GB:M11228; NID:G190333; PIDN:AAA60166.1; PID:G190334  
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
A:Title: Evolution and organization of the human protein C gene.  
A:Reference number: A25426; MUID:86120978; PMID:3511471  
A:Accession: A25426  
A:Molecule type: DNA  
A:Residues: 1-445,'L',446-461 <PLU>  
A:Cross-references: GB:M12712; NID:G190330; PIDN:AAA60165.1; PID:G190332  
R:Poster, D.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
A:Title: Characterization of a cDNA coding for human protein C.  
A:Reference number: A21781; MUID:84272714; PMID:6589623  
A:Accession: A21781  
A:Molecule type: mRNA  
A:Residues: 'Q',107-461 <F082>  
A:Cross-references: GB:X02059; NID:G190332; PIDN:AAA60164.1; PID:G190333  
R:Beckmann, R.J.; Schmidt, R.J.; Senterre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
Nucleic Acids Res. 13, 5233-5247, 1985  
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and i  
A:Reference number: A23789; MUID:85269639; PMID:2991859  
A:Accession: A23789  
A:Molecule type: mRNA  
A:Residues: 1-461 <BEC>  
A:Cross-references: GB:X02750; NID:G35689; PIDN:CAA26528.1; PID:G763120  
R:Mijerlich, J.P.; Broze Jr., G.J.  
J. Biol. Chem. 265, 11397-11404, 1990  
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m  
A:Reference number: A44605; MUID:90293094; PMID:1694179  
A:Contents: annotation; carbohydrate binding sites; activation peptide  
A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
R:Harrie, R.J.; Ling, V.T.; Spelmann, M.W.  
J. Biol. Chem. 267, 5102-5107, 1992  
A:Title: O-linked fucose is present in the first epidermal growth factor domain of facto  
A:Reference number: A44606; MUID:92184750; PMID:1544894  
A:Contents: annotation; beta-hydroxyaspartic acid  
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
C:Comment: Protein C is strongly enhanced by complexing with protein S. Protein C also f  
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
C:GeneticS:  
A:Gene: GDB:PROC  
A:Cross-references: GDB:120217; OMIM:176860  
A:Map position: 2q13-q21  
A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F/1-32/Domain: signal sequence #status predicted <SIG>  
 F/27-86/Domain: Gla domain homology <GLA>  
 F/33-42/Domain: propeptide #status predicted <PRO>  
 F/43-197/Product: protein C light chain #status predicted <LCH>  
 F/92-131/Domain: EGF homology <EG1>  
 F/140-175/Domain: EGF homology <EG2>  
 F/200-461/Product: protein C heavy chain #status predicted <HCH>  
 F/200-211/Domain: activation peptide #status experimental <APT>  
 F/212-445/Domain: trypsin homology <TRY>  
 F/48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
 F/59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D  
 F/106-111/Disulfide bonds: #status predicted  
 F/110/Binding site: carboxylate (Thr) (covalent) #status absent  
 F/113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F/139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F/211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
 F/253,299,402/Active site: His, Asp, Ser #status predicted  
 F/371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 49.2% Score 93; DB 1; Length 461;  
 Best Local Similarity 46.3%; Pred. No. 2.7e-08;  
 Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQSLKRXCRXXLCSPXXAEXIFRNXXRTQFW 41  
 Db 43 ANSFLELRHRSLERECEIEICDFEAKEIFQVNDTLAW 83

# RESULT 12

KEBO  
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine

N/Alternate names: Christmas factor

C/Species: Bos primigenius taurus (cattle)

C/Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999

C/Accession: A14757; B20274; I45891; A00923

R/Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davle, E.W.; Th  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979

A/Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa  
 A/Reference number: A14757; MUID:80056619; PMID:251916

A/Accession: A14757

A/Molecule type: protein

A/Residues: 1-63; 'T', 65-416 <NAT>

R/McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A/Reference number: A20274; MUID:83308813; PMID:6688526

A/Accession: B20274

A/Molecule type: protein

A/Residues: 59-63; 'X', 65-69 <MCM>

R/Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
 Nature 299, 178-180, 1982

A/Title: Molecular cloning of the gene for human anti-haemophilic factor IX.  
 A/Reference number: I45891; MUID:82212386; PMID:6287289

A/Accession: I45891

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 52-139 <CHO>  
 A/Cross-References: GB:J00007; NID:G163053; PIDN:AAA0520.1; PID:G163054

R/Haas, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,  
 J. Biochem. 104, 867-868, 1988

A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag  
 A/Reference number: A44556; MUID:89213399; PMID:3149637

A/Accession: A44556

A/Status: annotation

A/Note: structure and location of a carboxylate covalently bound to Ser

C/Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr  
 C/Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K

C/Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc  
 C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
 A/Pathway: blood coagulation intrinsic pathway

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F/1-16/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F/1-45/Domain: Gla domain homology (fragment) <GLA>  
 F/51-82/Domain: EGF homology <EG1>  
 F/88-124/Domain: EGF homology <EG2>  
 F/147-181/Domain: activation peptide #status experimental <APT>  
 F/182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F/7-8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #sta  
 F/18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide  
 F/53/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F/54/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F/158,168,173,261/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F/222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 47.1% Score 89; DB 1; Length 416;  
 Best Local Similarity 37.2%; Pred. No. 1.2e-07;  
 Matches 16; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 2 NGFLXXLRQSLKRXCRXXLCSPXXAEXIFRNXXRTQFW 44  
 Db 3 SGKLEFVRGNLERCEKCSFEAREVFENETKTEFWKQY 45

# RESULT 13

EXCH  
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken

N/Alternate names: virus-activating proteinase

C/Species: Gallus gallus (chicken)

C/Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text change 16-Jul-1999

C/Accession: S15838; S20380; S20381

R/Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na  
 FEBS Lett. 283, 281-285, 1991

A/Title: Primary structure of the virus activating protease from chick embryo. Its ident  
 A/Reference number: S15838; MUID:91257322; PMID:2044767

A/Accession: S15838

A/Status: not compared with conceptual translation

A/Molecule type: protein

A/Residues: 1-475 <SUZ>

A/Accession: S20380

A/Molecule type: protein

A/Residues: 41-55 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein

A/Residues: 241-246; 'X', 248-251, 'X', 253-261 <GOT>

A/Accession: S20381

A/Molecule type: protein



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GenCore version 5.1.4.D5\_4578  
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OW protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)

328.082 Million cell updates/sec

Title: 10Gln28Glu\_4

Sequence: 1 ANGFLXXLRQSLKRXCRXX.....XXAEXIFRNXXRTQFWVS 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 149   | 78.8        | 407    | 1  | FA7_BOVIN   |
| 2          | 131   | 69.3        | 444    | 1  | FA7_RABIT   |
| 3          | 123   | 65.1        | 466    | 1  | FA7_HUMAN   |
| 4          | 113   | 59.8        | 218    | 1  | TWGI_HUMAN  |
| 5          | 109   | 57.7        | 461    | 1  | PRTC_MOUSE  |
| 6          | 108   | 57.1        | 461    | 1  | PRTC_RAT    |
| 7          | 107   | 56.6        | 231    | 1  | TWGI_HUMAN  |
| 8          | 106   | 56.1        | 446    | 1  | FA7_MOUSE   |
| 9          | 102   | 54.0        | 459    | 1  | PRTC_PIG    |
| 10         | 97    | 51.3        | 456    | 1  | PRTC_BOVIN  |
| 11         | 96    | 50.8        | 488    | 1  | FA10_HUMAN  |
| 12         | 95    | 50.3        | 492    | 1  | FA10_BOVIN  |
| 13         | 94    | 49.7        | 490    | 1  | FA10_RABIT  |
| 14         | 93    | 49.2        | 461    | 1  | FA7_HUMAN   |
| 15         | 93    | 49.2        | 461    | 1  | PRTC_HUMAN  |
| 16         | 89    | 47.1        | 416    | 1  | FA7_BOVIN   |
| 17         | 87    | 46.0        | 475    | 1  | FA10_CHICK  |
| 18         | 86    | 44.5        | 458    | 1  | PRTC_RABIT  |
| 19         | 84    | 44.4        | 452    | 1  | FA7_CANFA   |
| 20         | 84    | 44.4        | 459    | 1  | FA7_MOUSE   |
| 21         | 78    | 41.3        | 622    | 1  | THRB_HUMAN  |
| 22         | 75    | 39.7        | 617    | 1  | THRB_RAT    |
| 23         | 75    | 39.7        | 618    | 1  | THRB_MOUSE  |
| 24         | 75    | 39.7        | 649    | 1  | PRTC_MOUSE  |
| 25         | 75    | 39.7        | 676    | 1  | PRTC_HUMAN  |
| 26         | 72    | 38.1        | 675    | 1  | PRTC_BOVIN  |
| 27         | 71    | 37.6        | 202    | 1  | TWGI_HUMAN  |
| 28         | 71    | 37.6        | 646    | 1  | PRTC_RABIT  |
| 29         | 70    | 37.0        | 226    | 1  | TWGI_HUMAN  |
| 30         | 69    | 36.5        | 376    | 1  | FA10_TROCA  |
| 31         | 69    | 36.5        | 400    | 1  | PRTC_HUMAN  |
| 32         | 69    | 36.5        | 625    | 1  | THRB_BOVIN  |
| 33         | 69    | 36.5        | 675    | 1  | PRTC_RAT    |

|    |    |      |      |   |            |                     |
|----|----|------|------|---|------------|---------------------|
| 34 | 65 | 34.4 | 396  | 1 | PRTC_BOVIN | P00744 bos taurus   |
| 35 | 62 | 32.8 | 475  | 1 | PRTC_MOUSE | Q08761 mus musculus |
| 36 | 56 | 29.6 | 613  | 1 | NCAP_IHNV  | P19691 infectious   |
| 37 | 53 | 28.0 | 604  | 1 | VE1_BPv2   | P11298 bovine papi  |
| 38 | 53 | 28.0 | 605  | 1 | VE1_BPv1   | P03116 bovine papi  |
| 39 | 43 | 22.8 | 484  | 1 | SUT2_YEAST | Q00772 saccharomyc  |
| 40 | 42 | 22.2 | 320  | 1 | GSHB_BUCAI | P57612 buchnera ap  |
| 41 | 41 | 21.7 | 184  | 1 | ADML_MOUSE | P97297 mus musculus |
| 42 | 41 | 21.7 | 363  | 1 | ADK_TOXGO  | Q9LWV2 toxoplasma   |
| 43 | 41 | 21.7 | 477  | 1 | PIB1_PETWA | P02678 petromyzon   |
| 44 | 41 | 21.7 | 529  | 1 | VGLF_MEASI | P26031 measles vir  |
| 45 | 41 | 21.7 | 1275 | 1 | RFBC_MTXXA | Q50864 myxococcus   |

## ALIGNMENTS

|          |   |           |      |         |
|----------|---|-----------|------|---------|
| RESULT 1 | FA7_BOVIN   | STANDARD; | PRT; | 407 AA. |
| ID       | P22457;   |           |      |         |
| AC       | 01-AUG-1991 (Rel. 19, Created)  |           |      |         |
| DT       | 01-AUG-1991 (Rel. 19, Last sequence update)                                       |           |      |         |
| DT       | 15-JUN-2002 (Rel. 41, Last annotation update)                                     |           |      |         |
| DE       | Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator). |           |      |         |
| GN       | F7.   |           |      |         |
| OS       | Bos taurus (Bovine).  |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                           |           |      |         |
| OC       | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;                 |           |      |         |
| OC       | Bovidae; Bovinae; Bos.  |           |      |         |
| OX       | NCBI_TaxID=9913;  |           |      |         |
| RN       | [1]   |           |      |         |
| RP       | SEQUENCE.   |           |      |         |
| RX       | MEDLINE=89008362; PubMed=3049594;   |           |      |         |
| RA       | Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,                     |           |      |         |
| RA       | Iwanaga S.;   |           |      |         |
| RT       | "Bovine factor VII. Its purification and complete amino acid                      |           |      |         |
| RT       | sequence.";   |           |      |         |
| RL       | J. Biol. Chem. 263:14868-14877(1988).   |           |      |         |
| RN       | [2]   |           |      |         |
| RP       | STRUCTURE OF CARBOHYDRATE ON SER-52.  |           |      |         |
| RX       | MEDLINE=89213999; PubMed=3149637;   |           |      |         |
| RA       | Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,                       |           |      |         |
| RA       | Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;                       |           |      |         |
| RT       | "A new trisaccharide sugar chain linked to a serine residue in bovine             |           |      |         |
| RT       | blood coagulation factors VII and IX.";   |           |      |         |
| RL       | J. Biochem. 104:867-868(1988).  |           |      |         |
| RN       | [3]   |           |      |         |
| RP       | STRUCTURE OF CARBOHYDRATE ON SER-52.  |           |      |         |
| RX       | MEDLINE=91344709; PubMed=2129367;   |           |      |         |
| RA       | Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;           |           |      |         |
| RT       | "A new trisaccharide sugar chain linked to a serine residue in the                |           |      |         |
| RT       | first BGF-like domain of clotting factors VII and IX and protein Z.";             |           |      |         |
| RL       | Adv. Exp. Med. Biol. 281:121-131(1990).   |           |      |         |
| CC       | - FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS              |           |      |         |
| CC       | CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR                |           |      |         |
| CC       | THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR                   |           |      |         |
| CC       | AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA                 |           |      |         |
| CC       | BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO                |           |      |         |
| CC       | FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.                          |           |      |         |
| CC       | - CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to                |           |      |         |
| CC       | form factor Xa.   |           |      |         |
| CC       | - SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED                  |           |      |         |
| CC       | BY A DISULFIDE BOND.  |           |      |         |
| CC       | - TISSUE SPECIFICITY: PLASMA.   |           |      |         |
| CC       | - PTM: THE VITAMIN K-DEPENDENT, ENZYMOLOGICALLY MODIFIED                          |           |      |         |
| CC       | GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND                        |           |      |         |
| CC       | CALCIUM.  |           |      |         |
| CC       | - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.                                     |           |      |         |
| CC       | - SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  |           |      |         |
| DR       | PIR; A31979; A31979.  |           |      |         |
| DR       | HSP; P08709; 1BP9.  |           |      |         |

DR MEROPS; S01.215; -  
 DR Interpro; IPR000152; Asx hydroxyl.  
 DR Interpro; IPR001314; Chymotrypsin.  
 DR Interpro; IPR000561; EGF-like.  
 DR Interpro; IPR000742; EGF-2.  
 DR Interpro; IPR001881; EGF-Ca.  
 DR Interpro; IPR002138; EGF-11.  
 DR Interpro; IPR002383; GLA blood.  
 DR Interpro; IPR001254; Ser protease\_Try.  
 DR Interpro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGFBLOOD.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxylglutamic acid;  
 KM EGF-like domain; Repeat.  
 FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.  
 FT DOMAIN 153 407 FACTOR VII HEAVY CHAIN.  
 FT ACT\_SITE 242 242 GLA-RICH.  
 FT ACT\_SITE 344 344 SUBSTRATE (BY SIMILARITY).  
 FT BINDING 336 338 BY SIMILARITY.  
 FT DISULFID 17 22 BY SIMILARITY.  
 FT DISULFID 50 61 BY SIMILARITY.  
 FT DISULFID 55 70 BY SIMILARITY.  
 FT DISULFID 72 81 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 98 112 BY SIMILARITY.  
 FT DISULFID 114 127 BY SIMILARITY.  
 FT DISULFID 135 162 BY SIMILARITY.  
 FT DISULFID 159 164 BY SIMILARITY.  
 FT DISULFID 178 194 BY SIMILARITY.  
 FT DISULFID 310 329 BY SIMILARITY.  
 FT DISULFID 340 368 BY SIMILARITY.  
 FT MOD\_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT CARBOHYD 52 52 O-LINKED (GLC. . .).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 407 AA; 44431 MW; 703ELFE0636F7P10 CRC64;

Query Match 78.8%; Score 149; DB 1; Length 407;  
 Best Local Similarity 68.2%; Pred. No. 5.2e-20;  
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANGLFLXXLRGSLRXRCRXLLCSFXXAEXIFRNXXKTRTFWVS 44  
 DB 1 ANGLFEELPGLSLERCRELCSPFEAAHEIFPNEEXTRFQWVS 44

RESULT 2  
 FA7\_RABIT STANDARD; PRT; 444 AA.  
 ID FA7\_RABIT ID P98139; P79224;  
 AC P98139; P79224;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
 GN F7.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93190306; PubMed=8383365;  
 RA Brothens A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";  
 RL Thromb. Res. Suppl. 69:231-238(1993).  
 RN [2]  
 RP REVISION TO 395.  
 RC TISSUE=Liver;  
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; U77477; AAB37326.1; -.  
 DR HSSP; P08709; 1FAK.  
 DR MEROPS; S01.215; -.  
 DR Interpro; IPR000152; Asx hydroxyl.  
 DR Interpro; IPR001314; Chymotrypsin.  
 DR Interpro; IPR000561; EGF-like.  
 DR Interpro; IPR000742; EGF-2.  
 DR Interpro; IPR001881; EGF-Ca.  
 DR Interpro; IPR002138; EGF-11.  
 DR Interpro; IPR002383; GLA blood.  
 DR Interpro; IPR001254; Ser protease\_Try.  
 DR Interpro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00059; GLA; 1.  
 DR SMART; SM00020; TRYD\_Spec; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYLU; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Layer; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KM EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT PROPEP 22 39 POTENTIAL.  
 FT CHAIN 40 191 FACTOR VII LIGHT CHAIN.  
 FT CHAIN 192 444 FACTOR VII HEAVY CHAIN.  
 FT DOMAIN 45 74 GLA-RICH.  
 FT DOMAIN 85 121 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 126 167 EGF-LIKE 2.  
 FT DOMAIN 192 444 SERINE PROTEASE.  
 FT SITE 191 192 CLEAVAGE (BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN) (BY SIMILARITY).  
 FT ACT\_SITE 232 232 BY SIMILARITY.  
 FT ACT\_SITE 281 281 BY SIMILARITY.  
 FT ACT\_SITE 383 383 BY SIMILARITY.  
 FT BINDING 377 377 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 56 61 BY SIMILARITY.  
 FT DISULFID 89 100 BY SIMILARITY.  
 FT DISULFID 94 109 BY SIMILARITY.  
 FT DISULFID 111 120 BY SIMILARITY.  
 FT DISULFID 130 141 BY SIMILARITY.  
 FT DISULFID 137 151 BY SIMILARITY.  
 FT DISULFID 153 166 BY SIMILARITY.  
 FT DISULFID 174 301 BY SIMILARITY.  
 FT DISULFID 198 203 BY SIMILARITY.  
 FT DISULFID 217 233 BY SIMILARITY.  
 FT DISULFID 349 368 BY SIMILARITY.  
 FT DISULFID 379 407 BY SIMILARITY.  
 FT MOD\_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.  
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 FT MOD\_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 102 102 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 444 AA; 49011 MW; 0461ABC4FE5427F8 CRC64;

Query Match 69.3%; Score 131; DB 1; Length 444;  
 Best Local Similarity 52.3%; Pred. No. 1.3e-16;  
 Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 1 ANGFLXLRQGLKRXKXLLSPKXAEIPFNXXKTRTFWWSY 44  
 DB 40 ANSFLELRPGSLRERCKELCSFEARREVFOSTERTKOFWITY 83

RESULT 3  
 FA7\_HUMAN STANDARD; PRT; 466 AA.  
 AC P08709; Q14339;  
 DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 DE conversion accelerator) (Eptacog alfa).  
 CN F7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86205965; PubMed=3486420;  
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,  
 RA Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor VII";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260948; PubMed=3037537;  
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
 RA Hagen F.S., Murray M.J.;  
 RT "Nucleotide sequence of the gene coding for human factor VII, a  
 RT vitamin K-dependent protein participating in blood coagulation";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS THR-353; GLN-413 AND LYS-445.  
 RA Rieder W.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=89088153; PubMed=3264725;  
 RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
 RA Pedersen A.H., Hedder U.;  
 RT "Amino acid sequence and posttranslational modifications of human  
 RT factor VIIa from plasma and transfected baby hamster kidney cells";  
 RL Biochemistry 27:785-7793(1988).  
 RN [5]  
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
 RX MEDLINE=91250411; PubMed=1904059;  
 RA Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,  
 RA Komiyama Y., Pedersen A.H., Kistiel W.;  
 RT "Human plasma and recombinant factor VII. Characterization of O-  
 RT glycosylations at serine residues 52 and 60 and effects of site-  
 RT directed mutagenesis of serine 52 to alanine";  
 RL J. Biol. Chem. 266:11051-11057(1991).  
 RN [6]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takeo T.,  
 RA Shimomishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [7]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Gaha A.,  
 RA Kongsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor";  
 RL Nature 380:41-46(1996).

[9] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RP MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 inhibited with a BPT mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Murenyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 molecule with reduced activity isolated from a clinically unaffected  
 male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Roderigo G., Casanato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferracci M., Patrascchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 (11His and 33Ser) in the human coagulation factor VII gene.";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamiya O., Kemball-Cook G., Marin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 polymorphism (SSCP) analysis in five dysfunctional variants of  
 coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RX MEDLINE=94264305; PubMed=8204879;  
 RA Chasing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blachman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Castelan G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 factors VII (294Ala-->Val) and X (334Ser-->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shitakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII Mle: homozygous asymptomatic type I deficiency caused by  
 an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr59Met mutation in factor VII of a patient with a hereditary  
 deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castelan G., Pinotti M., Ferraresi P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Biau O., Korostishevsky M.,  
 RA Zaitov R., Seligsohn U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN [21]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).  
 CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to  
 CC form factor Xa.  
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -I- TISSUE SPECIFICITY: PLASMA.  
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -I- PHARMACEUTICAL: Available under the names Niasase or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in  
 CC Query Match 65.1%; Score 123; DB 1; Length 466;  
 CC Best Local Similarity 52.3%; Pred. No. 4, 2e-15;  
 CC Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANGFLLXLRGSLRXCRXXLCSFXXAEXIFRNXXKTRPFWVS 44  
 DB 61 ANAFLEELRPGSLERCKEFGCSFEARREIFKDAERTKLFWSY 104  
 RESULT 4  
 TMG1 HUMAN  
 ID TMG1 HUMAN STANDARD; PRT; 218 AA.  
 AC 014658;  
 DT 15-JUN-2002 (rel. 41, Created)  
 DT 15-JUN-2002 (rel. 41, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-  
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein  
 DE 1).  
 GN PRG1 OR TMG1 OR PRGPI.  
 OS Homo sapiens (Human).



CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97404347; PubMed=9256434;  
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;  
 RT "Primary structure and tissue distribution of two novel proline-rich  
 gamma-carboxyglutamic acid proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.  
 CC -1- PTM: Glu residues are produced after subsequent posttranslational  
 CC modifications of glutamic acid by a vitamin K-dependent gamma-  
 CC carboxylase.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; AF009242; AAB67070.1; -.  
 DR HSSP; P00740; ICFH.  
 DR GENE; HGNC:9469; PRRG1.  
 DR MIM; 604428; -.  
 DR InterPro; IPR002383; GLA blood.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00069; GLA; 1.  
 DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.  
 DR K4 Gamma-carboxyglutamic acid; vitamin K; Transmembrane.  
 FT PROPEP 1 20  
 FT CHAIN 21 218  
 FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID  
 FT PROTEIN 1.  
 FT DOMAIN 21 83  
 FT TRANSEM 84 106  
 FT DOMAIN 107 218  
 FT DOMAIN 24 61  
 FT DOMAIN 131 135  
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 Query Match 59.8%; Score 113; DB 1; Length 218;  
 Best local Similarity 40.9%; Pred. No. 1,4e-13;  
 Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

RT "Isolation and characterization of a mouse protein C cDNA";  
 RL J. Biochem. 111:491-495(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=128/SVJ;  
 RX MEDLINE=96152576; PubMed=9493582;  
 RA Jabbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine gene encoding  
 RT anticoagulant protein C";  
 RL Thromb. Haemost. 79:310-316(1998).  
 RN [3]  
 RP SEQUENCE OF 274-434 FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=94318474; PubMed=8043441;  
 RA Murakawa M., Okumura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;  
 RT "A comparative study of partial primary structures of the catalytic  
 RT region of mammalian protein C";  
 RL Br. J. Haematol. 86:590-600(1994).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC DR EMBL; D10445; BAA01235.1; -.  
 DR EMBL; AF034569; AAC33795.1; -.  
 DR EMBL; D43755; BAA07812.1; -.  
 DR PIR; JX0210; JX0210.  
 DR HSSP; P04070; LPCU.  
 DR MEROPS; S01.218; -.  
 DR MGD; MGI:97771; Proc.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR002383; GLA blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_spec; 1.  
 DR PROSITE; PS00012; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA.1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Blood coagulation; Glycoprotein; Serine protease;
KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 212
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
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FT MOD_RES 57 57
FT MOD_RES 60 60
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FT MOD_RES 66 66
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FT MOD_RES 70 70
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FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
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FT DISULFID 91 110
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FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
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FT DISULFID 373 387
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FT DISULFID 398 426
FT CARBOHYD 214 240
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CARBOHYD 355 355
FT CONFLICT 328 328
FT CONFLICT 393 393
SQ SEQUENCE 461 AA; 51945 MW; 53FAA0085B19406E CRC64;

Query Match 57.7%; Score 109; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.7e-12;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

```

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DT 01-JUL-1993 (rel. 26, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoprotechombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cdna cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64336; CAA45617.1; -.
DR PIR; S18994; S18994.
DR PIR; S24312; S24312.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR pfam; PF00008; EGF_2.
DR pfam; PF00089; trypsin; 1.
DR pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.

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CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U66079; AAC33796.1; -.  
 CC DR HSSP; P08709; IBF9.  
 CC DR MEROPS; S01.215; -.  
 CC DR MGD; MG1:109325; F7.  
 CC DR InterPro; IPR000152; Asx\_hydroxyl.  
 CC DR InterPro; IPR001314; Chymotrypsin.  
 CC DR InterPro; IPR000561; EGF-like.  
 CC DR InterPro; IPR000742; EGF 2.  
 CC DR InterPro; IPR001881; EGF Ca.  
 CC DR InterPro; IPR002383; GLA\_blood.  
 CC DR InterPro; IPR001254; Ser\_protease\_Try.  
 CC DR InterPro; IPR000284; VitK\_dep\_GLA.  
 CC DR Pfam; PF00008; EGF; 2.  
 CC DR Pfam; PF00089; trypsin; 1.  
 CC DR Pfam; PF00594; gla; 1.  
 CC DR PRINTS; PR00722; CHYMOTRYPSIN.  
 CC DR PRINTS; PR00001; GLABLOOD.  
 CC DR SMART; SM00179; EGF\_CA; 1.  
 CC DR SMART; SM00001; EGF\_like; 1.  
 CC DR SMART; SM00069; GLA; 1.  
 CC DR SMART; SM00020; TRYP\_SPC; 1.  
 CC DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC DR PROSITE; PS00022; EGF\_1; 1.  
 CC DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 CC DR PROSITE; PS01187; EGF\_CA; 1.  
 CC DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 CC DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 CC Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 CC EGF-like domain; Repeat; Signal; Hydroxylation.  
 CC EGF-SIGNAL  
 CC FT SIGNAL 1 24  
 CC FT PROPEP 25 41  
 CC FT CHAIN 42 193  
 CC FT CHAIN 194 446  
 CC FT DOMAIN 47 76  
 CC FT DOMAIN 87 123  
 CC FT DOMAIN 128 169  
 CC FT DOMAIN 194 446  
 CC FT SITE 193 194  
 CC ACT SITE 224 234  
 CC FT ACT SITE 283 283  
 CC FT ACT SITE 385 385  
 CC FT BINDING 379 379  
 CC FT DISULFID 58 63  
 CC FT DISULFID 91 102

FT DISULFID 96 111 BY SIMILARITY.  
 FT DISULFID 113 122 BY SIMILARITY.  
 FT DISULFID 132 143 BY SIMILARITY.  
 FT DISULFID 139 153 BY SIMILARITY.  
 FT DISULFID 155 168 BY SIMILARITY.  
 FT DISULFID 176 203 BY SIMILARITY.  
 FT DISULFID 200 305 BY SIMILARITY.  
 FT DISULFID 219 235 BY SIMILARITY.  
 FT DISULFID 351 370 BY SIMILARITY.  
 FT DISULFID 381 409 BY SIMILARITY.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45C8C96E CRC64;  
 Query Match Score 106; DB 1; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 5,9e-12;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 ANGFLKXLRGSLRXRCXLLCSFPXAEKIFRNKXRTQFWWSY 44  
 DB 42 ANSLLELWPGSLERECNEQCSFEAREIFKSPERTKQFWIVY 85  
 RESULT 9  
 PRTC\_PIG STANDARD; PRT; 459 AA.  
 AC 09GLP2;  
 DT 16-OCT-2001 (rel. 40; Created)  
 DT 16-OCT-2001 (rel. 40; Last sequence update)  
 DT 15-JUN-2002 (rel. 41; Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 DE PROC.  
 GN Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RC MEDLINE=21121490; PubMed=11229814;  
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,  
 RA Kim H.K.W.;  
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional  
 RT protein modeling of membrane binding sites and comparative anatomy of  
 RT domains.";  
 RL Cell. Mol. Life Sci. 58:148-159 (2001).  
 CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that  
 CC regulates blood coagulation by inactivating factors Va and VIIa  
 CC in the presence of calcium ions and phospholipids.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved  
 CC into a light chain and a heavy chain held together by a disulfide  
 CC bond. The enzyme is then activated by thrombin, which cleaves a  
 CC tetradecapeptide from the amino end of the heavy chain; this  
 CC reaction, which occurs at the surface of endothelial cells, is  
 CC strongly promoted by thrombomodulin.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu  
 CC residues allows the modified protein to bind calcium.

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
 CC another site, beyond the GLA domain. This GLA-independent binding  
 CC site is necessary for the recognition of the  
 CC thrombin-thrombomodulin complex.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL: AF191307; AAC28380.1; -.  
 CC HSSP: P04070; 1PCU.  
 DR MEROPS: S01.218; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; glai; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00181; EGF; 2.  
 DR SMART: SM00001; EGF-like; 2.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TRYP\_Sec; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_Ca; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 KW SIGNAL 1 18  
 FT PROPEP 19 41  
 FT CHAIN 42 459  
 FT CHAIN 42 196  
 FT CHAIN 199 459  
 FT PEPTIDE 199 213  
 FT SITE 213 214  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 214 459  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67

FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 255 255  
 FT ACT\_SITE 301 301  
 FT ACT\_SITE 400 400  
 FT ACT\_SITE 400 400  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 321  
 FT DISULFID 240 256  
 FT DISULFID 371 385  
 FT DISULFID 396 424  
 FT CARBOHYD 138 138  
 FT CARBOHYD 292 292  
 FT CARBOHYD 353 353  
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC18C16D09 CRC64;  
 Query Match 54.0%; Score 102; DB 1; Length 459;  
 Best Local Similarity 45.5%; Pred. No. 3,4e-11;  
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;  
 Oy 1 ANGFLXLRQGSILKRXCKXKXLCSPYKAXEYIPRNXXRTQFWVSY 44  
 Db 42 ANSFLEELRPSLSRECKEETCDPEAREIRIONTENTWAFWSKY 85  
 RESULT 10  
 PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (BC 3,4,21.69)  
 DE (Antithrombin IIIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN [2]  
 RP SEQUENCE OF 40-194.  
 RX MEDLINE=85007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.;  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 RN [3]  
 RP REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN [4]  
 RP SEQUENCE OF 197-456.  
 RX MEDLINE=85007326; PubMed=6896877;  
 RA Stenflo J., Fernlund P.;  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RL J. Biol. Chem. 257:12180-12190(1982).

RN [5] PROCESSING, AND CALCIUM-BINDING DATA.  
 RP MEDLINE=83213513; PubMed=6304092;  
 RX Eamon N.L., Debaux L.E., Eamon C.T.;  
 RA "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
 RT domainless protein C.";  
 RN J. Biol. Chem. 258:5548-5553(1983).  
 RL [6]  
 RN PROCESSING, AND CALCIUM-BINDING DATA.  
 RP MEDLINE=83213514; PubMed=6406503;  
 RX Johnson A.E., Eamon N.L., Lane T.M., Eamon C.T.;  
 RA "Structural changes required for activation of protein C are induced  
 RT by Ca2+ binding to a high affinity site that does not contain gamma-  
 RL carboxyglutamic acid.";  
 RN J. Biol. Chem. 258:5554-5560(1983).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN, THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: K02435; AAA30685.1; -  
 DR PIR: A00928; KXBO.  
 DR HSSP: P04070; 1PCU.  
 DR MEROPS: S01.218; -  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; gla; 1.  
 DR SMART: SM00181; EGF; 2.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; Tryp\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF CA; 1.  
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 29  
 FT PROPEP 30 39

FT CHAIN 40 194 PROTEIN C LIGHT CHAIN.  
 FT CHAIN 197 456 PROTEIN C HEAVY CHAIN.  
 FT PEPTIDE 197 210 ACTIVATION PEPTIDE.  
 FT DOMAIN 94 129 EGF-LIKE 1.  
 FT DOMAIN 133 173 EGF-LIKE 2.  
 FT DOMAIN 211 456 SERINE PROTEASE.  
 FT MOD\_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 110 110 HYDROXYLATION.  
 FT ACT\_SITE 252 252 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 298 298 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 397 397 CHARGE RELAY SYSTEM.  
 FT DISULFID 56 61 BY SIMILARITY.  
 FT DISULFID 89 108 BY SIMILARITY.  
 FT DISULFID 98 103 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 119 128 BY SIMILARITY.  
 FT DISULFID 137 148 BY SIMILARITY.  
 FT DISULFID 144 157 BY SIMILARITY.  
 FT DISULFID 159 172 BY SIMILARITY.  
 FT DISULFID 180 318 INTERCHAIN.  
 FT DISULFID 237 253  
 FT DISULFID 253 368  
 FT DISULFID 368 382  
 FT DISULFID 393 421  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 366 366 F -> K.  
 FT VARIANT 82 82  
 FT CONFLICT 455 456  
 SQ SEQUENCE 456 AA; 51407 MW; CAAFE833FE94C209 CRC64;  
 Query Match 51.3%; Score 97; DB 1; Length 456;  
 Best Local Similarity 43.2%; Pred. No. 2.9e-10;  
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 ANGELXXLRGSLRXCRXXLCSFXAXEIPRXRXTRPGFWY 44  
 DB 40 ANSFLEBLRPGNVNRECSERVCSEFEAREIFQNTEDTMAFW 83  
 RESULT 11  
 ID PA10\_HUMAN STANDARD; PRT; 488 AA.  
 AC P00742; Q14340;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN P10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91216473; PubMed=1902434;  
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;  
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding  
 RL human coagulation factor X.";  
 RL Gene 99:291-294(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026600; PubMed=3768336;

RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;  
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 RT organization is essentially identical with that of factor IX and  
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 RL [3]  
 RN  
 RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X."; Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RL [4]  
 RN  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kail R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
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 RL [5]  
 RN  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid."; Biochemistry 22:2875-2884(1983).  
 RL [6]  
 RN  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X."; Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RL [7]  
 RN  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X."; Eur. J. Biochem. 218:153-163(1993).  
 RL [8]  
 RN  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X."; Gene 84:517-519(1989).  
 RL [9]  
 RN  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
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 RL [10]  
 RN  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural Basis for Chemical Inhibition of human blood coagulation  
 RT factor Xa."; Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.

CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 DR PIR; A25853; A25853.  
 DR PIR; A24478; A24478.  
 DR PDB; 1HCG; 08-MAY-95.  
 DR PDB; 1FAX; 29-OCT-97.  
 DR PDB; 1FXY; 17-JUN-98.  
 DR PDB; 1XKA; 23-MAR-99.  
 DR PDB; 1XKB; 23-MAR-99.  
 DR MEROPS; S01.216; -;  
 DR GlycoSiteDB; P00742; -;  
 DR Genew; HGNC:3528; F10.  
 DR MIM; 134530; -;  
 DR MIM; 227600; -;  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR002383; GLA\_dlood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
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 DR PRINTS; PR00001; GLABLOOD.  
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 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
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 FT SIGNAL 1 31 POTENTIAL.

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FT CHAIN       41      179     . FACTOR X HEAVY CHAIN.
FT CHAIN       183     488     . ACTIVATION PEPTIDE.
FT PROPEP      183     234     ACTIVATED FACTOR XA, HEAVY CHAIN.
FT CHAIN       225     488     EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN      86     122     EGF-LIKE 2.
FT DOMAIN      125     155     SERINE PROTEASE.
FT DOMAIN      235     488     GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES     47      47     GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES     54      54     GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES     56      56     GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES     59      59     GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES     66      66     GAMMA-CARBOXYGLUTAMIC ACID.
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FT CARBOHYD     199     199     O-LINKED (GALNAC. . .).
FT CARBOHYD     211     211     O-LINKED (GALNAC. . .).
FT CARBOHYD     221     221     N-LINKED (GLCNAC. . .).
FT CARBOHYD     231     231     /FTID-CAR 000012.
FT CARBOHYD     231     231     N-LINKED (GLCNAC. . .).
FT ACT_SITE     276     276     /FTID-CAR 000013.
FT ACT_SITE     322     322     CHARGE RELAY SYSTEM.
FT ACT_SITE     419     419     CHARGE RELAY SYSTEM.
FT DISULFID     90      101     CHARGE RELAY SYSTEM.
FT DISULFID     95      110
FT DISULFID     112     121
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Db 41 ANSFLBEMKKGHLERECMETCSYEAREVFESDSDKTNERMNTKY 84

RESULT 12
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AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RA MEDLINE=84247315; PubMed=6330671;
RX Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=8013053; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RN Biochemistry 19:659-667(1980).
RN [3]
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RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X."
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermodson W.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases."
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region."
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide."
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X."
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Teلمان O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding."
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnehaugen M., Ullner M., Persson E., Teلمان O.,
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RA Stenflo J., Drakenberg T.;  
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High  
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-  
 RT like domain in coagulation factor X";  
 RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,  
 RA Trewthell J.;  
 RT "The relative orientation of Gla and EGF domains in coagulation  
 RT factor X is altered by Ca2+ binding to the first EGF domain. A  
 RT combined NMR-small angle X-ray scattering study.";  
 RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
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 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
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 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 DR PROSITE; PS00240; TRYPSIN\_DOM.1.  
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DR PROSITE; PS00135; TRYPSIN\_SER.1.  
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.  
 KM SIGNAL  
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 FT PROPEP 24 40  
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 FT CHAIN 183 492 FACTOR X HEAVY CHAIN.  
 FT PROPEP 183 233 ACTIVATION PEPTIDE.  
 FT CHAIN 234 492 ACTIVATED FACTOR XA, HEAVY CHAIN.  
 FT PROPEP 476 492 MAY BE REMOVED BUT IS NOT NECESSARY FOR  
 FT ACTIVATION.  
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 125 165 EGF-LIKE 2.  
 FT DOMAIN 234 492 SERINE PROTEASE.  
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 FT MOD\_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.  
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 Db 41 ANSFLEBYKQGNLREHCEACSLSEAREVEDEAQTDFNSKY 84  
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 ID FA10\_RABIT STANDARD; PRT; 490 AA.  
 AC 019045.  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97256311; PubMed=9101642;  
 RA Penderuth U.R., Anderson K.D., James H.L.;  
 RT "Characterization of a full-length cDNA for rabbit factor X.";  
 RL Thromb. Res. 85:503-514(1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
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 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
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 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
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 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
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 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 DR MEROPS: S01.216; -.  
 DR Interpro: IPR000152; Asx\_hydroxyl.  
 DR Interpro: IPR001314; Chymotrypsin.  
 DR Interpro: IPR000561; EGF-like.  
 DR Interpro: IPR000742; EGF-2.  
 DR Interpro: IPR001881; EGF-Ca.  
 DR Interpro: IPR002383; GLA\_blood.  
 DR Interpro: IPR001254; Ser protease\_Try.  
 DR Interpro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; gla; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_1like; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TRYF\_Spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYFSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPsin\_HIS; 1.  
 DR PROSITE: PS00135; TRYPsin\_SER; 1.  
 DR GlycoProtein: Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KM Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
 FT PROPEP 41 40  
 FT CHAIN 21 180  
 FT CHAIN 184 490  
 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT DOMAIN 86 122  
 FT DOMAIN 125 165  
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 FA2\_HUMAN ID FA9\_HUMAN STANDARD; PRT; 461 AA.  
 AC P00740;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor IX precursor (BC 3.4.21.22) (Christmas factor).  
 GN F9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 OX (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86000558; PubMed=2994716;  
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;  
 RT "Nucleotide sequence of the gene for human factor IX (antithemophilic  
 factor B).";  
 RL Biochemistry 24:3736-3750 (1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85190593; PubMed=3857619;  
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84236100; PubMed=6329734;  
 RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,  
 RA Huddleston J.A., Brownlee G.G.;  
 RT "The gene structure of human anti-haemophilic factor IX.";  
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 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83220788; PubMed=6687940;  
 RA Jaye M., de la Salle H., Schamber F., Bailand A., Kohli V.,  
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 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a  
 unique 52-base synthetic oligonucleotide probe deduced from the amino  
 acid sequence of bovine factor IX.";  
 RT

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 RN [5]  
 RP SEQUENCE OF 36-326 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=84300526; PubMed=6089357;  
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;  
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 RL Sonat. Cell Mol. Genet. 10:465-473 (1984).  
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 RP SEQUENCE OF 290-359 FROM N.A.  
 RX MEDLINE=88127096; PubMed=3340835;  
 RA Stofler E.S., Koebel D.D., Sarkar G., Sommer S.S.;  
 RT "Genomic amplification with transcript sequencing.";  
 RL Science 239:491-494 (1988).  
 RN [7]  
 RP SEQUENCE OF 444-461 FROM N.A.  
 RX MEDLINE=94045330; PubMed=8236150;  
 RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,  
 RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;  
 RT "A deletion located in the 3' non translated part of the factor IX  
 RT gene responsible for mild haemophilia B.";  
 RL Thromb. Haemost. 70:370-371 (1993).  
 RN [8]  
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).  
 RX MEDLINE=90078229; PubMed=2592373;  
 RA Suehito K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
 RA Ogata K., Kamitani T., Saito H., Niho Y., Iwanaga S.;  
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by  
 RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell  
 RT chymase.";  
 RL J. Biol. Chem. 264:21257-21265 (1989).  
 RN [9]  
 RP HYDROXYLATION OF ASP-110.  
 RX MEDLINE=83308813; PubMed=6688526;  
 RA McMullen B.A., Fujikawa K., Kisiel W.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
 RT K-dependent blood coagulation zymogens.";  
 RL Biochem. Biophys. Res. Commun. 115:8-14 (1983).  
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 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=78194509; PubMed=659613;  
 RA di Sciopio R.G., Kurachi K., Davie E.W.;  
 RT "Activation of human factor IX (Christmas factor).";  
 RL J. Clin. Invest. 61:1528-1538 (1978).  
 RN [11]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185715; PubMed=6425296;  
 RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;  
 RT "Derivatives of blood coagulation factor IX contain a high affinity  
 RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";  
 RL J. Biol. Chem. 259:5698-5704 (1984).  
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 RP ERRATUM.  
 RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;  
 RL J. Biol. Chem. 260:2583-2583 (1985).  
 RN [13]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE.  
 RX MEDLINE=86189947; PubMed=3009023;  
 RA Bertley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
 RT "Defective propeptide processing of blood clotting factor IX caused  
 RT by mutation of arginine to glutamine at position -4.";  
 RL Cell 45:343-348 (1986).  
 RN [14]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325 (1989).

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 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;  
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 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
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 RP STRUCTURE OF CARBOHYDRATE ON SER-107.  
 RX MEDLINE=92386094; PubMed=1517205;  
 RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;  
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
 RT serine 61 through the fucose residue.";  
 RL J. Biol. Chem. 267:17520-17525 (1992).  
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 RP PHOSPHORYLATION OF SER-114.  
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 RT "Partial phosphorylation of serine-68 in EGF-I of human factor IX.";  
 RL (in) Abstracts of 11th international conference on methods in protein  
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 RN [18]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=20575397; PubMed=1113752;  
 RA Arruda V.R., Hagstrom J.N., Delich J., Heiman-Patterson T.,  
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 RT "Posttranslational modifications of recombinant myotube-synthesized  
 RT human factor IX.";  
 RL Blood 97:130-138 (2001).  
 RN [19]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=95229607; PubMed=7713897;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
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 RP STRUCTURE BY NMR OF 47-93.  
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 RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
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 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=97199336; PubMed=9047312;  
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 RP STRUCTURE BY NMR OF 91-133.  
 RX MEDLINE=91308127; PubMed=1854745;  
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;  
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 RT location of the calcium binding site in the first epidermal growth  
 RT factor like domain of blood coagulation factor IX.";  
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 RN [24]  
 RP STRUCTURE BY NMR OF 92-130.  
 RX MEDLINE=93284090; PubMed=1304885;  
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RA Tse A.G., Brownlee G.G., Campbell I.D.C.;  
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RX [25]  
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
RX MEDLINE=95310802; Pubmed=7606779;  
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RL domain: its role in protein-protein interactions";  
RN Cell 82:131-141(1995).  
RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.

Query Match 49.2%; Score 93; DB 1; Length 461;  
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Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps

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DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)  
DE (Autoproteolysin IIa) (Anticoagulant protein C) (Blood coagulation  
DE factor XIV).  
DE PROC.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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RP SEQUENCE FROM N.A.  
RX MEDLINE=85270390; Pubmed=2991887;  
RA Foster D.C., Yoshitake S., Davie E.W.;  
RT "The nucleotide sequence of the gene for human protein C";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85269639; Pubmed=2991859;  
RA Beckmann R.J., Schmidt R.J., Satterre R.F., Plutsky J., Crabtree G.R.;  
RL Long G.L.;  
RT "The structure and evolution of a 461 amino acid human protein C  
RT precursor and its messenger RNA, based upon the DNA sequence of  
RT cloned human liver cDNAs";  
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RP SEQUENCE FROM N.A.  
RX MEDLINE=86120978; Pubmed=3511471;  
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RX MEDLINE=84272714; Pubmed=5589623;  
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RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).  
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RP CARBOHYDRATE-LINKAGE SITE ASN-371.  
RX MEDLINE=90293094; Pubmed=16941179;

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RX MEDLINE=92164750; PubMed=1544894;  
RA Harris R.J., Ling P.B., Spellman M.W.;  
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RT domain of factor XII but not protein C.";  
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RP 3D-STRUCTURE MODELING OF 175-450.  
RX MEDLINE=94272342; PubMed=8003977;  
RA Fisher C.L., Greengard J.S., Griffin J.H.;  
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RT plasma factor activated protein C and its zymogen.";  
RL Protein Sci. 3:588-599(1994).  
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RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.  
RX MEDLINE=97157472; PubMed=9003757;  
RA Mather T., Oganesyan V., Hof P., Huber R., Foundling S., Esmon C.,  
RA Bode W.;  
RT "rmp 2.8 A crystal structure of Gla-domainless activated protein C.";  
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RP REVIEW ON PROC VARIANTS.  
RX MEDLINE=93190290; PubMed=8446940;  
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RA Sala N., Cooper D.N.;  
RT "Protein C deficiency: a database of mutations. For the Protein C & S  
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RT associated with two GLA domain mutations.";  
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 RX MEDLINE=92380660; PubMed=1511988;  
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;  
 RT "A novel homozygous missense mutation in the protein C (PROC) gene  
 RL causing recurrent venous thrombosis.";  
 RN Hum. Genet. 89:683-684(1992).  
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 RX MEDLINE=93250852; PubMed=1301959;  
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 RT electrophoresis.";  
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 RP VARIANT SER-334.  
 RX MEDLINE=92276939; PubMed=1593215;  
 RA Yamamoto K., Matsumita T., Sugitara I., Takamatsu J., Iwasaki E.,  
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 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.  
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 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND  
 RP V-388.  
 RX MEDLINE=93271391; PubMed=8499565;  
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 RA Bertina R.M.;  
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 RL Blood Coagul. Fibrinolysis 4:273-280(1993).  
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 RP VARIANT TRP-57.  
 RX MEDLINE=93271396; PubMed=8499568;  
 RA Millar D.S., Grundy C.B., Bignelli P., Moffat E.H., Martin R.,  
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 RT causing type 2 protein C deficiency and recurrent venous  
 RT thrombosis.";  
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 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.  
 RX MEDLINE=94122329; PubMed=8292730;  
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,  
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 RT "Genetic mutations in ten unrelated American patients with  
 RT symptomatic type 1 protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).  
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 RP VARIANT SER-423.  
 RX MEDLINE=94001606; PubMed=8398832;  
 RA Marchetti G., Patrachini P., Gemmati D., Castaman G., Rodeghiero F.,

RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;  
 RT "Symptomatic type II protein C deficiency caused by a missense  
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";  
 RL Br. J. Haematol. 84:285-289(1993).  
 RN [25]  
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).  
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(without alignments)  
196.288 Million cell updates/sec

Title: 10Gln28Glu\_4  
189  
Sequence: 1 ANGFLXXLRQSLKRCXCRXX.....XXAEXIFRNXXRTQFWVSX 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

SPTREMBL 21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 123   | 65.1        | 701    | 4 Q96PQ8  | Q96PQ8 homo sapien |
| 2          | 109   | 57.7        | 460    | 11 Q91WN8 | Q91WN8 mus musculu |
| 3          | 106   | 56.1        | 446    | 11 Q61109 | Q61109 mus musculu |
| 4          | 103   | 54.5        | 460    | 11 Q99PC6 | Q99PC6 mus musculu |
| 5          | 100   | 52.9        | 456    | 6 Q9TTR0  | Q9TTR0 canis famli |
| 6          | 96    | 50.8        | 482    | 11 Q63207 | Q63207 ratu        |
| 7          | 93    | 49.2        | 461    | 6 Q14316  | Q14316 homo sapien |
| 8          | 93    | 49.2        | 461    | 6 Q95ND7  | Q95ND7 pan troglod |
| 9          | 93    | 49.2        | 481    | 11 Q54740 | Q54740 mus musculu |
| 10         | 93    | 49.2        | 481    | 11 Q99L32 | Q99L32 mus musculu |
| 11         | 93    | 49.2        | 481    | 11 Q88947 | Q88947 mus musculu |
| 12         | 93    | 49.2        | 481    | 11 Q95ME8 | Q95ME8 bos tauris  |
| 13         | 89    | 47.1        | 49     | 6 Q9GMD9  | Q9GMD9 ornithorhyn |
| 14         | 89    | 47.1        | 49     | 6 Q28994  | Q28994 sus scrofa  |
| 15         | 82    | 43.4        | 138    | 6 Q90YK1  | Q90YK1 brachydanio |
| 16         | 80    | 42.3        | 433    | 13 Q90YK1 | Q90YK1 brachydanio |

|    |      |      |     |           |                    |
|----|------|------|-----|-----------|--------------------|
| 17 | 80   | 42.3 | 648 | 6 Q29094  | Q29094 sus scrofa  |
| 18 | 79   | 41.8 | 399 | 11 Q9CQW3 | Q9CQW3 mus musculu |
| 19 | 78   | 41.3 | 100 | 4 Q15253  | Q15253 homo sapien |
| 20 | 78   | 41.3 | 608 | 13 Q9PTW7 | Q9PTW7 struthio ca |
| 21 | 76.5 | 40.5 | 542 | 5 Q8T613  | Q8T613 halocynthia |
| 22 | 75   | 39.7 | 650 | 4 Q9NSD0  | Q9NSD0 homo sapien |
| 23 | 75   | 39.7 | 650 | 4 Q16519  | Q16519 homo sapien |
| 24 | 71   | 37.6 | 179 | 4 Q8TAS3  | Q8TAS3 homo sapien |
| 25 | 71   | 37.6 | 198 | 11 Q8R182 | Q8R182 mus musculu |
| 26 | 66   | 34.9 | 607 | 13 Q91001 | Q91001 gallus gall |
| 27 | 64   | 33.9 | 678 | 4 Q14393  | Q14393 homo sapien |
| 28 | 63   | 33.3 | 673 | 11 Q61592 | Q61592 mus musculu |
| 29 | 63   | 33.3 | 674 | 11 Q99K57 | Q99K57 mus musculu |
| 30 | 61   | 32.3 | 674 | 11 Q63772 | Q63772 ratu        |
| 31 | 58   | 30.7 | 25  | 11 Q90VH6 | Q90VH6 ratu        |
| 32 | 57   | 30.2 | 98  | 13 P82807 | P82807 notechis sc |
| 33 | 57   | 26.7 | 575 | 10 Q94E17 | Q94E17 oryza sativ |
| 34 | 50.5 | 26.7 | 608 | 10 Q9XRF3 | Q9XRF3 medicago sa |
| 35 | 50   | 26.5 | 472 | 13 Q98SU5 | Q98SU5 gasteroste  |
| 36 | 50   | 26.5 | 613 | 13 Q98SU6 | Q98SU6 gasteroste  |
| 37 | 50   | 26.5 | 910 | 13 Q98SU7 | Q98SU7 gasteroste  |
| 38 | 49.5 | 26.2 | 196 | 10 Q04284 | Q04284 belaginelia |
| 39 | 49.5 | 26.2 | 567 | 10 Q8W4J2 | Q8W4J2 arabidopsis |
| 40 | 49.5 | 26.2 | 603 | 10 Q9LPJ7 | Q9LPJ7 arabidopsis |
| 41 | 49.5 | 26.2 | 606 | 10 Q9SUG9 | Q9SUG9 arabidopsis |
| 42 | 49.5 | 26.2 | 651 | 10 Q8S218 | Q8S218 oryza sativ |
| 43 | 48.5 | 25.7 | 431 | 10 Q94EY5 | Q94EY5 arabidopsis |
| 44 | 48.5 | 25.7 | 492 | 10 Q9SMJ7 | Q9SMJ7 cicet ariet |
| 45 | 48.5 | 25.7 | 543 | 10 Q9MB23 | Q9MB23 arabidopsis |

## ALIGNMENTS

RESULT 1  
Q96PQ8 PRELIMINARY; PRT; 701 AA.  
ID Q96PQ8: 01-DEC-2001 (TREMBLrel. 19, Created)  
AC Q96PQ8: 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Factor VII active site mutant immunocognate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034;  
RA Hu Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
RT cells for immunotherapy in mouse models of prostatic cancer.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
RL EMBL; AF272774; AAK58686.1; -.  
DR InterPro: IPR000152; Asx hydroxyl.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF-2.  
DR InterPro: IPR001881; EGF\_CA.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR001254; Ser protease\_Try.  
DR InterPro: IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00047; Ig; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR SMART; SMO0181; EGF; 2.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 65.1%; Score 123; DB 4; Length 701;  
Best Local Similarity 52.3%; Pred. No. 7.9e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXRCXXLCSPFXAEXIFRNXXRTROPWVSY 44  
DB 61 ANAFLEELRPGLSLEKCEKQCSFEERAREIFKDAERTKLFWISY 104

## RESULT 2

ID 091MN8 PRELIMINARY; PRT; 460 AA.  
AC 091MN8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Similar to protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Strauberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013896; AAH13896.1; -.  
DR MGD; MGI:97771; Proc.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; GLA; 1.  
DR Pfam; PF00089; clypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 460 AA; 51818 MW; 0117F2668FCC274 CRC64;

Query Match 57.7%; Score 109; DB 11; Length 460;  
Best Local Similarity 45.5%; Pred. No. 1.9e-11;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXRCXXLCSPFXAEXIFRNXXRTROPWVSY 44  
DB 42 ANSFLERMPGSLERCEKQCSFEERAREIFQNVEDTLAFWIKY 85

## RESULT 3

ID 061109 PRELIMINARY; PRT; 446 AA.  
AC 061109;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Coagulation factor VII.  
GN F7 OR FVII.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96276538; PubMed=8701412;  
RA Iduegile E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
RA Castellino F.V.;  
RT "Characterization of a cDNA encoding murine coagulation factor VII";  
RT Thromb. Haemost. 75:481-487(1996).  
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
TRYPSIN FAMILY.

DR EMBL; U44795; AAC52570.1; -.  
DR HSSP; P08709; 1FAK.  
DR MEROPS; S01.215; -.  
DR MGD; MGI:109325; F7.  
DR InterPro; IPR002086; Aldehyde dehydr.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; GLA; 1.  
DR Pfam; PF00089; clypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00070; ALDEHYDE DEHYDR\_CYS; UNKNOWN\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
KW Serine protease.  
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BFEDA6870 CRC64;

Query Match 56.1%; Score 106; DB 11; Length 446;  
Best Local Similarity 47.7%; Pred. No. 6.6e-11;  
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLRXRCXXLCSPFXAEXIFRNXXRTROPWVSY 44  
DB 42 ANSLLEELMPGSLERCEKQCSFEERAREIFKSPERTKQFWIVY 85

## RESULT 4

ID 099PC6 PRELIMINARY; PRT; 460 AA.  
AC 099PC6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anticoagulant protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL;  
RA Korf I.;



RT "Complete sequence of UC72A01."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; AF318182; AK07918.1; -.  
DR HSSP; P04070; 1PCU.  
DR MEROPS; S01.218; -.  
DR MGD; MGI:97771; Proc.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF Ca.  
DR InterPro; IPR002383; GLA blood.  
DR InterPro; IPR001254; Ser protease\_Try.  
DR InterPro; IPR000294; vitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00181; EGF\_2.  
DR SMART; SM00001; EGF\_like; 2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; tryp\_sec; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01166; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease.  
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;  
Query Match 54.5%; Score 103; DB 11; Length 460;  
Best Local Similarity 43.2%; Pred. No. 2.4e-10;  
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 ANGFLXLRQSLKRXCRXXLCSFXAXEIRFNXXRRQFWVS 44  
Db 42 ANSFLEWRPGLRECEMEICDLEAQEIFQNVEDTLAFWIKY 85  
RESULT 5  
Q9TTRO PRELIMINARY; PRT; 456 AA.  
AC Q9TTRO;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Protein C precursor.  
GN PROC.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,  
RA Brenig B.,  
RT "Molecular characterization and chromosomal assignment of the canine  
RT protein C gene."  
RL Mamm. Genome 10:135-139 (1999).  
RN [2]  
RX SEQUENCE FROM N.A.  
RX MEDLINE=93371952; PubMed=10443005;  
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.,  
RT "Analysis of canine protein C gene polymorphisms."  
RL Anim. Genet. 30:237-238 (1999).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.

DR EMBL; AJ001979; CAA05126.1; -.  
DR HSSP; P04070; 1PCU.  
DR MEROPS; S01.218; -.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF Ca.  
DR InterPro; IPR002383; GLA blood.  
DR InterPro; IPR001254; Ser protease\_Try.  
DR InterPro; IPR000294; vitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00181; EGF\_2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; tryp\_sec; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01166; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease; Signal.  
FT SIGNAL 1 42  
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.  
FT FT 193 194 PROTEIN C CONNECTING DIPEPTIDE.  
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.  
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59F CRC64;  
Query Match 52.9%; Score 100; DB 6; Length 456;  
Best Local Similarity 43.2%; Pred. No. 8.4e-10;  
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 ANGFLXLRQSLKRXCRXXLCSFXAXEIRFNXXRRQFWVS 44  
Db 43 ANSFLEIRAGSLRECEMEICDFEAKKEIFQNVDDTLAWYSKY 86  
RESULT 6  
Q63207 PRELIMINARY; PRT; 482 AA.  
AC Q63207;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Factor X.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE=96093366; PubMed=8578539;  
RA Stanton C., Ross R.P., Hutson S., Wallin R.,  
RT "Evidence for competition between vitamin K-dependent clotting factors  
RT for intracellular processing by the vitamin K-dependent gamma-  
RT carboxylase."  
RL Thromb. Res. 80:63-73 (1995).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; X79807; CAA56202.1; -.  
DR HSSP; P00742; 1XKA.  
DR MEROPS; S01.216; -.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.

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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GlA; 1.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00017; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 50.8%; Score 96; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 4.7e-09;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRQSLKRXCRXXLCSPXXAEXIFRNXXRTROFWSY 44
Db 41 ANSFEEIKKGNLRECEVEICSPFEAREVFEDNEKTEFMKXY 84

RESULT 7
O14316 PRELIMINARY; PRT; 456 AA.
AC O14316;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL; AL033403; CAA21954.1; -.
CC EMBL; X55008; CAB38245.2; -.
DR HSRP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.

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DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GlA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 49.2%; Score 93; DB 4; Length 456;
Best Local Similarity 41.9%; Pred. No. 1.6e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NGFLXXLRQSLKRXCRXXLCSPXXAEXIFRNXXRTROFWSY 44
Db 44 SKGLEFPVQGNLERCEMEKCSFEAREVFENTERTTFMKXY 86

RESULT 8
O95ND7 PRELIMINARY; PRT; 461 AA.
AC O95ND7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE F9 (Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RT Genes Genet. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GlA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

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DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KM Hydrolase; Serine protease.  
 SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 49.2%; Score 93; DB 6; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 1.6e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRQSLXRCXRLCSFXAXEYIFRNXXRTROFWVS 44  
 Db 49 SGKLEEFVQGNLERECMEKCSFEARREVFEKTEFTFWKQY 91

## RESULT 9

Q95ND6 PRELIMINARY; PRT; 461 AA.  
 AC Q95ND6; (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 20, Last sequence update)  
 DE Coagulation factor XI.  
 GN P9.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxId=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=505;  
 RA Saita Y.;  
 RT "Comparison of DNA and protein polymorphisms between humans and  
 RT chimpanzees.";  
 RL Genes Genet. Syst. 0:0-0(2001).  
 DR EMBL; AB062471; BAB58886.1; JOINED.  
 DR EMBL; AB062459; BAB58886.1; JOINED.  
 DR EMBL; AB062461; BAB58886.1; JOINED.  
 DR EMBL; AB062463; BAB58886.1; JOINED.  
 DR EMBL; AB062465; BAB58886.1; JOINED.  
 DR EMBL; AB062467; BAB58886.1; JOINED.  
 DR EMBL; AB062469; BAB58886.1; JOINED.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VltK\_dep\_GLA.  
 DR Pfam; PF00008; G1a; 1.  
 DR Pfam; PF000594; G1a; 1.  
 DR Pfam; PF00089; trypsin.1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
 DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_2.  
 DR PROSITE; PS00011; GLUT CARBOXYLATION; UNKNOWN\_1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KM Hydrolase; Serine protease.  
 SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 49.2%; Score 93; DB 6; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 1.6e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRQSLXRCXRLCSFXAXEYIFRNXXRTROFWVS 44  
 Db 49 SGKLEEFVQGNLERECMEKCSFEARREVFEKTEFTFWKQY 91

RESULT 10  
 054740 PRELIMINARY; PRT; 481 AA.

AC 054740; (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6).  
 GN F10 OR F10.  
 OS Mus musculus (Mouse).  
 OS Plasmid plb1escrpt.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;  
 RX MEDLINE=98454993; PubMed=9783672;  
 RA Heidemann H.H., Kontemann R.E.;  
 RT "Cloning and recombinant expression of mouse coagulation factor X.";  
 RL Thromb. Res. 92:33-41(1998).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL; AJ222677; CAA10933.1; -.  
 DR HSP; P00742; 1XKA.  
 DR MEROPS; S01.216; -.  
 DR MED; MGI:103107; F10.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VltK\_dep\_GLA.  
 DR Pfam; PF00008; G1a; 2.  
 DR Pfam; PF00594; G1a; 1.  
 DR Pfam; PF00089; trypsin.1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYPSIN; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLUT CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;  
 KW Repeat; Serine protease; Signal.  
 FT SIGNAL 1 40 POTENTIAL.  
 FT CHAIN 41 481 COAGULATION FACTOR X.  
 SQ SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D97AE CRC64;

Query Match 49.2%; Score 93; DB 11; Length 481;  
 Best Local Similarity 31.8%; Pred. No. 1.7e-08;  
 Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQSLXRCXRLCSFXAXEYIFRNXXRTROFWVS 44  
 Db 41 ANSFEEFKGNLERECMEKCSFEARREVFEKTEFTFWKQY 84

## RESULT 11

Q99LJ2 PRELIMINARY; PRT; 481 AA.  
 AC Q99LJ2;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Coagulation factor X.  
 GN F10.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubeberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; LXKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF-2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.7e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRQGSILRXCRXXLCSPFXAEXIFRNXXRTPQFWVS 44
DB 41 ANSFEEFFKGNLRECMETICSYEEVRELFEDDEKTKYWTXY 84

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## RESULT 12

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ID 088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; Pubmed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;

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RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC6345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; LXKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF-2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E5F9D271E CRC64;

Query Match 49.2%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.7e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRQGSILRXCRXXLCSPFXAEXIFRNXXRTPQFWVS 44
DB 41 ANSFEEFFKGNLRECMETICSYEEVRELFEDDEKTKYWTXY 84

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## RESULT 13

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ID 095ME8 PRELIMINARY; PRT; 49 AA.
AC 095ME8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amarat E.J.;
RA "Partial sequence of bovine F9 coding gene.";
RT

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10Gln28Glu\_4  
Perfect score: 189  
Sequence: 1 ANGFLXXLRQGSLLKRCXCRXX.....XXAEXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA: \*  
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3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
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| 1          | 156   | 82.5        | 44     | 3  | US-08-955-636-4  |
| 2          | 127   | 67.2        | 44     | 3  | US-08-955-636-30 |
| 3          | 126   | 66.7        | 44     | 3  | US-08-955-636-26 |
| 4          | 124   | 65.6        | 44     | 3  | US-08-955-636-27 |
| 5          | 123   | 65.1        | 44     | 3  | US-08-955-636-3  |
| 6          | 123   | 65.1        | 406    | 1  | US-08-293-778-24 |
| 7          | 123   | 65.1        | 406    | 1  | US-08-295-411-5  |
| 8          | 123   | 65.1        | 406    | 1  | US-08-955-471-5  |
| 9          | 123   | 65.1        | 406    | 5  | PCT-US92-10242-5 |
| 10         | 123   | 65.1        | 444    | 1  | US-08-475-845-2  |
| 11         | 123   | 65.1        | 444    | 1  | US-08-327-690-2  |
| 12         | 123   | 65.1        | 444    | 2  | US-08-660-289-2  |
| 13         | 123   | 65.1        | 444    | 2  | US-08-537-807-2  |
| 14         | 123   | 65.1        | 444    | 2  | US-08-871-003-2  |
| 15         | 123   | 65.1        | 444    | 3  | US-08-464-233-2  |
| 16         | 123   | 65.1        | 444    | 4  | US-09-189-607-2  |
| 17         | 123   | 65.1        | 444    | 4  | US-09-378-907-2  |
| 18         | 123   | 65.1        | 444    | 5  | PCT-US94-05779-2 |
| 19         | 123   | 65.1        | 466    | 1  | US-07-882-202A-4 |
| 20         | 123   | 65.1        | 466    | 1  | US-08-021-615A-4 |
| 21         | 123   | 65.1        | 466    | 1  | US-08-321-777-4  |
| 22         | 123   | 65.1        | 466    | 4  | US-09-009-217-14 |
| 23         | 123   | 65.1        | 466    | 4  | US-09-009-656-14 |
| 24         | 123   | 65.1        | 466    | 5  | PCT-US93-04493-4 |
| 25         | 120   | 63.0        | 44     | 3  | US-08-955-636-28 |
| 26         | 119   | 63.0        | 44     | 3  | US-08-955-636-29 |
| 27         | 109   | 57.7        | 41     | 1  | US-08-229-280-4  |

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|----|-----|------|-----|---|------------------|--------------------|
| 28 | 101 | 53.4 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appli  |
| 29 | 101 | 53.4 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appli  |
| 30 | 101 | 53.4 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appli  |
| 31 | 101 | 53.4 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appli  |
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| 33 | 101 | 53.4 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appli  |
| 34 | 101 | 53.4 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appli  |
| 35 | 98  | 51.9 | 44  | 3 | US-08-955-636-23 | Sequence 2, Appli  |
| 36 | 98  | 51.9 | 44  | 3 | US-08-955-636-24 | Sequence 2, Appli  |
| 37 | 97  | 51.3 | 44  | 3 | US-08-955-636-2  | Sequence 2, Appli  |
| 38 | 96  | 50.8 | 448 | 1 | US-08-225-411-3  | Sequence 3, Appli  |
| 39 | 96  | 50.8 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appli  |
| 40 | 96  | 50.8 | 448 | 5 | PCT-US92-10068-1 | Sequence 1, Appli  |
| 41 | 96  | 50.8 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appli  |
| 42 | 95  | 50.3 | 44  | 3 | US-08-955-636-35 | Sequence 35, Appli |
| 43 | 95  | 50.3 | 487 | 2 | US-08-469-486-53 | Sequence 53, Appli |
| 44 | 95  | 50.3 | 487 | 2 | US-08-469-658-53 | Sequence 53, Appli |
| 45 | 95  | 50.3 | 492 | 1 | US-08-469-486-2  | Sequence 2, Appli  |

## ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      82.5%; Score 156; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.4e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 ANGFLXXLRQGSLLKRCXCRXXCXFXAEXIFRNXXRTQFWVSY 44
Db 1 ANGFLXXLRPGSLKRCXCRXXCXFXAEXIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```

```
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```
Query Match          67.2%; Score 127; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 5,1e-15;
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      1 ANGFLLXLRQGSILRXCRXXLCSPXXAEXIFRNXXRTROPFWVS 44
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 ANAFLLXLRQGSILRXCRXXQCSPXXARXIFPDAXRTKLFWISY 44
```

RESULT 3

```
US-08-955-636-26
/ Sequence 26, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelstuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26
```

```
Query Match          66.7%; Score 126; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 7,6e-15;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 ANGFLLXLRQGSILRXCRXXLCSPXXAEXIFRNXXRTROPFWVS 44
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 ANAFLLXLRQGSILRXCRXXQCSPXXARXIFPDAXRTKLFWISY 44
```

RESULT 4

```
US-08-955-636-27
/ Sequence 27, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelstuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 27
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```
Query Match          65.6%; Score 124; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 1,7e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      1 ANGFLLXLRQGSILRXCRXXLCSPXXAEXIFRNXXRTROPFWVS 44
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 ANAFLLXLRQGSILRXCRXXQCSPXXARXIFPDAXRTKLFWISY 44
```

RESULT 5

```
US-08-955-636-3
/ Sequence 3, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelstuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
```

```
Query Match          65.1%; Score 123; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 2,5e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      1 ANGFLLXLRQGSILRXCRXXLCSPXXAEXIFRNXXRTROPFWVS 44
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 ANAFLLXLRQGSILRXCRXXQCSPXXARXIFPDAXRTKLFWISY 44
```

RESULT 6

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US-08-293-778-24
/ Sequence 24, Application US/08293778
/ Patent No. 5580560
/ GENERAL INFORMATION:
/ APPLICANT: Nicolaissen, Else M.
/ APPLICANT: Bjorn, Soren E.
/ APPLICANT: Wiberg, Finn C.
/ APPLICANT: Woodbury, Richard
/ TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
/ STREET: 405 Lexington Avenue, 62nd Floor
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10174-6201
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/293,778
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/104,509
/ FILING DATE:
/ APPLICATION NUMBER: DK 3235/87
/ FILING DATE: 25-JUN-1987
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/434,149
/ FILING DATE: 13-NOV-1989
/ PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agila, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129.224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 65.1%; Score 123; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 2.4e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGLXRXCRXLCSPFXXAEXIFPNXXRTROFWVS 44  
Db 1 ANAFLELRPGSLRYCKYQCSFYARIFPDARTKLFWISY 44

RESULT 7  
US-08-295-411-5  
Sequence 5, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-295-411-5

Query Match 65.1%; Score 123; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 2.4e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGLXRXCRXLCSPFXXAEXIFPNXXRTROFWVS 44  
Db 1 ANAFLELRPGSLRYCKYQCSFYARIFPDARTKLFWISY 44

RESULT 8  
US-08-955-471-5  
Sequence 5, Application US/08955471  
Patent No. 5968751  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,471  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/295,411  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153...406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-955-471-5

Query Match 65.1%; Score 123; DB 2; Length 406;  
Best Local Similarity 52.3%; Pred. No. 2.4e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGLXXLRGSLXRCXRLCSFXXAEXIFRNXXRTQFWWSY 44  
DB 1 ANAFLELRPGSLERCKEQCSFEERARIFKDAERTKLFWSY 44

RESULT 9  
PCT-US92-10242-5

Sequence 5, Application PC/TUS9210242  
GENERAL INFORMATION:  
APPLICANT: Griffen, John H.  
APPLICANT: Meesters, Rolf  
TITLE OR INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OR INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 North Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10242  
FILING DATE: 19921118

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRO472P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"

FEATURE:  
NAME/KEY: Region  
LOCATION: 153...406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
PCT-US92-10242-5

Query Match 65.1%; Score 123; DB 5; Length 406;  
Best Local Similarity 52.3%; Pred. No. 2.4e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ANGLXXLRGSLXRCXRLCSFXXAEXIFRNXXRTQFWWSY 44  
DB 1 ANAFLELRPGSLERCKEQCSFEERARIFKDAERTKLFWSY 44

RESULT 10  
US-08-475-845-2  
Sequence 2, Application US/08475845  
Patent No. 578965

GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OR INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,845  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,690  
FILING DATE: 24-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-475-845-2

FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"

Query Match 65.1%; Score 123; DB 1; Length 444;  
Best Local Similarity 52.3%; Pred. No. 2.6e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ANGLXXLRGSLXRCXRLCSFXXAEXIFRNXXRTQFWWSY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEERARIFKDAERTKLFWSY 82

RESULT 11  
US-08-327-690-2

```
; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match 65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
```

```
QY 1 ANGFLXXLRQSLXRCXKXLCSPXXAXIFRNXXRTROFWVSY 44
Db 39 ANAFLEELRPGSLERCKEBCSFEEARIEIFKDAERTKLFWISY 82
```

```
RESULT 12
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
```

```
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2
```

```
Query Match 65.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
```

```
QY 1 ANGFLXXLRQSLXRCXKXLCSPXXAXIFRNXXRTROFWVSY 44
Db 39 ANAFLEELRPGSLERCKEBCSFEEARIEIFKDAERTKLFWISY 82
```

```
RESULT 13
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 65.1%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 2,6e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLLRQGSILRXCRXXLCFXXAEXIFRNXXRTROFWVS 44  
DB 39 ANAFLEELRPGSLERCKECCSFEEAREIFXDAERTKLFWISY 82

RESULT 14  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5937864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 65.1%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 2,6e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLLRQGSILRXCRXXLCFXXAEXIFRNXXRTROFWVS 44  
DB 39 ANAFLEELRPGSLERCKECCSFEEAREIFXDAERTKLFWISY 82

RESULT 15  
US-08-464-233-2  
Sequence 2, Application US/08464233  
Patent No. 6039944  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,233  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-233-2

Query Match 65.1%; Score 123; DB 3; Length 444;  
Best Local Similarity 52.3%; Pred. No. 2,6e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLLRQGSILRXCRXXLCFXXAEXIFRNXXRTROFWVS 44  
DB 39 ANAFLEELRPGSLERCKECCSFEEAREIFXDAERTKLFWISY 82

Search completed: March 19, 2003, 15:16:17  
Job time : 10.75 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using SW model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds  
(without alignments)  
280.876 Million cell updates/sec

Title: 10Gln28G1U\_4  
Perfect score: 189  
Sequence: 1 ANAFLLXRLRGSILKRCXCRXX.....XXAEXIFRNXXRRQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep:.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep:.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep:.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep:.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB pep:.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep:.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep:.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US05\_PUBCOMB pep:.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep:.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep:.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep:.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 123   | 65.1        | 406    | 9  | US-10-109-498-1    |
| 2          | 98    | 51.9        | 419    | 9  | US-10-182-263-6    |
| 3          | 93    | 49.2        | 415    | 10 | US-09-118-748-2    |
| 4          | 93    | 49.2        | 419    | 9  | US-10-182-263-1    |
| 5          | 93    | 49.2        | 419    | 9  | US-10-182-263-3    |
| 6          | 93    | 49.2        | 419    | 9  | US-10-182-263-4    |
| 7          | 93    | 49.2        | 419    | 9  | US-10-182-263-5    |
| 8          | 93    | 49.2        | 419    | 9  | US-09-978-917A-4   |
| 9          | 93    | 49.2        | 461    | 9  | US-10-182-263-2    |
| 10         | 93    | 49.2        | 461    | 9  | US-09-978-917A-2   |
| 11         | 93    | 49.2        | 461    | 9  | US-10-132-829-5    |
| 12         | 93    | 49.2        | 461    | 10 | US-09-884-901-3    |
| 13         | 70    | 37.0        | 209    | 9  | US-09-759-130B-313 |
| 14         | 70    | 37.0        | 209    | 9  | US-09-759-130B-310 |
| 15         | 70    | 37.0        | 225    | 9  | US-09-759-130B-356 |
| 16         | 53    | 28.0        | 208    | 9  | US-09-759-130B-355 |
| 17         | 53    | 28.0        | 225    | 9  | US-09-759-130B-353 |
| 18         | 53    | 28.0        | 225    | 9  | US-09-759-130B-353 |
| 19         | 43    | 22.8        | 332    | 10 | US-09-848-852A-3   |

|    |      |      |     |    |                   |                   |
|----|------|------|-----|----|-------------------|-------------------|
| 20 | 43   | 22.8 | 484 | 10 | US-09-801-368-334 | Sequence 334, App |
| 21 | 40.5 | 21.4 | 197 | 9  | US-10-076-622-516 | Sequence 516, App |
| 22 | 40.5 | 21.4 | 197 | 12 | US-10-007-805-516 | Sequence 516, App |
| 23 | 40.5 | 21.4 | 232 | 9  | US-10-076-622-517 | Sequence 517, App |
| 24 | 40.5 | 21.4 | 232 | 12 | US-10-007-805-517 | Sequence 517, App |
| 25 | 40.5 | 21.4 | 243 | 9  | US-09-938-418-7   | Sequence 7, Appli |
| 26 | 40.5 | 21.4 | 243 | 9  | US-10-045-992-4   | Sequence 4, Appli |
| 27 | 40.5 | 21.4 | 243 | 9  | US-10-063-547-122 | Sequence 122, App |
| 28 | 40.5 | 21.4 | 243 | 9  | US-10-174-590-366 | Sequence 366, App |
| 29 | 40.5 | 21.4 | 243 | 9  | US-10-176-758-366 | Sequence 366, App |
| 30 | 40.5 | 21.4 | 243 | 9  | US-10-063-616-122 | Sequence 122, App |
| 31 | 40.5 | 21.4 | 243 | 9  | US-10-175-737-366 | Sequence 366, App |
| 32 | 40.5 | 21.4 | 243 | 9  | US-10-063-502-122 | Sequence 122, App |
| 33 | 40.5 | 21.4 | 243 | 9  | US-10-076-622-514 | Sequence 514, App |
| 34 | 40.5 | 21.4 | 243 | 9  | US-10-173-706-366 | Sequence 366, App |
| 35 | 40.5 | 21.4 | 243 | 9  | US-10-175-738-366 | Sequence 366, App |
| 36 | 40.5 | 21.4 | 243 | 9  | US-10-175-738-366 | Sequence 366, App |
| 37 | 40.5 | 21.4 | 243 | 9  | US-10-176-482-366 | Sequence 366, App |
| 38 | 40.5 | 21.4 | 243 | 9  | US-10-176-757-366 | Sequence 366, App |
| 39 | 40.5 | 21.4 | 243 | 9  | US-10-176-913-366 | Sequence 366, App |
| 40 | 40.5 | 21.4 | 243 | 9  | US-10-180-552-366 | Sequence 366, App |
| 41 | 40.5 | 21.4 | 243 | 9  | US-10-180-557-366 | Sequence 366, App |
| 42 | 40.5 | 21.4 | 243 | 9  | US-10-173-700-366 | Sequence 366, App |
| 43 | 40.5 | 21.4 | 243 | 9  | US-10-174-572-366 | Sequence 366, App |
| 44 | 40.5 | 21.4 | 243 | 9  | US-10-174-579-366 | Sequence 366, App |
| 45 | 40.5 | 21.4 | 243 | 9  | US-10-174-582-366 | Sequence 366, App |

## ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Publication No. US2003004908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286, 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      65.1%, Score 123, DB 9, Length 406;
Best Local Similarity 75.0%; Pred. No. 9.7e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Cy 1 ANAFLLXRLRGSILKRCXCRXXLCSFXAEXIFRNXXRRQFWVSY 44
Db 1 ANAFLLXRLRGSILKRCXCRXXLCSFXAEXIFRNXXRRQFWVSY 44

RESULT 2
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
```

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          51.9%; Score 98; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2,5e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFW 41

RESULT 3
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, Jinli
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match          49.2%; Score 93; DB 10; Length 415;
Best Local Similarity 41.9%; Pred. No. 1,8e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRQGSIXRCXKXLCSPXXAEXIFRNXXRTROFW 44
DB 3 SGTLEEFVQGNLERECMEKCSFEARAEVENTERTTEFWKQY 45

RESULT 4
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1,9e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFW 41

RESULT 5
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1,9e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCXKXLCSPXXAEXIFRNXXRTROFW 41
DB 1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFW 41

RESULT 6
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4
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Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLROGSLXRCXKXLCSPFXAEXIFPNXXRTROFW 41
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 7
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLROGSLXRCXKXLCSPFXAEXIFPNXXRTROFW 41
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 8
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match          49.2%; Score 93; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1.9e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLROGSLXRCXKXLCSPFXAEXIFPNXXRTROFW 41
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 9
US-10-182-263-2
; Sequence 2, Application US/10182263
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; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match          49.2%; Score 93; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLROGSLXRCXKXLCSPFXAEXIFPNXXRTROFW 41
Db 43 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 83

RESULT 10
US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match          49.2%; Score 93; DB 9; Length 461;
Best Local Similarity 46.3%; Pred. No. 2e-08;
Matches 19; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXLROGSLXRCXKXLCSPFXAEXIFPNXXRTROFW 41
Db 43 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFW 83

RESULT 11
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
; FILE REFERENCE: 6627-PALL170
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; PRIOR APPLICATION NUMBER: US 09/608,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 312  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-759-1308-312

Query Match 37.0%; Score 70; DB 9; Length 209;  
Best Local Similarity 38.2%; Pred. No. 0.0001;  
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXCRXXLCSFXXAEXIFRNXXRTQFWVSY 44  
DB 46 GNLERECNEELCNYEAREIFVEDKTIAPWQEX 79

## RESULT 15

US-09-759-1308-310  
; Sequence 310, Application US/09759130B  
; Publication No. US20030022279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirst, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; TITLE OF INVENTION: USES.  
; FILE REFERENCE: MP100-535OMNIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: US 09/608,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 310  
; LENGTH: 226  
; TYPE: PRT

; ORGANISM: Homo sapiens  
; US-09-759-1308-310

Query Match 37.0%; Score 70; DB 9; Length 226;  
Best Local Similarity 38.2%; Pred. No. 0.0001;  
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLRXCRXXLCSFXXAEXIFRNXXRTQFWVSY 44  
DB 63 GNLERECNEELCNYEAREIFVEDKTIAPWQEX 96

Search completed: March 20, 2003, 13:30:15  
Job time : 10.375 secs

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GenCore version 5.1.4\_p5\_4578  
(c) 1993 - 2003 CompuGen Ltd.

iel

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; Search time 31.375 Seconds
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186.869 Million cell updates/sec
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.....XXAFXIFRNXXRTRQFWVS 44

sidues  
rameters: 908470

33

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predicted by chance to have a score of the result being printed total score distribution.

## VARIATIONS

|   | Description          |
|---|----------------------|
| 6 | Bovine factor VII    |
| 6 | Bovine factor VII    |
| 2 | Modified GIIa domain |
| 2 | Modified GIIa domain |
| 0 | Modified GIIa domain |
| 1 | Modified GIIa domain |
| 1 | Human factor VII G   |
| 5 | Human factor VII g   |
| 0 | Mutant blood coag    |
| 1 | Mutant blood coag    |

|    |     |      |     |    |           |                   |
|----|-----|------|-----|----|-----------|-------------------|
| 15 | 120 | 63.2 | 406 | 23 | AAU771199 | Human coagulation |
| 14 | 120 | 63.2 | 406 | 23 | AAU771198 | Human coagulation |
| 43 | 120 | 63.2 | 406 | 23 | AAU771197 | Human coagulation |
| 42 | 120 | 63.2 | 406 | 23 | AAU771196 | Human coagulation |
| 41 | 120 | 63.2 | 406 | 23 | AAU771195 | Human coagulation |
| 40 | 120 | 63.2 | 406 | 23 | AAU771194 | Human coagulation |
| 39 | 120 | 63.2 | 406 | 23 | AAU771193 | Human coagulation |
| 38 | 120 | 63.2 | 406 | 23 | AAU771192 | Human coagulation |
| 37 | 120 | 63.2 | 406 | 23 | AAU771191 | Human coagulation |
| 36 | 120 | 63.2 | 406 | 23 | AAU771190 | Human coagulation |
| 35 | 120 | 63.2 | 406 | 23 | AAU771189 | Human coagulation |
| 34 | 120 | 63.2 | 406 | 23 | AAU771188 | Human coagulation |
| 33 | 120 | 63.2 | 406 | 23 | ABB80072  | Human coagulation |
| 32 | 120 | 63.2 | 406 | 23 | ABB80071  | Human coagulation |
| 31 | 120 | 63.2 | 406 | 23 | ABB80070  | Human coagulation |
| 30 | 120 | 63.2 | 406 | 23 | ABB80069  | Human coagulation |
| 29 | 120 | 63.2 | 406 | 23 | ABB80068  | Human coagulation |
| 28 | 120 | 63.2 | 406 | 23 | ABB80067  | Human coagulation |
| 27 | 120 | 63.2 | 406 | 22 | ABB84865  | Mutant blood coag |
| 26 | 120 | 63.2 | 406 | 22 | ABB84864  | Mutant blood coag |
| 25 | 120 | 63.2 | 406 | 22 | AAAB84867 | Mutant blood coag |
| 24 | 120 | 63.2 | 406 | 22 | AAAB84866 | Wild-type human b |
| 23 | 120 | 63.2 | 406 | 22 | AAAB84865 | Human FVII mutant |
| 22 | 120 | 63.2 | 406 | 22 | AAAB84864 | Human FVII mutant |
| 21 | 120 | 63.2 | 406 | 22 | AAAB84863 | Human FVII mutant |
| 20 | 120 | 63.2 | 406 | 22 | AAAB84862 | Human FVII mutant |
| 19 | 120 | 63.2 | 406 | 22 | AAAB84861 | Human FVII mutant |
| 18 | 120 | 63.2 | 406 | 22 | AAAB84860 | Human FVII mutant |
| 17 | 120 | 63.2 | 406 | 22 | AAAB84859 | Human FVII mutant |
| 16 | 120 | 63.2 | 406 | 22 | AAAB84858 | Human FVII mutant |
| 15 | 120 | 63.2 | 406 | 22 | AAAB84857 | Human FVII mutant |
| 14 | 120 | 63.2 | 406 | 22 | AAAB84856 | Human FVII mutant |
| 13 | 120 | 63.2 | 406 | 18 | AAAB84855 | Modified blood co |
| 12 | 120 | 63.2 | 406 | 14 | AAAB84854 | Factor VII (VII)  |
| 11 | 120 | 63.2 | 406 | 14 | AAAB84853 | Factor VII (VII)  |

## ALIGNMENTS

|  |                     |
|--|---------------------|
| UUT 1  |                     |
| 18306  |                     |
| AAV18306 standard; peptide; 44 Aa.                                   |                     |
| AAV18306;  |                     |
| 17-AUG-1999 (first entry)  |                     |
| Bovine factor VII GLA domain.  |                     |
| GLA domain; vitamin K-dependent protein; clotting disorder; therapy. |                     |
| Bos taurus.  |                     |
| Key  | Location/Qualifiers |
| Misc-difference 1..44  |                     |
| /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"           |                     |
| WO9920767-A1.  |                     |
| 29-APR-1999.   |                     |
| 20-OCT-1998;   | 98WO-US22152.       |
| 23-OCT-1997;   | 97US-0955636.       |
| (MINU ) UNIV MINNESOTA.  |                     |
| Nelaeestuen Gl.  |                     |
| WPI, 1999-288309/24.   |                     |

```
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 81.6%; Score 155; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.8e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANGFLXXLRQGSIXRCXRLCSFXXAFXIFRNXXRTROFWVS 44
    |||||
DB 1 ANGFLXXLRPGLRXCRXRLCSFXXAHXIFRNXXRTROFWVS 44

RESULT 2
AAB36396
ID AAB36396 standard; peptide; 44 AA.
AC
XX AAB36396;
XX
DT 27-FEB-2001 (first entry)
XX
DE Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
OS Bos taurus.
XX
FN WO200066753-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11416.
XX
PR 29-APR-1999; 99US-0302239.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
XX WPI; 2001-007226/01.
XX
DR
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
XX Disclosure; Page 12; 81pp; English.
XX
PS The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot
```

```
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;

Query Match 81.6%; Score 155; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 5.8e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANGFLXXLRQGSIXRCXRLCSFXXAFXIFRNXXRTROFWVS 44
    |||||
DB 1 ANGFLXXLRPGLRXCRXRLCSFXXAHXIFRNXXRTROFWVS 44

RESULT 3
AAV18312
ID AAV18312 standard; peptide; 44 AA.
AC
XX AAV18312;
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
PN WO9920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22152.
XX
PR 23-OCT-1997; 97US-0955636.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
DR
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 80; 86pp; English.
XX
PS This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 67.9%; Score 129; DB 20; Length 44;
Best Local Similarity 77.3%; Pred. No. 1.5e-14;
Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```





CC GLA domain is useful for increasing clot formation and for treating a  
 CC bleeding disorder, including thrombosis and clotting disorders such as  
 CC haemophilia A, haemophilia B and liver disease. The present sequence  
 CC represents a wild type human factor VII GLA domain sequence, given in  
 CC the exemplification of the present invention.

XX Sequence 44 AA;

Query Match 63.2%; Score 120; DB 22; Length 44;  
 Best Local Similarity 75.0%; Pred. No. 5.2e-13;  
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGLXRXCRXXLCSFXXAFIFRNXXRTQFWVS 44  
 Db 1 ANAFLELRPGSLRERCKEQQCSFEAREIFPDARTKLFWISY 44

RESULT 9  
 AAB84870 ID AAB84870 standard; Protein; 401 AA.

XX AAB84870;  
 XX 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-31).

KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;  
 KM mutant; mutein.

OS Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Misc-difference 311..317

FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp  
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

XX 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19463.

PT Mutant of blood coagulant factor VII, used for substitution therapy in  
 PT the treatment of hemophilia -

PS Claim 14; Page 20-21; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII  
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present  
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an  
 CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 63.2%; Score 120; DB 22; Length 401;  
 Best Local Similarity 52.3%; Pred. No. 4.3e-12;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGLXRXCRXXLCSFXXAFIFRNXXRTQFWVS 44  
 Db 1 ANAFLELRPGSLRERCKEQQCSFEAREIFPDARTKLFWISY 44

RESULT 10

AAB84871 ID AAB84871 standard; Protein; 401 AA.

AC AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;  
 KM mutant; mutein.

OS Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Misc-difference 235..239

FT /note= "Wild-type Val-Pro-Gly-Thr substituted by  
 Asp-Arg-Lys-Thr-Leu"

FT Misc-difference 311..317  
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp  
 -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

PT Mutant of blood coagulant factor VII, used for substitution therapy in  
 PT the treatment of hemophilia -

PS Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII  
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present  
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an  
 CC agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 63.2%; Score 120; DB 22; Length 401;  
 Best Local Similarity 52.3%; Pred. No. 4.3e-12;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGLXRXCRXXLCSFXXAFIFRNXXRTQFWVS 44  
 Db 1 ANAFLELRPGSLRERCKEQQCSFEAREIFPDARTKLFWISY 44

RESULT 11

ID AAR35764 standard; protein; 406 AA.

XX AAR35764;

DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

KM PC: protein C; IX; Factor IX; X; Factor X; PT: prothrombin; VII;  
 KM Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;  
 KM exosite; catalytic activity.

OS Homo sapiens.

XX

[illegible]

|    |  |
|----|--|
| KM | thrombocytopenia; von Willebrand's disease; plasma substitute. |
| XX | Homo sapiens.  |
| OS | Synthetic.   |
| XX |  |
| PH | Key  |
| FT | Modified-site  |
| FT | Location/Qualifiers  |
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| FT | /note= "gamma-carboxyglutamic acid"                            |
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| FT | 14   |
| FT | /label= OTHER  |
| FT | /note= "gamma-carboxyglutamic acid"                            |
| FT | 16   |
| FT | /label= OTHER  |
| FT | /note= "gamma-carboxyglutamic acid"                            |
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| FT | /note= "gamma-carboxyglutamic acid"                            |
| FT | 20   |
| FT | /label= OTHER  |
| FT | /note= "gamma-carboxyglutamic acid"                            |
| FT | 17..22   |
| FT | /note= "gamma-carboxyglutamic acid"                            |
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| FT | /label= OTHER  |
| FT | /note= "gamma-carboxyglutamic acid"                            |
| FT | 29   |
| FT | /label= OTHER  |
| FT | /note= "gamma-carboxyglutamic acid"                            |
| FT | 32..33   |
| FT | /note= "proteolytic site"                                      |
| FT | 35   |
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| FT | /note= "gamma-carboxyglutamic acid"                            |
| FT | 38..39   |
| FT | /note= "proteolytic site"                                      |
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| FT | /note= "proteolytic site"                                      |
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| FT | /note= "proteolytic site"                                      |
| FT | 50..61   |
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| FT | 135..162   |
| FT | /note= "beta-hydroxy-aspartic acid"                            |
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| FT | /note= "proteolytic site"                                      |
| FT | 145  |
| FT | /note= "proteolytic site"                                      |
| FT | 159..164   |
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| FT | 178..194   |
| FT | /note= "glycosylation site"                                    |
| FT | 193  |
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| FT | 242  |
| FT | /note= "glycosylation site"                                    |
| FT | 344  |
| FT | /note= "glycosylation site"                                    |
| FT | 290..291   |
| FT | /note= "proteolytic site in unmodified factor VII"             |
| FT | 290  |
| FT | /note= "proteolytic site in unmodified factor VII"             |
| FT | 310..329   |
| FT | /note= "proteolytic site in unmodified factor VII"             |
| FT | 315..316   |
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| FT | 310..329   |
| FT | /note= "proteolytic site in unmodified factor VII"             |
| FT | 315..316   |
| FT | /note= "proteolytic site in unmodified factor VII"             |



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FT /note= "glycosylation site"
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FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393
FT /note= "proteolytic site"
FT Cleavage-site 396..397
FT /note= "proteolytic site"
FT Cleavage-site 402..403
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FT
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FT
FT
FT 03-DEC-1996.
FT
FT
FT 13-NOV-1989; 89US-0434149.
FT
FT
FT 09-AUG-1993; 93US-0104509.
FT 13-NOV-1989; 89US-0434149.
FT 12-JUN-1992; 92US-0898248.
FT 22-AUG-1994; 94US-0293778.
FT
FT
FT (NOVO ) NOVO-NORDISK AS.
FT
FT Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
FT WPI: 1997-033523/03.
FT
FT Mutated human factor VII or VIIa proteins - with amino acid
FT substitutions to improve proteolytic stability
FT
FT Example 3; Page -: 28pp; English.
FT
FT Modified human factor VII or VIIa proteins are stabilised against
FT proteolytic cleavage by substitution of one of the residues Lys32,
FT Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
FT Lys341 by an amino acid that provides a proteolytically more stable
FT peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
FT Gly, Thr, Ala or Ser. The modified proteins are useful for treating
FT bleeding disorders such as thrombocytopenia and von Willebrand's
FT disease. They are also suitable for addition to plasma substitutes.
FT The present sequence is a specific example of a modified factor VII
FT protein.
FT
FT
FT Sequence 406 AA;
SQ
Query Match 63.2%; Score 120; DB 18; Length 406;
Best Local Similarity 52.3%; Pred. No. 4,4e-12;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
Oy 1 ANGFLXLRQSGLXRCRXXLCSFXXAIFRNXXRTQRFWSY 44
Db 1 ANAFLELRPGSLERCKEKCSEFARERIFDAERTKLFWSY 44

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FT /note= "gamma-carboxylutamic acid"
FT Modified-site 7
FT /label= OTHER
FT /note= "gamma-carboxylutamic acid"
FT Modified-site 14
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FT Modified-site 20
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FT Modified-site 25
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FT /note= "gamma-carboxylutamic acid"
FT Modified-site 29
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FT Cleavage-site 32..33
FT /note= "gamma-carboxylutamic acid"
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FT Disulfide-bond 55..70
FT Modified-site 63
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FT /note= "glycosylation site"
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FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note= "proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 315
FT /note= "native Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide
FT bond"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393

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FT      /note= "proteolytic site"
FT      396..397
FT      /note= "proteolytic site"
FT      402..403
FT      /note= "proteolytic site"
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XX
XX      03-DEC-1996.
XX
XX      13-NOV-1989;      89US-0434149.
XX
XX      09-AUG-1993;      93US-0104509.
XX      13-NOV-1989;      89US-0434149.
XX      12-JUN-1992;      92US-0898248.
XX      22-AUG-1994;      94US-0293778.
XX
XX      (NOVO ) NOVO-NORDISK AS.
XX
XX      Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX      WPI; 1997-033523/03.
XX
XX      Mutated human factor VII or VIIa proteins - with amino acid
XX      substitutions to improve proteolytic stability
XX
XX      Example 4; Page -; 28pp; English.
XX
XX      Modified human factor VII or VIIa proteins are stabilised against
XX      proteolytic cleavage by substitution of one of the residues Lys32,
XX      Lys81, Ile62, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX      Lys341 by an amino acid that provides a proteolytically more stable
XX      peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX      Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX      bleeding disorders such as thrombocytopenia and von Willebrand's
XX      disease. They are also suitable for addition to plasma substitutes.
XX      The present sequence is a specific example of a modified factor VII
XX      protein.
XX
XX      Sequence      406 AA;
XX
XX      Query Match      63.2%; Score 120; DB 18; Length 406;
XX      Best Local Similarity 52.3%; Pred. No. 4.4e-12;
XX      Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
XX
XX      QY      1 ANGFLXXLRQGSILRXCRXXLCSPXXAFXIFRNXXRTQPFWSY 44
XX      1 ANAFLELRPGSLERCKEQCSFEBAREIFXDAERTKLFWISY 44
XX
XX      DB
XX
XX      RESULT 14
XX      AAU77745
XX      ID      AAU77745 standard; protein; 406 AA.
XX
XX      AC      AAU77745;
XX
XX      DT      05-JUN-2002 (first entry)
XX
XX      DE      Human factor VIIa active site mutant.
XX
XX      KW      Factor VIIa; human; shock heat treatment; protein stability;
XX      protein manufacture; protein conformation; mutant; mutein.
XX
XX      OS      Homo sapiens.
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      Active-site      193
XX      FT      Active-site      /note= "Member of the factor VIIa catalytic triad"
XX      FT      Active-site      242
XX      FT      Active-site      /note= "Member of the factor VIIa catalytic triad"
XX      FT      Active-site      344
XX      FT      Active-site      /note= "Member of the factor VIIa catalytic triad"

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FT      Misc-difference 344
FT      /label= Gly, Met, Thr
FT      /note= "Preferably Ala. Wild type Ser"
XX
XX      WO200177141-A1.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-DK00234.
XX
XX      06-APR-2000; 2000DK-0000573.
XX      17-APR-2000; 2000US-197650P.
XX
XX      (NOVO ) NOVO NORDISK AS.
XX
XX      Mathiesen F;
XX      WPI; 2001-657162/75.
XX
XX      Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX      involves a shock heat treatment -
XX
XX      Disclosure; Page -; 22pp; English.
XX
XX      The invention describes a method of stabilising a polypeptide involving
XX      shock heat treatment of the polypeptide. The method is useful in a
XX      pharmaceutical composition, in the industrial or large scale method of
XX      manufacturing a polypeptide, also as a unit operation during preparation,
XX      purification, recovery and/or formulation of polypeptides. The shock heat
XX      treatment improves the protein stability without substantial loss of
XX      biological activity. The method can be applied to change polypeptide
XX      conformation in a very fast and non-invasive manner. The polypeptide
XX      formed is stable. The method is also useful for decreasing the
XX      association of the polypeptide. This sequence represents a modified
XX      human factor VIIa protein, mutated at the catalytic site, described
XX      in the invention.
XX      Note: This sequence does not appear in the specification but has
XX      been obtained using information given in the invention.
XX
XX      Sequence      406 AA;
XX
XX      Query Match      63.2%; Score 120; DB 22; Length 406;
XX      Best Local Similarity 52.3%; Pred. No. 4.4e-12;
XX      Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
XX
XX      QY      1 ANGFLXXLRQGSILRXCRXXLCSPXXAFXIFRNXXRTQPFWSY 44
XX      1 ANAFLELRPGSLERCKEQCSFEBAREIFXDAERTKLFWISY 44
XX
XX      DB
XX
XX      RESULT 15
XX      AAM52171
XX      ID      AAM52171 standard; Protein; 406 AA.
XX
XX      AC      AAM52171;
XX
XX      DT      07-FEB-2002 (first entry)
XX
XX      DE      Human FVII SEQ ID NO 1.
XX
XX      KW      Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX      cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease;
XX      myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
XX      OS      Homo sapiens.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      Misc-difference 6      /label= Glu, OTHER
XX      FT      Misc-difference /note= "OTHER = gamma carboxyglutamic acid"
XX      FT      Misc-difference 7      /label= Glu, OTHER
XX      FT      Misc-difference /note= "OTHER = gamma carboxyglutamic acid"

```

FT Misc-difference 14  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 16  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 19  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 20  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 25  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 26  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 29  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Misc-difference 35  
 /label= Glu, OTHER  
 /note= "OTHER = gamma carboxyglutamic acid"  
 FT  
 FT Modified-site 52  
 /note= "O-glycosylated"  
 FT  
 FT Modified-site 60  
 /note= "O-glycosylated"  
 FT  
 FT Modified-site 145  
 /note= "O-glycosylated"  
 FT  
 FT Cleavage-site 152..153  
 /note= "proteolytic cleavage site converting FVII zymogen  
 to an activated form, comprising two chains  
 linked by a single disulphide bridge"  
 FT  
 FT Modified-site 322  
 /note= "N-glycosylated"  
 FT  
 FT  
 PN WO200158935-A2.  
 XX 16-AUG-2001.  
 XX  
 XX 12-FEB-2001; 2001WO-DK00094.  
 XX  
 PR 11-FEB-2000; 2000DK-0000218.  
 PR 18-OCT-2000; 2000DK-0001558.  
 XX  
 PA (MAXY-) MAXYGEN APS.  
 XX  
 PI Andersen KV, Pedersen AH, Bornaes C;  
 XX WPI; 2001-581807/65.  
 DR N-PSDB; AAI99982.  
 XX  
 PT New conjugate, useful for treating Factor VIIa related diseases or  
 PT disorders such as haemophilia, liver disease, myocardial infarction and  
 PT deep-vein thrombosis, comprises non-polypeptide group covalently  
 PT attached to polypeptide group -  
 XX  
 XX  
 PS Claim 1; Page 81-83; 89pp; English.  
 XX  
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
 CC polypeptide conjugates, comprising at least one non-polypeptide group  
 CC covalently attached to a polypeptide, where the amino acid sequence of  
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
 CC least one amino acid residue containing an attachment group for the  
 CC non-polypeptide group has been introduced or removed. The FVIIa  
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and  
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
 CC diseases or disorders such as haemophilia, liver disease, myocardial  
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
 CC have increased functional in vivo half life and/or increased plasma half  
 CC life, increased bioavailability and or reduced sensitivity to proteolytic  
 CC degradation. Consequently medical treatment using the conjugates has a

CC number of advantages over currently available such as longer duration  
 CC between injections.  
 XX  
 SQ Sequence 406 AA;  
 Query Match 63.2%; Score 120; DB 22; Length 406;  
 Best Local Similarity 75.0%; Pred. No. 4.4e-12;  
 Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 Gy 1 ANGLFXLRLROGLRXCRXXLCSFXXAFIFRNXXRTRQFWVS 44  
 Db 1 ANAFLXLRPGSLRXKCKXKXCSFXXARXIFKDXARLFWISY 44

Search completed: March 19, 2003, 14:51:15  
 Job time : 32.4375 secs

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GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using SW model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10GLN28PHE\_4  
Perfect score: 190  
Sequence: 1 ANGFLXXLRQSLXRXCRXX.....XXAFXIFRNXXRTQFWVSX 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 148   | 77.9        | 407    | 1 KPE07  | coagulation factor |
| 2          | 128   | 67.4        | 443    | 2 I46932 | coagulation factor |
| 3          | 120   | 63.2        | 466    | 1 KFHU7  | coagulation factor |
| 4          | 104   | 54.7        | 461    | 1 JX0210 | protein C (activat |
| 5          | 103   | 54.2        | 461    | 1 S18994 | protein C (activat |
| 6          | 94    | 49.5        | 456    | 1 KXBO   | protein C (activat |
| 7          | 93    | 48.9        | 482    | 1 EXRT   | coagulation factor |
| 8          | 93    | 48.9        | 488    | 1 EXHU   | coagulation factor |
| 9          | 92    | 48.4        | 492    | 1 EXBO   | coagulation factor |
| 10         | 90    | 47.4        | 461    | 1 KFHU   | coagulation factor |
| 11         | 89    | 46.8        | 461    | 1 KXHU   | protein C (activat |
| 12         | 87    | 45.8        | 622    | 1 TBHU   | thrombin (EC 3.4.2 |
| 13         | 86    | 45.3        | 416    | 1 KPEO   | coagulation factor |
| 14         | 84    | 44.2        | 475    | 1 EXCH   | coagulation factor |
| 15         | 84    | 44.2        | 617    | 2 S10511 | thrombin (EC 3.4.2 |
| 16         | 84    | 44.2        | 618    | 2 A35827 | thrombin (EC 3.4.2 |
| 17         | 81    | 42.6        | 452    | 1 A30351 | coagulation factor |
| 18         | 81    | 42.6        | 459    | 2 J00419 | coagulation factor |
| 19         | 78    | 41.1        | 625    | 1 TBBO   | thrombin (EC 3.4.2 |
| 20         | 77    | 40.5        | 642    | 2 S53433 | plasma protein S p |
| 21         | 72    | 37.9        | 642    | 2 S53434 | plasma protein S p |
| 22         | 72    | 37.9        | 642    | 1 KKHUS  | plasma protein S p |
| 23         | 69    | 36.3        | 675    | 1 KXROS  | plasma protein S p |
| 24         | 68    | 35.8        | 646    | 2 S38819 | plasma protein S p |
| 25         | 66    | 34.7        | 422    | 1 KKHUZ  | plasma protein S p |
| 26         | 66    | 34.7        | 675    | 1 KKHUS  | plasma protein S p |
| 27         | 62    | 32.6        | 396    | 1 KXBOZ  | plasma protein Z - |
| 28         | 61    | 32.1        | 678    | 2 B48089 | growth arrest-spec |
| 29         | 60    | 31.6        | 673    | 2 A48089 | growth arrest-spec |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 59   | 31.1 | 675  | 1 KXMS   | plasma protein S p  |
| 31 | 58   | 30.5 | 674  | 2 I55476 | growth potentiatin  |
| 32 | 52   | 27.4 | 605  | 1 W1WLB  | E1 protein - bovin  |
| 33 | 52   | 27.4 | 620  | 1 W1WLB2 | E1 protein - bovin  |
| 34 | 48   | 25.3 | 413  | 1 VHAVNH | nucleoprotein - in  |
| 35 | 46.5 | 24.5 | 594  | 2 D84859 | probable MAP kinase |
| 36 | 46.5 | 24.5 | 603  | 2 C96575 | probable MAP kinase |
| 37 | 45.5 | 23.9 | 576  | 2 C96763 | probable MAP kinase |
| 38 | 45.5 | 23.9 | 2133 | 2 T42763 | coagulation factor  |
| 39 | 45   | 23.7 | 448  | 2 T18710 | hypothetical prote  |
| 40 | 45   | 23.7 | 687  | 2 T08528 | probable DNA topoi  |
| 41 | 44.5 | 23.4 | 304  | 2 AF2942 | 5-dehydro-4-deoxyg  |
| 42 | 44.5 | 23.4 | 304  | 2 D98340 | 5-dehydro-4-deoxyg  |
| 43 | 43   | 22.6 | 536  | 2 E70066 | hypothetical prote  |
| 44 | 43   | 22.6 | 1171 | 2 T31635 | hypothetical prote  |
| 45 | 43   | 22.6 | 1217 | 2 T21403 | hypothetical prote  |

## ALIGNMENTS

## RESULT 1

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:8908362; PMID:3049594

A:Accession: A31979

A:Molecule type: Protein

A:Residues: 1-407 <TAK>

R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:8330813; PMID:6688526

A:Accession: C20274

A:Molecule type: Protein

A:Residues: 58-62, 'X', 64-68 <MCM>

A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44566; PMID:8921399; PMID:3149637

A:Contents: annotation

A:Note: structure and location of covalently bound carbohydrate

C:Function: catalyzes the proteolytic activation of coagulation factor X in the prese

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAI>

F:1-44/Domain: Gla domain homology (fragment) <GLA>

F:50-81/Domain: EGF homology <EGF>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6-7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:152/Binding site: carboxylate (Ser) (covalent) #status experimental

F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental

F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-Ile (coagulation factor XIa) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:1290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match 77.9%; Score 148; DB 1; Length 407;

Best Local Similarity 68.2%; Pred. No. 3,66-18;

Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```

Oy      1  ANGFLXXLRQGSIXRXCRRXXLCSPFXAXFIFRNXXTRQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1  ANGFLLEELRPSLERRCREELCSFEERAHETFRNEERTROWVSY 44

RESULT 2
146932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
A:Accession: I46932
R:Brothers, A.B.; Clarke, B.U.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A>Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: I46932; MUID:93190306; PMID:8383365
A:Accession: I46932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:S56300; NID:9266294; PID:9266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:124-83/Domain: Gla domain homology <GLA>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match      67.4%; Score 128; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 1,3e-14;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Oy      1  ANGFLXXLRQGSIXRXCRRXXLCSPFXAXFIFRNXXTRQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      40 ANSFLLELRPGSLERRCREELCSFEERAEVFGSTERTKQFWIRY 83

RESULT 3
KHFU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
A:Accession: A28322; A28319; A1186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldean, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murd
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A>Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OHA>
A:Cross-references: GB:J02933; NID:9180333; PIDN:AAA51983.1; PID:9180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A>Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A28319; MUID:86205965; PMID:3486420
A:Accession: A28319
A:Molecule type: mRNA
A:Residues: 1-466 <THA>
A:Cross-references: GB:M13232; NID:9182799; PIDN:AAA8040.1; PID:9182801
R:Rithm, L.; Bjornen, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A>Title: Amino acid sequence and posttranslational modifications of human factor VII-a F
A:Reference number: A90539; MUID:89088153; PMID:3364725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjornen, S.; Foster, D.C.; Thim, L.; Wiiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A>Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A:Reference number: A40529; MUID:91250411; PMID:1904059
A:Content: annotation; carbohydrate binding sites
R:Persson, E.; Petersen, L.C.

```

```

Eur. J. Biochem. 224, 293-300, 1995
A>Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PBR>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen
coagulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domain: Gla domain homology <GLA>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:110-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66-67;74;76;79;80;85;86;89;95/Modified site: gamma-carboxylglutamic acid (Glu) #status e
F:77-82;110-121;115-130;132-141;151-162;158-172;174-187;195-332;219-224;238-254;370-389;
F:112;120/Binding site: carboxylate (Ser) (covalent) #status experimental
F:123/Modified site: epsilon-beta-hydroxyaspartic acid (Asp) #status absent
F:205;382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-116 (coagulation factor XIIa) #status experimental
F:253;302;404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor XIa) #status predicted

Query Match      63.2%; Score 120; DB 1; Length 466;
Best Local Similarity 52.3%; Pred. No. 3.5e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy      1  ANGFLXXLRQGSIXRXCRRXXLCSPFXAXFIFRNXXTRQFWVSY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61 ANAFLELRPSLERRCREELCSFEEREIFDAERTKLFWSY 104

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
A:Accession: JX0210
R:Nade, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A>Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:9220385; PIDN:BAA01235.1; PID:9220386
A:Experimental source: liver
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that rec
B.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <GLA>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196;199-461/Product: protein C #status predicted <PC>
F:42-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACP>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

```

F:122-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
 F:214,299,355/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 54.7% Score 104; DB 1; Length 461;  
 Best Local Similarity 45.5% Pred. No. 2,3e-10;  
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAFXIFRNXXRTQFWVS 44  
 Db 42 ANSFLEVRPGSLERECMEICDFEQAQEIFQVNETLAFWIKY 85

RESULT 5  
 S18994  
 Protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
 C:Accession: S18994; S24312  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 A:Description: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S18994

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OK>  
 A:Cross-references: EMBL:X64336; NID:g56962; PIDD:CAA45617.1; PID:g56963  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 Biochim. Biophys. Acta 1131, 329-332, 1992  
 A:Title: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <OK>

A:Cross-references: EMBL:X64336; NID:g56962; PIDD:CAA45617.1; PID:g56963

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase

F:1-12/Domain: signal sequence #status predicted <SIG>

F:127-85/Domain: Gla domain homology <GLA>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-461/Product: protein C #status predicted <PC>

F:91-130/Domain: EGF homology <EG1>

F:139-174/Domain: EGF homology <EG2>

F:213-445/Domain: trypsin homology <TRY>

F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat

F:215,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted

F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 54.2% Score 103; DB 1; Length 461;  
 Best Local Similarity 45.5% Pred. No. 3.5e-10;  
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAFXIFRNXXRTQFWVS 44  
 Db 42 ANSFLEVRPGSLERECMEICDFEQAQEIFQVNETLAFWIKY 85

RESULT 6

KXBO

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N:Alternate names: autoprothrombin IIA; plasma protein C

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence\_revision 17-Mar-1997 #text\_change 16-Jul-1999

C:Accession: A26250; A18385; A18386; A00928

R:Long, G.L.; Balagej, R.M.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100

A:Accession: A26250

A:Molecule type: mRNA

A:Residues: 1-456 <LON>

R:Fernlund, P.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982

A:Title: Amino acid sequence of the light chain of bovine protein C.

A:Reference number: A18385; MUID:83007325; PMID:6896876

A:Accession: A18385

A:Molecule type: protein

A:Residues: 40-194 <PER>

A>Note: 82-Lys was also found

R:Drakeberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A:Title: beta-hydroxyaspartic acid in vitamin K-dependent protein C.

A:Reference number: A19316; MUID:83169769; PMID:6572939

A:Contents: annotation; revision to residue 110

R:Stenflo, J.; Fernlund, P.

J. Biol. Chem. 257, 12180-12190, 1982

A:Title: Amino acid sequence of the heavy chain of bovine protein C.

A:Reference number: A18386; MUID:83007326; PMID:6896877

A:Accession: A18386

A:Molecule type: protein

A:Residues: 197-454, 'PV' <STE>

R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.

J. Biol. Chem. 258, 5548-5553, 1983

A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless P

A:Reference number: A37541; MUID:8321513; PMID:6304092

A:Contents: annotation; activation; calcium binding

R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.

J. Biol. Chem. 258, 5554-5560, 1983

A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin

A:Reference number: A37542; MUID:8321514; PMID:6406503

A:Contents: annotation; activation; calcium binding

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re

s.

C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c

bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>

F:124-83/Domain: Gla domain homology <GLA>

F:30-39/Domain: propeptide #status predicted <PRO>

F:40-194/Product: protein C light chain #status experimental <LCH>

F:98-128/Domain: EGF homology <EG1>

F:137-172/Domain: EGF homology <EG2>

F:197-456/Product: protein C heavy chain #status experimental <HCH>

F:197-210/Domain: activation peptide #status experimental <AP>

F:211-440/Domain: trypsin homology <TRY>

F:45,46,53,55,58,59,62,64,65,66,74/Modified site: gamma-carboxyglutamic acid (Glu) #statu

F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #statu

F:136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted

F:252,298,397/Active site: His, Asp, Ser #status predicted

F:366/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 49.5% Score 94; DB 1; Length 456;  
 Best Local Similarity 43.2% Pred. No. 1.4e-08;  
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAFXIFRNXXRTQFWVS 44  
 Db 40 ANSFLELRPGVNERECSEVCEFEAREIFQVNETLAFWVSFY 83

RESULT 7

EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C.Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000  
 C.Accession: S49075; J04670; E50191; PS0190; 162745  
 R.Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 Thromb. Res. 80, 63-73, 1995  
 A>Title: Evidence for competition between vitamin K-dependent clotting factors for intra  
 A.Reference number: A58498; MUID:96093366; PMID:8578539  
 A.Accession: S49075  
 A.Molecule type: mRNA  
 A.Residues: 1-482 <STA2>  
 A.Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
 A.Note: submitted to the EMBL Data Library, June 1994  
 A.Note: neither the complete nucleic acid sequence nor the complete translation are show  
 R.Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 Gene 169, 269-273, 1996  
 A>Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
 A.Reference number: J04670; MUID:96194815; PMID:8647460  
 A.Accession: J04670  
 A.Molecule type: mRNA  
 A.Residues: 1-482 <STA2>  
 A.Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
 A.Experimental source: COS-1 cell  
 R.Enyoji, K.; Miyazaki, K.; Kato, H.  
 J. Biochem. 109, 890-898, 1991  
 A>Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
 A.Reference number: PS0190; MUID:92041742; PMID:1718949  
 A.Accession: PS0191  
 A.Molecule type: protein  
 A.Residues: 41-58, 'X', 60-65 <ENU1>  
 A.Accession: PS0190  
 A.Molecule type: protein  
 A.Residues: 183-186, 'X', 188-207 <ENU2>  
 R.Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A>Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
 A.Reference number: 146196; MUID:94222160; PMID:8168596  
 A.Accession: 162745  
 A.Status: preliminary; translated from GB/EMBL/DDBJ  
 A.Molecule type: DNA  
 A.Residues: 295-383, 'G', 385-455 <MUR>  
 A.Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:g455396  
 C.Function:  
 A.Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A.Pathway: blood coagulation  
 C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: signal sequence #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:183-231/Domain: activation peptide #status predicted <APT>  
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F:232-460/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:57-62,70-101,95-110,112-121,123-140,136-149,151-164,172-340,238-243,258-275,388-402,41  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:187/Binding site: carboxylate (Aan) (covalent) #status experimental  
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F:218/Binding site: carboxylate (Aan) (covalent) #status predicted  
 F:231-232/Cleavage site: Arg-1le (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 48.9%; Score 93; DB 1; Length 482;  
 Best Local Similarity 36.4%; Pred. No. 2,1e-08;  
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGLXXLRQGSIXRYCRXXLGFXXAFXFRNXXRTROGWVSY 44  
 DB 41 ANSFPEIKKGNIRECEVERICSFEEAREVEFDNEKTEFFMNX 84

RESULT 8  
 EXHU  
 Coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human  
 M.Alternate names: Stuart Factor  
 C.Species: Homo sapiens (man)  
 C.Date: 15-Nov-1984 #sequence revision 02-May-1994 #text\_change 08-Dec-2000  
 C.Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; A00  
 R.Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davle, E.W.  
 Biochemistry 25, 5098-5102, 1986  
 A>Title: Gene for human factor X: a blood coagulation factor whose gene organization is  
 A.Reference number: A24478; MUID:87026600; PMID:3768336  
 A.Accession: A24478  
 A.Molecule type: DNA  
 A.Residues: 1-488 <LEV>  
 A.Cross-references: GB:L29433; GB:M4327; NID:g459809; PIDN:AAA52764.1; PID:g182831  
 R.Wessler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.  
 Gene 99, 291-294, 1991  
 A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag  
 A.Reference number: J00917; MUID:91216473; PMID:1902434  
 A.Accession: J00917  
 A.Molecule type: mRNA  
 A.Residues: 1-488 <MES>  
 A.Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390  
 R.Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davle, E.W.  
 J. Biol. Chem. 267, 7395-7401, 1992  
 A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagul  
 A.Reference number: A42485; MUID:92218390; PMID:1313796  
 A.Accession: A42485  
 A.Molecule type: DNA  
 A.Residues: 1-15 <MIA>  
 A.Experimental source: liver  
 A.Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)  
 R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
 Gene 41, 311-314, 1986  
 A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
 A.Reference number: A25853; MUID:86221713; PMID:3011603  
 A.Accession: A25853  
 A.Molecule type: mRNA  
 A.Residues: 19-284, 'E', 288-488 <KAU>  
 A.Cross-references: GB:M2613; NID:g180335; PIDN:AAA51984.1; PID:g180336  
 R.Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
 A>Title: Characterization of an almost full-length cDNA coding for human blood coagulation  
 A.Reference number: A22208; MUID:85216545; PMID:2582420  
 A.Accession: A22208  
 A.Molecule type: mRNA  
 A.Residues: 13-441, 'S', 443-488 <FUN>  
 A.Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841  
 R.Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davle, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
 A>Title: Characterization of a cDNA coding for human factor X.  
 A.Reference number: A21284; MUID:84222026; PMID:6587384  
 A.Accession: A21284  
 A.Molecule type: mRNA  
 A.Residues: 13-284, 'E', 289-488 <LE2>  
 A.Cross-references: GB:K01886  
 R.McMillen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howard, W.N.; Kwa, E.Y.; Weiss  
 Biochemistry 22, 2875-2884, 1983  
 A>Title: Complete amino acid sequence of the light chain of human blood coagulation fact  
 A.Reference number: A20362; MUID:83257207; PMID:6871167  
 A.Accession: A20362  
 A.Molecule type: protein  
 A.Residues: 41-179 <MCN>  
 R.Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A.Reference number: S39414; MUID:94062825; PMID:8243461  
 A.Accession: S39415  
 A.Molecule type: protein  
 A.Residues: 183-234 <INO>  
 A.Note: glycosylation sites  
 A.Note: identification and characterization of beta-hydroxyaspartic acid  
 R.Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanham, K.; Lyman, G.



Gene 84, 517-519, 1989  
 A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
 A:Reference number: I54051; MUID:90128299; PMID:2612918  
 A:Accession: I54051  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:Cross-references: GB:M31297; NID:9183860; PIDN:AAA52636.1; PID:9553330  
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla  
 J. Mol. Biol. 232, 947-966, 1993  
 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A49458; MUID:93360277; PMID:8355279  
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 C:Genetics:  
 A:Gene: GDB:F10  
 A:Cross-references: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A>Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-23/Domain: signal sequence #status predicted <PRO>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-238/Domain: activation peptide #status experimental <APT>  
 F:233-488/Product: coagulation factor X heavy chain #status experimental <ACT>  
 F:235-462/Domain: trypsin homology <TRY>  
 F:46/47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:57-62/Disulfide bonds: #status predicted  
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:119,211/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:122,231/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:234-235/Cleavage site: Arg-115, Asp, Ser #status experimental  
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 48.9%; Score 93; DB 1; Length 488;  
 Best Local Similarity 36.4%; Pred. No. 2.2e-08;  
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLXRCRXLLCSFXXAFIFNXXRTROFWYSY 44  
 DB 41 ANSFLBEMKXGHLERCEWERTCSYERAREVFEDSDXTNEFMNRY 84

RESULT 9  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Dates: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
 A:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Funig, M.R.; Campbell, R.M.; MacGillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; MUID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FUN>  
 A:Cross-references: GB:X00673; NID:9192; PIDN:CAA25286.1; PID:9193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochemistry 19, 659-667, 1980  
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735

A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102; 'N', 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GRFG', 446-492 <T  
 A>Note: carboxylate binding sites and disulfide bonds were determined  
 R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Ohlén, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; MUID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A>Note: beta-hydroxyaspartic acid site  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196; 199-209; 216-233 <INO>  
 A>Note: carbohydrate binding sites  
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D  
 Biochemistry 11, 4899-4903, 1972  
 A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
 A:Reference number: A12453; MUID:73053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic  
 A:Reference number: A38024; MUID:84185716; PMID:6546930  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of tw  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
 C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <APT>

F.234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F.234-461/Domains: trypsin homology <TRY>  
 F.461-475.54.56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #S  
 F.57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-311/Sulfide bonds: #status F  
 F.103/Modified site: epsilon-beta-hydroxyaspartic acid (Asp) #status experimental  
 F.200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F.208-485/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F.218/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F.233-233/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat  
 F.240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental  
 F.275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 48.4%; Score 92; DB 1; Length 492;  
 Best Local Similarity 38.6%; Pred. No. 3.3e-08;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXRQSGSLKRXCRXXLCSPXXAFKIFRXRXRTQRFVSY 44  
 DB 41 ANSFLEEVKQGNLERECLEACSLSEARREVFEDAEQDFEWSKY 84

RESULT 10  
 KFHU  
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
 N:Alternate names: antihemophilic factor B; Christmae factor  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #ext change 15-Sep-2000  
 C:Accession: A00922; A57570; A30511; A32989; A22673; A23377; A37546; A30623; A60486; A20  
 R.Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.  
 Biochemistry 24, 3736-3750, 1985  
 A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B) .  
 A:Reference number: A00922; PMID:8600558; PMID:2294716  
 A:Accession: A00922  
 A:Molecule type: DNA  
 A:Residues: 1-461 <YOS>  
 A:Cross-references: GB:K02402; NID:9182612; PIDN:AA59620.1; PID:9182613  
 R.Ansen, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro  
 EMBO J. 3, 1053-1060, 1984  
 A>Title: The gene structure of human anti-haemophilic factor IX.  
 A:Reference number: A37570; PMID:84236100; PMID:6329734  
 A:Accession: A37570  
 A:Molecule type: DNA  
 A:Residues: 1-461 <ANS>  
 A:Cross-references: GB:K02048  
 R.Reltsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
 Blood 72, 1074-1076, 1988  
 A>Title: The putative factor IX gene promoter in hemophilia B Leyden.  
 A:Reference number: A30511; PMID:88327116; PMID:3416069  
 A:Accession: A30511  
 A:Molecule type: DNA  
 A:Residues: 8-24 <REI>  
 A:Cross-references: EMBL:X55008; NID:g311288; PIDN:CA38245.2; PID:g4469253  
 R.Koeberl, D.D.; Bottema, C.D.K.; Buurstedde, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor  
 A:Reference number: A32989; PMID:89371752; PMID:2773937  
 A:Accession: A32989  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 30-92 <KOB>  
 R.McGraw, R.A.; Davis, L.M.; Noves, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985  
 A>Title: Evidence for a prevalent polymorphism in the activation peptide of human coagulat  
 A:Reference number: A22673; PMID:85190593; PMID:3857619  
 A:Accession: A22673  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', 195-461 <MCG>  
 A:Cross-references: GB:M11309; NID:9180552; PIDN:AA52023.1; PID:9180553  
 R.Note: the authors translated the codon ACA for residue 29 as Tyr  
 R.Jay, W.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Finkel, A.; Tolstoch  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A>Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba  
 A:Reference number: A21337; PMID:83220788; PMID:6687940

A:Accession: A21337  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', 195-461 <JAY>  
 A:Cross-references: GB:J00137; NID:g182610; PIDN:AA52763.1; PID:g182611  
 R.Jagdeeswaran, P.; Lavelle, D.E.; Kahl, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A>Title: Isolation and characterization of human factor IX cDNA: identification of Tag I  
 A:Reference number: A37546; PMID:84300526; PMID:6089357  
 A:Accession: A37546  
 A:Molecule type: mRNA  
 A:Residues: 38-193, 'T', 195-326 <JAG>  
 A:Cross-references: GB:M35672  
 R.Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
 A>Title: Isolation and characterization of a cDNA coding for human factor IX.  
 A:Reference number: A30623; PMID:83065193; PMID:6959130  
 A:Accession: A30623  
 A:Molecule type: mRNA  
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',  
 A:Cross-references: GB:J00136; NID:g182608; PIDN:AA59726.1; PID:g182609  
 R.Ritarakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
 Vox Sang. 58, 21-29, 1990  
 A>Title: Development of an immunoaffinity process for factor IX purification.  
 A:Reference number: A60486; PMID:90194857; PMID:231207  
 A:Accession: A60486  
 A:Molecule type: protein  
 A:Residues: 47-52, 'X', 55-60, 'X', 62, 'XX', 65 <THA>  
 R.McMullen, B.A.; Fujikawa, K.; Kistel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; PMID:83308813; PMID:6688526  
 A:Accession: A20274  
 A:Molecule type: protein  
 A:Residues: 105-109, 'X', 111-115 <MCX>  
 R.Ballard, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall  
 Eur. J. Biochem. 172, 565-572, 1988  
 A>Title: Characterisation of two differently processed forms of human recombinant factor  
 A:Reference number: S02527; PMID:88166735; PMID:3280312  
 A:Accession: S02527  
 A:Molecule type: protein  
 A:Residues: 29-63 <BAL>  
 A>Note: processed forms expressed in recombinant system  
 R.Jallat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dieterle, A.; Faure, T.; Meulien,  
 EMBO J. 9, 3295-3301, 1990  
 A>Title: Characterization of recombinant human factor IX expressed in transgenic mice an  
 A:Reference number: S12058; PMID:91006024; PMID:2209546  
 A:Accession: S12058  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-68 <JAL>  
 A>Note: processed forms expressed in recombinant system  
 R.Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Canpbe  
 EMBO J. 9, 475-480, 1990  
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium  
 A:Reference number: S12377; PMID:90151623; PMID:2406129  
 A:Accession: S12377  
 A:Molecule type: protein  
 A:Residues: 92-130 <HAN>  
 A>Note: NMR detection of calcium binding by domain expressed in recombinant system  
 R.de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum,  
 Thromb. Haemost. 70, 370-371, 1993  
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi  
 A:Reference number: I59612; PMID:94054330; PMID:8235150  
 A:Accession: I59612  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 444-461 <RES>  
 A:Cross-references: GB:S66752; NID:g439773; PIDN:AA52858.1; PID:g439774  
 R.Stotler, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.  
 Science 239, 491-494, 1988  
 A>Title: Genomic amplification with transcript sequencing.  
 A:Reference number: I59529; PMID:88127096; PMID:3340835  
 A:Accession: I59529

A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 290-359 <RE2>  
 A:Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623  
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; In  
 Biochemistry 33, 5167-5171, 1994  
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin  
 A:Reference number: A54255; MUID:94227047; PMID:8172892  
 A:Accession: A54255  
 A:Molecule type: protein  
 A:Residues: 'D',204,'X',206-211,212,'D',214,'X',216-221,'D', <AGA>  
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate  
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.  
 J. Clin. Invest. 61, 1528-1538, 1978  
 A:Title: Activation of human factor IX (Christmas factor).  
 A:Reference number: A18483; MUID:78194509; PMID:659613  
 A:Contents: annotation; activation; active site; carbohydrate binding  
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984  
 A:Reference number: A37569  
 A:Contents: annotation  
 A:Note: 194-Thr was also found  
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
 J. Biol. Chem. 259, 5698-5704, 1984  
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
 A:Reference number: A37543; MUID:84185715; PMID:6425296  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
 J. Biol. Chem. 260, 2583, 1985  
 A:Reference number: A37544  
 A:Contents: annotation; calcium binding, correction  
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
 Cell 45, 343-348, 1986  
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation  
 A:Reference number: A37545; MUID:86189947; PMID:3009023  
 A:Contents: annotation; signal sequence cleavage site  
 R:Shuto, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takematsu, J.; Ogata, K.; Kamiya,  
 J. Biol. Chem. 264, 21257-21265, 1989  
 A:Title: Blood clotting factor IX (BM) Nagoya: substitution of arginine 180 by tryptophan  
 A:Reference number: A30622; MUID:90078229; PMID:2592373  
 A:Contents: annotation; sequence of mutant B(M) Nagoya  
 A:Note: carboxylation, glycosylation, and cleavage sites  
 R:Barton, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle  
 submitted to the Brookhaven Protein Data Bank, November 1991  
 A:Reference number: A51252; PDB:1IXA  
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
 A:Note: recombinant form expressed in yeast  
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str  
 C:Genetics:  
 A:Gene: GDB:F9  
 A:Cross-references: GDB:119900; OMIM:306900  
 A:Map position: Xq27.1-Xq27.2  
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
 A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan  
 F:1-28/Domain: signal sequence #status experimental <STIG>  
 F:29-46/Domain: propeptide #status experimental <PPT>  
 F:31-91/Domain: Gla domain homology <Gla>  
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:97-128/Domain: EGF homology <EG1>  
 F:134-170/Domain: EGF homology <EG2>  
 F:192-226/Domain: activation peptide #status experimental <ACT>  
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:227-461/Domain: trypsin homology <TRY>  
 F:53,54,61,63,66,67,72,73,76,79,86/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D  
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental  
 F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental  
 Query Match 47.4%; Score 90; DB 1; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 6.9e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 2 NGFLXLRQGSIXRCRXKCSFXKAFIFRNXXRTROFWYSY 44  
 Db 49 SGKLEEFVQNLNERCWEKCSFEAREVFENTERTEFWKQY 91  
 RESULT 11  
 KCHU  
 protein C (activated) (EC 3.4.21.69) precursor - human  
 N:Alternate names: autoprothrombin IIA; plasma protein C  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
 R:Postel, D.C.; Yoshitake, S.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
 A:Title: The nucleotide sequence of the gene for human protein C.  
 A:Reference number: A22331; MUID:85270390; PMID:2991887  
 A:Accession: A22331  
 A:Molecule type: DNA  
 A:Residues: 1-461 <FOS1>  
 A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334  
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
 A:Title: Evolution and organization of the human protein C gene.  
 A:Reference number: A25426; MUID:86120978; PMID:3511471  
 A:Accession: A25426  
 A:Molecule type: DNA  
 A:Residues: 1-445,'L',446-461 <PLU>  
 A:Reference number: GB:M2712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
 R:Postel, D.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
 A:Title: Characterization of a cDNA coding for human protein C.  
 A:Reference number: A21781; MUID:84272714; PMID:6589623  
 A:Accession: A21781  
 A:Molecule type: mRNA  
 A:Residues: 'G',107-461 <FOS2>  
 A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323  
 R:Beckmann, R.U.; Schmidt, R.U.; Sauter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
 Nucleic Acids Res. 13, 5233-5247, 1985  
 A:Title: The structure and evolution of the 461 amino acid human protein C precursor and i  
 A:Reference number: A23789; MUID:85269639; PMID:2991859  
 A:Accession: A23789  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <BEC>  
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120  
 R:Millerich, J.P.; Broze Jr., G.J.  
 J. Biol. Chem. 265, 11397-11404, 1990  
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m  
 A:Reference number: A44605; MUID:90293094; PMID:1654179  
 A:Contents: annotation; carbohydrate binding sites; activation peptide  
 A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
 R:Harris, R.J.; Ling, V.T.; Spellman, M.W.  
 J. Biol. Chem. 267, 5102-5107, 1992  
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor  
 A:Reference number: A44606; MUID:92184750; PMID:1544894  
 A:Contents: annotation; beta-hydroxyaspartic acid  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
 Activation of factor Va is strongly enhanced by complexing with protein S. Protein C also f  
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
 C:Genetics:  
 A:Gene: GDB:PROC  
 A:Cross-references: GDB:120317; OMIM:176860  
 A:Map position: 2q13-2q21  
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:127-86/Domain: Gla domain homology <Glu>  
 F:133-442/Domain: propeptide #status predicted <PRO>  
 F:43-197/Product: protein C light chain #status predicted <LCH>  
 F:92-131/Domain: EGF homology <EG1>  
 F:140-175/Domain: EGF homology <EG2>  
 F:200-461/Product: protein C heavy chain #status predicted <HCH>  
 F:200-211/Domain: activation peptide #status experimental <APT>  
 F:212-445/Domain: trypsin homology <TRY>  
 F:48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
 F:59-64,92-105,101-120,123-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D  
 F:106-111/Disulfide bonds: #status predicted  
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent  
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:133,290,335/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
 F:253,299,402/Active site: His, Asp, Ser #status predicted  
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 46.8%; Score 89; DB 1; Length 461;  
 Best Local Similarity 46.3%; Pred. No. 1e-07;  
 Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLXRCRXLCSPFXAFIFRNXXRTROPW 41  
 DB 43 ANSFLELRHSHSLRECEIEICFENAKELFQVNDTLAFW 83

RESULT 12

thrombin (EC 3.4.21.5) precursor [validated] - human  
 N:Alternate names: coagulation factor II  
 N:Contains: prothrombin  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #ext change 08-Dec-2000  
 A:Accession: A29351; A00914; B00914; A37549; A37550; I51952  
 R:Degeen, S.J.F.; Davie, E.W.  
 Biochemistry 26, 6165-6177, 1987  
 A>Title: Nucleotide sequence of the gene for human prothrombin.  
 A:Reference number: A29351; PMID:88077877; PMID:2825773  
 A:Accession: A29351  
 A:Molecule type: DNA  
 A:Residues: 1-622 <DEG>  
 A:Cross-references: GB:M17262; GB:M33691; NID:9556069; PIDN:AAC63054.1; PID:G339641  
 R:Degeen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.  
 Biochemistry 22, 2087-2097, 1983  
 A>Title: Characterization of the complementary deoxyribonucleic acid and gene coding for  
 A:Reference number: A00914; PMID:83331469; PMID:6305407  
 A:Accession: A00914  
 A:Molecule type: mRNA  
 A:Residues: 8-163, 'N', 165-622 <DE2>  
 A:Cross-references: GB:V00595; GB:J00307; NID:G37128; PIDN:CMA23842.1; PID:G1335344  
 A:Accession: B00914  
 A:Molecule type: DNA  
 A:Residues: 168-311 <DE3>  
 R:Walt, D.A.; Hewett-Emlert, D.; Seeger, W.H.  
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977  
 A:Reference number: A37549; PMID:77193964; PMID:266717  
 A:Accession: A37549  
 A:Molecule type: protein  
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,  
 R:Butkowsk, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.  
 J. Biol. Chem. 252, 4942-4957, 1977  
 A>Title: Primary structure of human prothrombin 2 and alpha-thrombin.  
 A:Reference number: A37550; PMID:77207112; PMID:873923  
 A:Accession: A37550  
 A:Molecule type: protein  
 A:Residues: 315-334, 'N', 336-348, 'N', 350-366, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-  
 J. Biol. Chem. 261, 13210-13215, 1986  
 A:Reference number: A37551; PMID:87008532; PMID:3759958

A:Contents: annotation; activation cleavages  
 R:MacGillivray, R.T.; Irwin, D.M.; Quinto, E.R.; Stone, J.C.  
 Ann. N. Y. Acad. Sci. 485, 73-79, 1986  
 A>Title: Recombinant genetic approaches to functional mapping of thrombin.  
 A:Reference number: I51952; PMID:87182874; PMID:3471151  
 A:Accession: I51952  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2, 'R', 5-100 <RES>  
 A:Cross-references: GB:M3031; NID:g190723; PIDN:AA60220.1; PID:g190724  
 C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds  
 C:Comment: can be removed either by factor Xa or thrombin, the cleavage into light and heavy chain  
 ter 314-Arg, are released in natural blood clotting.  
 C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.  
 C:Comment: The gamma-carboxyglutamate residues bind calcium ions, result from the carboxy/  
 ent interaction with the negatively charged phospholipid membrane surface.  
 C:Comment: The prothrombin precursor is synthesized in the liver.  
 C:Genetics:  
 A:Gene: GDB:F2  
 A:Cross-references: GDB:119894; OMIM:176930  
 A:Map position: 11p11-11q12  
 A:Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-43/Domain: propeptide #status predicted <PRO>  
 F:128-87/Domain: Gla domain homology <Glu>  
 F:44-622/Product: prothrombin #status experimental <MAT>  
 F:44-327/Domain: activation peptide #status experimental <APT>  
 F:108-186/Domain: kringle homology <KR1>  
 F:213-291/Domain: kringle homology <KR2>  
 F:328-622/Product: thrombin light chain #status experimental <LCH>  
 F:364-622/Product: thrombin heavy chain #status experimental <HCH>  
 F:364-613/Domain: trypsin homology <TRY>  
 F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:60-65,90-103,108-186,129-157,157-181,213-291,234-274,262-286/Disulfide bonds: #status  
 F:121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:336-482,536-550,564-594/Disulfide bonds: #status predicted  
 F:391-407/Disulfide bonds: #status experimental  
 F:406,462/Active site: His, Asp #status predicted  
 F:16/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:568/Active site: Ser #status experimental

Query Match 45.8%; Score 87; DB 1; Length 622;  
 Best Local Similarity 38.6%; Pred. No. 3.1e-07;  
 Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANGFLXXLRGSLXRCRXLCSPFXAFIFRNXXRTROPW 44  
 DB 44 ANTFLEVRKGNLRECVETCSYERAFALSSRTDTVFMKY 87

RESULT 13

KFEBO

coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
 N:Alternate names: Christmas factor  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 30-Nov-1980 #sequence revision 03-Aug-1994 #ext change 16-Jul-1999  
 A:Accession: A14757; B20274; I48891; A00923  
 R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; T  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
 A>Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac  
 A:Reference number: A14757; PMID:80056619; PMID:291316  
 A:Accession: A14757  
 A:Molecule type: protein  
 A:Residues: 1-63, 'T', 65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; PMID:83308813; PMID:6688526  
 A:Accession: B20274  
 A:Molecule type: protein



| Query Match | Score | DB 2; | Length |
|-------------|-------|-------|--------|
| 44.2%       | 84;   | DB 2; | 617;   |

Best Local Simultaneously 35.3%; Freq. NO. 12-00;  
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Best Local Simultaneously 35.3%; Freq. NO. 12-00;  
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

2 NGFLXLRGSLRXCRXXLCSFXKAFXIFRNXXRTRQFWVS 44

2 NGF LMAUHQSS LAKACCKAAALCSF AAMFAVF NNAKAR INQFWVS I 43  
:<| | :| | :| | :| |  
qy

Search completed: March 19, 2003, 15:00:59  
Job time : 30.125 secs

Job time : 30.125 secs

GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)  
328.082 Million cell updates/sec

Title: 10Gln28PHE\_4  
Perfect score: 190  
Sequence: 1 ANGFLXHLRQCSLXRXCRXX.....XXAFXIFPNXXRTQFWVSX 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 148   | 77.9        | 407    | 1     | FA7_BOVIN   |
| 2          | 128   | 67.4        | 444    | 1     | FA7_RABIT   |
| 3          | 120   | 63.2        | 466    | 1     | FA7_HUMAN   |
| 4          | 110   | 57.9        | 218    | 1     | TWGI_HUMAN  |
| 5          | 104   | 54.7        | 461    | 1     | PRTC_MOUSE  |
| 6          | 103   | 54.2        | 231    | 1     | TWGI_HUMAN  |
| 7          | 103   | 54.2        | 446    | 1     | FA7_MOUSE   |
| 8          | 103   | 54.2        | 461    | 1     | PRTC_RAT    |
| 9          | 99    | 52.1        | 459    | 1     | PRTC_PIG    |
| 10         | 97    | 51.1        | 490    | 1     | FA10_RABIT  |
| 11         | 94    | 49.5        | 456    | 1     | PRTC_BOVIN  |
| 12         | 93    | 48.9        | 488    | 1     | FA10_HUMAN  |
| 13         | 92    | 48.4        | 492    | 1     | FA10_BOVIN  |
| 14         | 90    | 47.4        | 461    | 1     | FA9_HUMAN   |
| 15         | 89    | 46.8        | 621    | 1     | PRTC_HUMAN  |
| 16         | 87    | 45.8        | 622    | 1     | THRB_HUMAN  |
| 17         | 86    | 45.3        | 416    | 1     | FA9_BOVIN   |
| 18         | 84    | 44.2        | 475    | 1     | FA10_CHICK  |
| 19         | 84    | 44.2        | 617    | 1     | THRB_RAT    |
| 20         | 84    | 44.2        | 618    | 1     | THRB_MOUSE  |
| 21         | 82    | 43.2        | 458    | 1     | PRTC_RABIT  |
| 22         | 81    | 42.6        | 452    | 1     | FA9_CANFA   |
| 23         | 81    | 42.6        | 459    | 1     | FA9_MOUSE   |
| 24         | 78    | 41.1        | 625    | 1     | THRB_BOVIN  |
| 25         | 72    | 37.9        | 646    | 1     | PRTC_MACMU  |
| 26         | 72    | 37.9        | 649    | 1     | PRTC_HUMAN  |
| 27         | 69    | 36.3        | 675    | 1     | PRTC_BOVIN  |
| 28         | 68    | 35.8        | 202    | 1     | TWGI_HUMAN  |
| 29         | 68    | 35.8        | 646    | 1     | PRTC_RABIT  |
| 30         | 67    | 35.3        | 226    | 1     | TWGI_HUMAN  |
| 31         | 66    | 34.7        | 376    | 1     | FA10_TROCA  |
| 32         | 66    | 34.7        | 400    | 1     | PRTC_HUMAN  |
| 33         | 66    | 34.7        | 675    | 1     | PRTC_RAT    |

|    |      |      |      |   |            |                      |
|----|------|------|------|---|------------|----------------------|
| 34 | 62   | 32.6 | 396  | 1 | PRTC_BOVIN | P00744 bos taurus    |
| 35 | 59   | 31.1 | 675  | 1 | PRTC_MOUSE | Q08761 mus musculus  |
| 36 | 52   | 27.4 | 604  | 1 | VE1_BRV2   | P11298 bovine papill |
| 37 | 52   | 27.4 | 605  | 1 | VE1_BRV1   | P03116 bovine papill |
| 38 | 48   | 25.3 | 413  | 1 | NCAP_IHNV  | P19691 infectious    |
| 39 | 45.5 | 23.9 | 2133 | 1 | FA8_PIG    | P12263 sus scrofa    |
| 40 | 42.5 | 22.4 | 105  | 1 | UL03_HCMVA | P16775 human cytom   |
| 41 | 42   | 22.1 | 320  | 1 | GSHB_BUCAI | P57612 buchnera ap   |
| 42 | 41   | 21.6 | 97   | 1 | YCRB_MYCA  | P45619 mycoplasma    |
| 43 | 41   | 21.6 | 184  | 1 | ADML_MOUSE | P97297 mus musculus  |
| 44 | 41   | 21.6 | 371  | 1 | LST_NEIMA  | O91UV5 neisseria m   |
| 45 | 41   | 21.6 | 371  | 1 | LST_NEIMB  | P72097 neisseria m   |

## ALIGNMENTS

```

RESULT 1
ID   FA7_BOVIN
AC   P22457;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
DE   accelerator).
GN   P7.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   MEDLINE=89008362; PubMed=3049594;
RX   Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA   Iwanaga S.;
RT   "Bovine factor VII. Its purification and complete amino acid
RT   sequence.";
RL   J. Biol. Chem. 263:14868-14877(1988).
RN   [2]
RP   STRUCTURE OF CARBOHYDRATE ON SER-52.
RX   MEDLINE=89213999; PubMed=3149637;
RA   Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA   Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
RT   "A new trisaccharide sugar chain linked to a serine residue in bovine
RT   blood coagulation factors VII and IX.";
RL   J. Biochem. 104:867-868(1988).
RN   [3]
RP   STRUCTURE OF CARBOHYDRATE ON SER-52.
RX   MEDLINE=91344709; PubMed=2129367;
RA   Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;
RT   "A new trisaccharide sugar chain linked to a serine residue in the
RT   first EGF-like domain of clotting factors VII and IX and protein Z.";
RL   Adv. Exp. Med. Biol. 281:121-131(1990).
CC   -!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC   CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC   THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC   AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC   BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC   FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC   -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-lle bond in factor X to
CC   form factor Xa.
CC   -!- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC   BY A DISULFIDE BOND.
CC   -!- TISSUE SPECIFICITY: PLASMA.
CC   -!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC   GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC   CALCIUM.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
DR   PIR, A31979; A31979.
DR   HSBP, P08709; 1BP9.

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DR  MEROPS: S01.215; -.
DR  InterPro: IPR000152; Asx_hydroxyl.
DR  InterPro: IPR001314; Chymotrypsin.
DR  InterPro: IPR000561; EGF-like.
DR  InterPro: IPR000742; EGF_2.
DR  InterPro: IPR001881; EGF_Ca.
DR  InterPro: IPR001438; EGF_II.
DR  InterPro: IPR002383; GLA_blood.
DR  InterPro: IPR001254; Ser_protease_Try.
DR  InterPro: IPR000294; VitK_dep_GLA.
DR  Pfam: PF00008; EGF_2.
DR  Pfam: PF00089; trypsin; 1.
DR  Pfam: PF00594; gla; 1.
DR  PRINTS: PR00722; CHYMOTRYPSIN.
DR  PRINTS: PR00010; EGFBLD.
DR  PRINTS: PR00001; GLABLOOD.
DR  SMART: SM00179; EGF_CA; 1.
DR  SMART: SM00001; EGF_like; 1.
DR  SMART: SM00069; GLA_1.
DR  SMART: SM00020; TYP_SPC; 1.
DR  PROSITE: PS00010; ASX_HYDROXYL; 1.
DR  PROSITE: PS00022; EGF_1; 1.
DR  PROSITE: PS01186; EGF_2; 2.
DR  PROSITE: PS01187; EGF_CA; 1.
DR  PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR  PROSITE: PS00240; TRYPSIN_DOM; 1.
DR  PROSITE: PS00134; TRYPSIN_HIS; 1.
DR  PROSITE: PS00135; TRYPSIN_SER; 1.
DR  PROSITE: PS00135; TRYPSIN_SER; 1.
DR  HydroLae: Serine protease; Blood coagulation; Zymogen; Glycoprotein;
DR  Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
DR  EGF-like domain; Repeat.
DR  CHAIN 1 152
DR  DOMAIN 6 35
DR  DOMAIN 46 82
DR  DOMAIN 87 128
DR  DOMAIN 153 407
DR  SITE 152 153
DR  ACT_SITE 193 193
DR  ACT_SITE 242 242
DR  ACT_SITE 344 344
DR  BINDING 338 338
DR  DISULFID 17 22
DR  DISULFID 50 61
DR  DISULFID 55 70
DR  DISULFID 72 81
DR  DISULFID 91 102
DR  DISULFID 98 112
DR  DISULFID 114 127
DR  DISULFID 135 164
DR  DISULFID 159 164
DR  DISULFID 178 194
DR  DISULFID 310 329
DR  DISULFID 340 368
DR  MOD_RES 6 6
DR  MOD_RES 7 7
DR  MOD_RES 14 14
DR  MOD_RES 16 16
DR  MOD_RES 19 19
DR  MOD_RES 20 20
DR  MOD_RES 25 25
DR  MOD_RES 26 26
DR  MOD_RES 29 29
DR  MOD_RES 35 35
DR  MOD_RES 52 52
DR  CARBOHYD 145 145
DR  CARBOHYD 203 203
DR  SEQUENCE 407 AA; 44431 MW; 703EFED636F7F10 CRC64;
Query Match 77.9%; Score 148; DB 1; Length 407;
Best Local Similarity 68.2%; Pred. No. 3.5e-19;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 1 ANGELXXLRGSLXRCXRLCSFPXXAFIIFRNXXRTROFWY 44
DB 1 ANGFEELPGLSLERCRBELCSFEENHEIFNNEERTROFWY 44

RESULT 2
ID FA7_RABIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=93190306; PubMed=8383365;
RA Brothens A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII.";
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyses one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U77477; AAB37326.1; -.
DR HSSP; P08709; 1FAK.
DR MEROPS; S01.215; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.

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DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxylutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
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FT MOD_RES 55 55
FT MOD_RES 58 58
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FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 102 102
FT CARBOHYD 212 241
FT CARBOHYD 242 261
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABCF55427F8 CRC64;

Query Match 67.4%; Score 128; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 1,6e-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
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DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Bptacog alfa).
DE
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.V., Kistiel W., Kurauchi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.V.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
[3]
RN SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toch B.J., Yi Q., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
[4]
RN SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RT Biochemistry 27:7785-7793(1988).
[5]
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wilberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RT J. Biol. Chem. 266:11051-11057(1991).
[6]
RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RT J. Biol. Chem. 264:20320-20325(1989).
[7]
RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RT Adv. Exp. Med. Biol. 281:121-131(1990).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96115641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kitzhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RT Nature 380:41-46(1996).
```

RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPI mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=96367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Glibert G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Wede T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrarchi P., Gemmati D., Derosa V., Pinotti M.,  
 RA Rodorigo G., Casanato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferrati M., Patrarchi P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 RT (115His and 333Ser) in the human coagulation factor VII gene.";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=96061028; PubMed=8242057;  
 RA Takamiya O., Kemballi-Cook G., Marin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RX MEDLINE=94264305; PubMed=8204879;  
 RA Ching S., Clarke B., Srichara S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Caecaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (394Ala-->Val) and X (334Ser-->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohwaki K., Hayashi T., Wada H., Minamikawa K., Shitakawa S.,  
 RA Suzuki M.;  
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain."

|  |  |                              |
|--|--|------------------------------|
| RL   | Thromb. Haemost.   | 71:773-777 (1994).           |
| RN   | [18]   |                              |
| RP   | VARIANT MET-419.   |                              |
| RX   | MEDLINE=96247510; PubMed=8652821;                                      |                              |
| RA   | Ardini A.A., Mannucci P.M., Bauer K.A.;                                |                              |
| RT   | "A Thrombotic mutation in factor VII of a patient with a hereditary    |                              |
| RL   | Blood 87:5085-5094(1996).  |                              |
| RN   | [19]   |                              |
| RP   | VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.                  |                              |
| RX   | MEDLINE=97001216; PubMed=8844208;                                      |                              |
| RA   | Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,     |                              |
| RT   | Lunghi B., Rodeghiero F., Marchetti G.;                                |                              |
| RL   | "Mutation pattern in clinically asymptomatic coagulation factor VII    |                              |
| RN   | deficiency.";  |                              |
| RP   | Hum. Mutat. 8:108-115(1996).   |                              |
| RL   | [20]   |                              |
| RP   | VARIANT VAL-304.   |                              |
| RX   | MEDLINE=97037613; PubMed=8883260;                                      |                              |
| RA   | Tanary H., Fromovich Y., Shalom L., Reich Z., Dym O., Ianir N.,        |                              |
| RT   | Brenner B., Paz M., Luder A.S., Blau O., Korostelevsky M.,             |                              |
| RL   | Zelzov R., Seligsohn U.;   |                              |
| RT   | "A1a244Val is a common, probably ancient mutation causing factor VII   |                              |
| RL   | deficiency in Moroccan and Iranian Jews.;"                             |                              |
| RP   | Thromb. Haemost. 76:283-291(1996).                                     |                              |
| RN   | [21]   |                              |
| RP   | VARIANTS MALTA THR-194 AND VAL-304.                                    |                              |
| RX   | MEDLINE=96112461; PubMed=9452082;                                      |                              |
| RA   | Alshinawi C., Securti C., Galides R., Aguilina A., Felice A.E.;        |                              |
| RT   | "Two new missense mutations (P134T and A244V) in the coagulation       |                              |
| RL   | factor VII gene.";   |                              |
| RN   | Hum. Mutat. Suppl. 1:S189-S191(1998).                                  |                              |
| CC   | -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS |                              |
| CC   | CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR     |                              |
| CC   | THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR        |                              |
| CC   | AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA      |                              |
| CC   | BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO     |                              |
| CC   | FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.               |                              |
| CC   | -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to     |                              |
| CC   | form factor Xa.  |                              |
| CC   | -I- SUBUNIT: HETEROIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED      |                              |
| CC   | BY A DISULFIDE BOND.   |                              |
| CC   | -I- ALTERNATIVE PRODUCTS: 2 isoforms, A (shown here) and B; are        |                              |
| CC   | produced by alternative splicing.                                      |                              |
| CC   | -I- TISSUE SPECIFICITY: PLASMA.  |                              |
| CC   | -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME        |                              |
| CC   | GUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND              |                              |
| CC   | CALCIUM.   |                              |
| CC   | -I- DISEASE: DEFECTS IN F7 CAN CAUSE CONGULOPATHY.                     |                              |
| CC   | -I- PHARMACEUTICAL: Available under the names Niaslate or Novoseven    |                              |
| CC   | (Novo Nordisk). Used for the treatment of bleeding episodes in         |                              |
| Query Match:   | 63.2%;   | Score 120; DB 1; Length 466; |
| Best Local Similarity  | 52.3%;   | Pred. No. 4.8e-14;           |
| Matches 23; Conservativity 5; Mismatches 16; Indels 0; Gaps 0              |  |                              |
| Oy   | 1 ANGFLXLRQGSIXRXCRRXLCSFFXAIFRNXXRTROFWWSY 44                         |                              |
| Dd   | 61 ANAFLEELRPGSLERCKEBCQCSFEFAHEIRFDARILTFWISY 104                     |                              |
| RESULT 4   |  |                              |
| TWG1_HUMAN   | STANDARD;  | PRT; 218 AA.                 |
| ID_O14668;   |  |                              |
| DT 15-JUN-2002 (Rel. 41, Created)  |  |                              |
| DT 15-JUN-2002 (Rel. 41, Last sequence update)                             |  |                              |
| DE Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline- |  |                              |
| rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein      |  |                              |
| 1).  |  |                              |
| PRGI OR TWG1 OR PRGP1.   |  |                              |
| GN Homo sapiens (Human).   |  |                              |

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
  gamma-carboxyglutamic acid proteins.";
  Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997)".
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PM: Gla residues are produced after subsequent posttranslational
  modifications of glutamic acid by a vitamin K-dependent gamma-
  carboxylase.
CC -----
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CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; ICFH.
DR Genew; HGNC:9469; PRRG1.
DR MIM; 604428; -.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT PROTEIN 1.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 84 106
FT FT DOMAIN 107 218
FT FT DOMAIN 24 61
FT FT DOMAIN 131 135
FT FT POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AE98 CRC64;
Query Match 57.9%; Score 110; DB 1; Length 218;
Best Local Similarity 40.9%; Pred. No. 1,5e-12;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
OY 1 ANGFLXLRQGLRXCRXXLCSPFXAEPFNXXRTQFWWSY 44
Db 21 ANGFEERIQGNIERCKEKFCTFEBARAFENNEKTEKFWSY 64

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RT      "Isolation and characterization of a mouse protein C cDNA.";
RL      [2]
RN      J. Biochem. 111:491-495(1992).
RP      SEQUENCE FROM N.A.
RX      STRAIN=129/SvJ;
RX      MEDLINE=98152576; PubMed=9493582;
RA      Jalburt L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA      Castellino F.J.;
RT      "Nucleotide structure and characterization of the murine gene encoding
RT      anticoagulant protein C.";
RL      Thromb. Haemost. 79:310-316(1998).
RN      [3]
RP      SEQUENCE OF 274-434 FROM N.A.
RC      STRAIN=BALB/c;
RC      MEDLINE=94318474; PubMed=8043441;
RX      Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RA      "A comparative study of partial primary structures of the catalytic
RT      region of mammalian protein C.";
RL      Br. J. Haematol. 86:590-600(1994).
CC      -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC      REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC      IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC      -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC      and villi.
CC      -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC      INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC      BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC      TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC      REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC      STRONGLY PROMOTED BY THROMBOMODULIN.
CC      -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC      -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC      GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC      -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC      ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC      SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC      THROMBIN-THROMBOMODULIN COMPLEX.
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC      -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; D10445; BAA01235.1; -.
DR      EMBL; AF034569; AAC33795.1; -.
DR      EMBL; D43755; BAA07812.1; -.
DR      PIR; JX0210; JX0210.
DR      HSSP; P04070.1PCU.
DR      MEROPS; S01.218; -.
DR      MGD; MGI:97771; Proc.
DR      InterPro; IPR000152; Aex_hydroxy1.
DR      InterPro; IPR001314; Chymotrypsin.
DR      InterPro; IPR000561; EGF-like.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR002383; GLA_Blood.
DR      InterPro; IPR001254; Ser_protease_Try.
DR      InterPro; IPR000294; Vitk_dep_GLA.
DR      Pfam; PF00008; EGF_2.
DR      Pfam; PF00089; trypsin. 1.
DR      Pfam; PF00594; gla. 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      PRINTS; PR00001; GLABLOOD.
DR      SMART; SM00179; EGF_CA_1.
DR      SMART; SM00001; EGF_like_1.
DR      SMART; SM00069; GLA_1.
DR      SMART; SM00020; TRY_Spc_1.
DR      PROSITE; PS00010; ASX_HYDROXYL_1.
DR      PROSITE; PS00022; EGF_1; 1.

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DR PROSITE; P501186; EGF 2; 2.
DR PROSITE; P501187; EGF_Ca; 1.
DR PROSITE; P500011; GLU_CARBOXYLATION; 1.
DR PROSITE; P500240; TRYPsin_DOM; 1.
DR PROSITE; P500134; TRYPsin_HIS; 1.
DR PROSITE; P500135; TRYPsin_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1
FT PROPE 34
FT CHAIN 42
FT CHAIN 196
FT PEPTIDE 199
FT SITE 212
FT SITE 213
FT DOMAIN 96
FT DOMAIN 135
FT DOMAIN 213
FT MOD_RES 47
FT MOD_RES 48
FT MOD_RES 48
FT MOD_RES 55
FT MOD_RES 57
FT MOD_RES 60
FT MOD_RES 61
FT MOD_RES 66
FT MOD_RES 67
FT MOD_RES 70
FT MOD_RES 70
FT ACT_SITE 112
FT ACT_SITE 253
FT ACT_SITE 299
FT ACT_SITE 402
FT DISULFID 58
FT DISULFID 91
FT DISULFID 100
FT DISULFID 104
FT DISULFID 121
FT DISULFID 139
FT DISULFID 146
FT DISULFID 161
FT DISULFID 182
FT DISULFID 238
FT DISULFID 373
FT DISULFID 398
FT CARBOHYD 214
FT CARBOHYD 290
FT CARBOHYD 355
FT CONFLICT 328
FT CONFLICT 393
SQ SEQUENCE 461 AA; 51945 MW; 53FA0B5B194D6E CRC64;

Query Match
Best Local Similarity 45.7%; Score 104; DB 1; Length 461;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXKRCXXLCSEFXAXFIFRNXXKRTQGFWSY 44
Db 42 ANSFLEMRPGLSLEKCEMEICDFEEAOEIFQVNEVDLAFWIKY 85

RESULT 6
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC O9BBD7;
DT 15-JUN-2002 (Rel. 41, Created)
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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RX MEDLINE=2117044; PubMed=1171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Glu residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
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CC -----
CC DR EMBL; AF326350; AAK00955.1; -.
CC DR HSSP; P00740; ICFH.
CC DR InterPro; IPR002383; Glu blood.
CC DR InterPro; IPR000294; Glu_dep_GLA.
CC DR Pfam; PF00594; gla; 1.
CC DR PRINTS; PR00001; GLABLOOD.
CC DR SMART; SM00069; GLA; 1.
CC DR PROSITE; P500011; GLU_CARBOXYLATION; 1.
CC KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
CC FT PROPEP 1
CC FT CHAIN 20
CC FT DOMAIN 20
CC FT TRANSMEM 79
CC FT DOMAIN 102
CC FT DOMAIN 231
CC FT DOMAIN 231
CC SQ SEQUENCE 231 AA; 25848 MW; 8A373E48490D81 CRC64;

Query Match
Best Local Similarity 40.9%; Score 103; DB 1; Length 231;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXKRCXXLCSEFXAXFIFRNXXKRTQGFWSY 44
Db 20 ANSFLEMRPGLSLEKCEMEICSEYBEKVEFNKERTMEFWKGY 63

RESULT 7
FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

RX MEDLINE=97127167; PubMed=8972017;  
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine blood  
 coagulation factor VII gene."  
 RL Thromb. Haemost. 76:957-964(1996).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
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 CC -----  
 CC EMBL: U66079; AAC3796.1; -  
 CC HSSP: P08709; 1BR9.  
 DR MEROPS: S01.215; -  
 DR MGD: MGI:109325; F7.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF-2.  
 DR InterPro: IPR001881; EGF-Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VltK\_dep\_GLA.  
 DR Pfam: PF00008; EGF; 2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; gla; 1.  
 DR PRINTS: PRO0722; CHYMOTRYPSIN.  
 DR PRINTS: PRO0001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_like; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; Tryp\_Sec; 1.  
 DR PROSITE: PS00010; Asx\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GU\_CARBOXYLATION; 1.  
 DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolyase: Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 KM EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 193  
 FT CHAIN 194 446  
 FT DOMAIN 47 76  
 FT DOMAIN 87 123  
 FT DOMAIN 128 169  
 FT DOMAIN 194 446  
 FT SITE 193 194  
 FACTOR IXA, OR THROMBIN (BY SIMILARITY).

FT ACT SITE 234 234 BY SIMILARITY.  
 FT ACT SITE 283 283 BY SIMILARITY.  
 FT ACT SITE 385 385 BY SIMILARITY.  
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 96 111 BY SIMILARITY.  
 FT DISULFID 113 122 BY SIMILARITY.  
 FT DISULFID 132 143 BY SIMILARITY.  
 FT DISULFID 139 153 BY SIMILARITY.  
 FT DISULFID 155 168 BY SIMILARITY.  
 FT DISULFID 176 303 BY SIMILARITY.  
 FT DISULFID 200 205 BY SIMILARITY.  
 FT DISULFID 219 235 BY SIMILARITY.  
 FT DISULFID 351 370 BY SIMILARITY.  
 FT DISULFID 381 409 BY SIMILARITY.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A5C96B CRC64;  
 Query Match 54.2%; Score 103; DB 1; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 5.5e-11;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;  
 Qy 1 ANGFLXLIROGSLRXCRXXLCSFYXAFXIFPNXRXTRQFWVS 44  
 Db 42 ANSLLEELMPGSLRECNBEGCSFEAREIFRSPERTQFWIV 85  
 RESULT 8  
 ID PRTC\_RAT STANDARD; PRT; 461 AA.  
 AC P31394;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=liver;  
 RX MEDLINE=92329550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C";  
 RL Biochim. Biophys. Acta 1131:329-332(1992)  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.

| FT                    | MOD_RES   | 67  | 67                 | GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY). |
|-----------------------|---|---|--------------------|---|
| FT                    | MOD_RES   | 70  | 70                 | GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY). |
| FT                    | MOD_RES   | 112   | 112                | HYDROXYLATION (BY SIMILARITY).              |
| FT                    | ACT_SITE  | 254   | 254                | CHARGE RELAY SYSTEM.                        |
| FT                    | ACT_SITE  | 300   | 300                | CHARGE RELAY SYSTEM.                        |
| FT                    | ACT_SITE  | 402   | 402                | CHARGE RELAY SYSTEM.                        |
| FT                    | DISULFID  | 58  | 63                 | BY SIMILARITY.                              |
| FT                    | DISULFID  | 91  | 110                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 100   | 105                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 104   | 119                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 121   | 130                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 139   | 150                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 146   | 159                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 161   | 174                | INTERCHAIN (BY SIMILARITY).                 |
| FT                    | DISULFID  | 182   | 320                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 239   | 255                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 373   | 387                | BY SIMILARITY.                              |
| FT                    | DISULFID  | 398   | 426                | BY SIMILARITY.                              |
| FT                    | CARBOHYD  | 215   | 215                | N-LINKED (GLCNAC. . .) (POTENTIAL).         |
| FT                    | CARBOHYD  | 291   | 291                | N-LINKED (GLCNAC. . .) (POTENTIAL).         |
| FT                    | CARBOHYD  | 355   | 355                | N-LINKED (GLCNAC. . .) (POTENTIAL).         |
| SO                    | SEQUENCE  | 461 AA;                                     | 51912 MM;          | 8A4CP93664EDACD5 CRC64;                     |
| Query Match           |   | 54.2%;                                      | Score 103;         | DB 1; Length 461;                           |
| Best Local Similarity |   | 45.5%;                                      | Pred. No. 5.7e-11; |   |
| Matches               | 20;   | Conservative                                | 4;                 | Mismatches 20; Indels 0; Gaps 0;            |
| Oy                    | 1   | ANGFLXXLRQSLKRXCRXLCSEFXAPXIRPNXXRTQPNVSY   | 44                 |   |
| Db                    | 42  | ANSFLIEVRAAGSLERECMEICDFEEAEOITQNVEDTLAFIKY | 85                 |   |
| RESULT 9              |   |   |                    |   |
| PTC_PIG               |   |   |                    |   |
| ID_PRTC_PIG           | STANDARD;   | PRT;  | 459 AA.            |   |
| AC                    | Q9GUP2;   |   |                    |   |
| DT                    | 16-OCT-2001 (Rel. 40, Created)  |   |                    |   |
| DT                    | 16-OCT-2001 (Rel. 40, Last sequence update)   |   |                    |   |
| DT                    | 15-JUN-2002 (Rel. 41, Last annotation update)   |   |                    |   |
| DE                    | Vitamin-K dependent protein C precursor (EC 3.4.21.69)  |   |                    |   |
| DE                    | (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).   |   |                    |   |
| DE                    | PROC.   |   |                    |   |
| GN                    | Sus scrofa (Pig).   |   |                    |   |
| OS                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |   |                    |   |
| OC                    | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.   |   |                    |   |
| OX                    | NCBI_TaxId=9823;  |   |                    |   |
| RN                    | [1]   |   |                    |   |
| RP                    | SEQUENCE FROM N.A.  |   |                    |   |
| RC                    | TISSUE=Liver;   |   |                    |   |
| RX                    | MEDLINE=21121490; PubMed=11229814;  |   |                    |   |
| RA                    | Grilmm D.R., Colcer M.B., Braunschweig M., Alexander L.J., Neame P.J., Kim H.K.W.;  |   |                    |   |
| RT                    | "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains";  |   |                    |   |
| RT                    | Cell. Mol. Life Sci. 58:148-159(2001).  |   |                    |   |
| RL                    | - FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIa in the presence of calcium ions and phospholipide.  |   |                    |   |
| CC                    | - CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.   |   |                    |   |
| CC                    | - SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin. |   |                    |   |
| CC                    | - TISSUE SPECIFICITY: Plasma; synthesized in the liver.   |   |                    |   |
| CC                    | - PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.   |   |                    |   |

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
 CC another site, beyond the GLA domain. This GLA-independent binding  
 CC site is necessary for the recognition of the  
 CC thrombin-thrombomodulin complex.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL; AF191307; AAC28380.1; --  
 CC HSSP; P04070; 1PCU.  
 DR HSSP; P04070; 1PCU.  
 DR MEROPS; S01.218; --  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VtK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00001; EGF\_like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spe; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 41  
 FT CHAIN 42 459  
 FT CHAIN 42 196  
 FT CHAIN 199 459  
 FT CHAIN 199 213  
 FT SITE 213 214  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 214 459  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67

FT MOD\_RES 70 70  
 FT ACT\_SITE 112 112  
 FT ACT\_SITE 255 255  
 FT ACT\_SITE 301 301  
 FT ACT\_SITE 400 400  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 321  
 FT DISULFID 240 256  
 FT DISULFID 371 385  
 FT CARBOHYD 138 138  
 FT CARBOHYD 292 292  
 FT CARBOHYD 353 353  
 SQ SEQUENCE 459 AA; 5186 MW; 8541AAC14CCT16D09 CRC64;  
 Query Match 52.1%; Score 99; DB 1; Length 459;  
 Best Local Similarity 45.5%; Pred. No. 3e-10;  
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;  
 OY 1 ANGFLXLRQGSGLKRXCRXXLCSPFYXAFYFRNXXRTQFWVS 44  
 DB 42 ANSFLELRPSLSRECKEETCDFEAREIFONTENTWAFMSKY 85  
 RESULT 10  
 FA10\_RABIT STANDARD; PRT; 490 AA.  
 AC 019045;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN Flt.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CC NCBI\_TaxID=9986;  
 RN [1]  
 RP MEDLINE=97256311; PubMed=9101642;  
 RX Pendurthi U.R., Anderson K.D., James H.L.;  
 RA "Characterization of a full-length cDNA for rabbit factor X.";  
 RL Thromb. Res. 85:503-514 (1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)  
 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF003200; AAB62542.1; -.  
 DR HSSP: P00742; IHCG.  
 DR MEROPS: S01.216; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF 2.  
 DR InterPro: IPR001881; EGF\_CA.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; Vitk\_deg\_GLA.  
 DR Pfam: PF00008; EGF 2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; gla; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_like; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; Tryp\_Spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPsin\_SER; 1.  
 DR PROSITE: PS00135; TRYPsin\_HIS; 1.  
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KM Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
 FT PROPEP 1 40  
 FT CHAIN 41 180  
 FT CHAIN 184 490  
 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT DOMAIN 86 122  
 FT DOMAIN 125 165  
 FT DOMAIN 233 490  
 FT MOD\_RES 46 46  
 FT MOD\_RES 47 47  
 FT MOD\_RES 54 54  
 FT MOD\_RES 56 56  
 FT MOD\_RES 59 59  
 FT MOD\_RES 60 60  
 FT MOD\_RES 65 65  
 FT MOD\_RES 66 66  
 FT MOD\_RES 69 69  
 FT MOD\_RES 72 72  
 FT MOD\_RES 75 75  
 FT MOD\_RES 79 79  
 FT MOD\_RES 103 103  
 FT ACT\_SITE 274 274

FT ACT\_SITE 320 320 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 417 417 CHARGE RELAY SYSTEM.  
 FT DISULFID 90 101 BY SIMILARITY.  
 FT DISULFID 95 110 BY SIMILARITY.  
 FT DISULFID 112 121 BY SIMILARITY.  
 FT DISULFID 129 140 BY SIMILARITY.  
 FT DISULFID 136 149 BY SIMILARITY.  
 FT DISULFID 151 164 BY SIMILARITY.  
 FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 229 244 BY SIMILARITY.  
 FT DISULFID 259 275 BY SIMILARITY.  
 FT DISULFID 368 402 BY SIMILARITY.  
 FT DISULFID 413 441 BY SIMILARITY.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85A2A6D11 CRC64;  
 Query Match 51.1%; Score 97; DB 1; Length 490;  
 Best Local Similarity 38.6%; Pred. No. 7.4e-10;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;  
 Qy 1 ANGFLXXLRQGSIXRXCRXXLCSFXXAFXIFRNXXRTQFWWSY 44  
 Db 41 ANSFLLELKKNLERECMEHCSEYEEALVFEDREKTNFEFNKY 84  
 RESULT 11  
 ID PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxId=9913;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=85014826; PubMed=6091100;  
 RX Long G.L., Balagaje R.M., McGilivray R.T.A.;  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN [2]  
 RP SEQUENCE OF 40-194.  
 RA MEDLINE=83007325; PubMed=6896876;  
 RX Fernlund P., Stenflo J.;  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 RN [3]  
 RP REVISION TO 110.  
 RA MEDLINE=83169769; PubMed=6572939;  
 RX Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN [4]  
 RP SEQUENCE OF 197-456.  
 RA MEDLINE=83007326; PubMed=6896877;  
 RX Stenflo J., Fernlund P.;  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RL J. Biol. Chem. 257:12180-12190(1982).  
 RN [5]  
 RP PROCESSING, AND CALCIUM-BINDING DATA.  
 RA MEDLINE=83213513; PubMed=6304092;  
 RX Esmen N.L., Debaule L.E., Esmen C.T.;  
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
 domainless protein C";



RL J. Biol. Chem. 258:5548-5553 (1983).  
 [6]  
 RP PROCESSING AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213514; PubMed=6406503;  
 RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;  
 RT "Structural changes required for activation of protein C are induced  
 by Ca<sup>2+</sup> binding to a high affinity site that does not contain gamma-  
 carboxyglutamic acid."  
 RL J. Biol. Chem. 258:5554-5560 (1983).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 -----  
 CC EMBL, K02435, AAA30685.1; -.  
 DR PIR, A00928; KXBO.  
 DR HSP, P04070; 1PCU.  
 DR HESOP, S01.218; -.  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF-Ca.  
 DR InterPro: IPR001254; Ser protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin\_1.  
 DR Pfam: PF00594; gla\_1.  
 DR SMART, SM00181; EGF\_2.  
 DR SMART, SM00069; GLA\_1.  
 DR SMART, SM00020; Tryp\_SPC\_1.  
 DR PROSITE, PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE, PS00022; EGF\_2\_1.  
 DR PROSITE, PS01186; EGF\_2\_2.  
 DR PROSITE, PS01187; EGF-Ca\_1.  
 DR PROSITE, PS00011; GLU CARBOXYLATION\_1.  
 DR PROSITE, PS00240; TRYPSIN\_DOM\_1.  
 DR PROSITE, PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 DR PROSITE, PS00135; TRYPSIN\_SER\_1.  
 KM Blood coagulation; Glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1  
 FT NON TER 1  
 FT PROPEP 30 29  
 FT CHAIN 40 194  
 FT CHAIN 157 456  
 FT PEPTIDE 197 210  
 FT DOMAIN 94 129  
 FT DOMAIN 133 173  
 FT DOMAIN 211 456  
 FT DOMAIN 211 456  
 SERINE PROTEASE.

FT MOD RES 45 45  
 FT MOD RES 46 46  
 FT MOD RES 53 53  
 FT MOD RES 55 55  
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 FT MOD RES 62 62  
 FT MOD RES 64 64  
 FT MOD RES 65 65  
 FT MOD RES 68 68  
 FT MOD RES 74 74  
 FT MOD RES 110 110  
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 FT ACT SITE 298 298  
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 FT DISULFID 102 117  
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 FT DISULFID 137 148  
 FT DISULFID 144 157  
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 FT CARBOHYD 366 366  
 FT VARIAT 82 82  
 FT CONFLICT 455 456  
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 Db 40 ANSFLEELRPGNVERECSEVECFEAREIEFONTEDTWAFWSFY 83  
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 ID FA10 HUMAN STANDARD; PRT; 488 AA.  
 AC P00742; Q14340;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91216473; PubMed=1902434;  
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;  
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding  
 human coagulation factor X."  
 RT Gene 99:291-294 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026600; PubMed=3768336;  
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;  
 RT "Gene for human factor X: a blood coagulation factor whose gene  
 organization is essentially identical with that of factor IX and  
 protein C."  
 RT Biochemistry 25:5098-5102 (1986).  
 RN [3]

RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RN [4]  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA.";  
 RT Gene 41:311-314(1986).  
 RN [5]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83557207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasaogawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RT Biochemistry 22:2875-2884(1983).  
 RN [6]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [7]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RT Eur. J. Biochem. 218:153-163(1993).  
 RN [8]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RT Gene 84:517-519(1989).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RT J. Mol. Biol. 232:947-966(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoro H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC EMBL; K01886; AAA52486.1; -;  
 CC EMBL; M33297; AAA52636.1; -;  
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 CC PIR; A25853; A25853.  
 CC PIR; A24478; A24478.  
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 CC PDB; 1FAK; 29-OCT-97.  
 CC PDB; 1FXV; 17-JUN-98.  
 CC PDB; 1XKA; 23-MAR-99.  
 CC PDB; 1XKB; 23-MAR-99.  
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 CC MIM; 227600; -;  
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 CC InterPro; IPR001314; Chymotrypsin.  
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 CC InterPro; IPR000742; EGF 2.  
 CC InterPro; IPR001881; EGF Ca.  
 CC InterPro; IPR002383; GLA\_blood.  
 CC InterPro; IPR001254; Ser\_protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00008; EGF; 2.  
 CC Pfam; PF00089; trypsin; 1.  
 CC Pfam; PF00594; gla; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00001; GLABLOOD.  
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 CC SMART; SM00001; EGF\_like; 1.  
 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; TRYP\_Spc; 1.  
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 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 CC PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SRR; 1.  
 CC GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 CC signal; Zymogen; EGF-like domain; Repeat; 3d-structure.  
 CC FT SIGNAL 1 31 POTENTIAL.  
 CC FT PROPEP 32 40  
 CC FT CHAIN 41 179 FACTOR X LIGHT CHAIN.  
 CC FT CHAIN 183 488 FACTOR X HEAVY CHAIN.  
 CC FT PROPEP 183 234 ACTIVATION PEPTIDE.  
 CC FT CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.  
 CC FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
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FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .).
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FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 48.9%; Score 93; DB 1; Length 488;
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Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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DB 41 ANSFLKMKHLEKRECEMETCSYSEAREVEFSDXTNEFMNXY 84

RESULT 13
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492 (1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=676735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neureath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor)."
RL Biochemistry 19:659-667 (1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kiesel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14 (1983).

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RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neureath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086 (1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X."
RL Eur. J. Biochem. 218:153-163 (1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053114; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neureath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases."
RL Biochemistry 11:4899-4903 (1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363 (1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region."
RL J. Biol. Chem. 259:5705-5710 (1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide."
RL J. Biol. Chem. 261:4008-4014 (1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X."
RL Biochemistry 29:8111-8118 (1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding."
RL Biochemistry 31:5974-5983 (1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunneharagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X."
RL J. Biol. Chem. 267:19642-19649 (1992).
RN [13]

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RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,  
 RA Trewheella J.;  
 RT "The relative orientation of Gla and EGF domains in coagulation  
 factor X is altered by Ca<sup>2+</sup> binding to the first EGF domain. A  
 RT combined NMR-small angle X-ray scattering study.";  
 RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -----  
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 CC -----  
 DR EMBL; X00673; CAA25286.1; -.  
 DR PIR; A00925; EXBO.  
 DR PDB; 1APO; 31-JAN-94.  
 DR PDB; 1CCF; 31-MAY-94.  
 DR PDB; 1MHE; 15-MAY-97.  
 DR PDB; 1MHF; 15-MAY-97.  
 DR MEROPS; S01.216; -.  
 DR GlycosultedB; P00743; -.  
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 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
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 DR InterPro; IPR000294; VitK\_dep\_GLA.  
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 DR Pfam; PF00584; gla; 1.  
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 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_1like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
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 DR PROSITE; PS00022; EGF\_1; 1.  
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 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KM Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT STGNL 1 23  
 FT PROPEP 24 40

| FT | CHAIN    | 41  | 180 | FACTOR X LIGHT CHAIN.                               |
|----|----------|-----|-----|---|
| FT | CHAIN    | 183 | 492 | FACTOR X HEAVY CHAIN.                               |
| FT | PROPEP   | 183 | 233 | ACTIVATION PEPTIDE.                                 |
| FT | CHAIN    | 234 | 492 | ACTIVATED FACTOR XA, HEAVY CHAIN.                   |
| FT | PROPEP   | 476 | 492 | MAY BE REMOVED BUT IS NOT NECESSARY FOR ACTIVATION. |
| FT | DOMAIN   | 86  | 122 | EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).            |
| FT | DOMAIN   | 125 | 165 | EGF-LIKE 2.   |
| FT | DOMAIN   | 224 | 492 | SERINE PROTEASE.                                    |
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| FT | ACT_SITE | 321 | 321 | CHARGE RELAY SYSTEM.                                |
| FT | ACT_SITE | 418 | 418 | CHARGE RELAY SYSTEM.                                |
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| FT | MOD_RES  | 47  | 47  | GAMMA-CARBOXYGLUTAMIC ACID.                         |
| FT | MOD_RES  | 54  | 54  | GAMMA-CARBOXYGLUTAMIC ACID.                         |
| FT | MOD_RES  | 56  | 56  | GAMMA-CARBOXYGLUTAMIC ACID.                         |
| FT | MOD_RES  | 59  | 59  | GAMMA-CARBOXYGLUTAMIC ACID.                         |
| FT | MOD_RES  | 60  | 60  | GAMMA-CARBOXYGLUTAMIC ACID.                         |
| FT | MOD_RES  | 65  | 65  | GAMMA-CARBOXYGLUTAMIC ACID.                         |
| FT | MOD_RES  | 66  | 66  | GAMMA-CARBOXYGLUTAMIC ACID.                         |

Query Match 48.4%; Score 92; DB 1; Length 492;  
 Best Local Similarity 38.6%; Pred. No. 66-09;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXLRGSLXRCXKXLCFFXAFXIFRNXXTRQFWWSY 44  
 DB 41 ANSFLFVKGNDRECELBACGLEBARFEDAEQTFDEWMSY 84

RESULT 14  
 FA9\_HUMAN STANDARD; PRT; 461 AA.  
 ID FA9\_HUMAN  
 AC P00740;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).  
 GN P9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 ON [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86000558; PubMed=2994716;  
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;  
 RT "Nucleotide sequence of the gene for human factor IX (antihemophilic  
 RT factor B).";  
 RL Biochemistry 24:3736-3750(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85190593; PubMed=3857619;  
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,  
 RA Graham J.B., Stafford D.W.;  
 RT "Evidence for a prevalent dimorphism in the activation peptide of  
 RT human coagulation factor IX.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84236100; PubMed=6329734;  
 RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,  
 RA Huddleston J.A., Brownlee G.G.;  
 RT "The gene structure of human anti-haemophilic factor IX.";  
 RL EMBO J. 3:1053-1060(1984).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83220788; PubMed=6687940;  
 RA Jave M., de la Salle H., Schamber F., Ballard A., Kohl V.,  
 RA Findel A., Tolstoshev P., Lecocq J.P.;  
 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a  
 RT unique 52-base synthetic oligonucleotide probe deduced from the amino  
 RT acid sequence of bovine factor IX.";

- RL Nucleic Acids Res. 11:2325-2335(1983).  
 RN [5]  
 RP SEQUENCE OF 36-326 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=84300526; PubMed=6089357;  
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;  
 RT "Isolation and characterization of human factor IX cDNA:  
 RT identification of Tag 1 polymorphism and regional assignment.";  
 RL Sonat. Cell Mol. Genet. 10:465-473(1984).  
 RN [6]  
 RP SEQUENCE OF 290-359 FROM N.A.  
 RX MEDLINE=88127096; PubMed=3340835;  
 RA Stofler E.S., Koebel D.D., Sarkar G., Sommer S.S.;  
 RT "Genomic amplification with transcript sequencing.";  
 RL Science 239:491-494(1988).  
 RN [7]  
 RP SEQUENCE OF 444-461 FROM N.A.  
 RX MEDLINE=94054330; PubMed=8236150;  
 RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,  
 RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;  
 RT "A deletion located in the 3' non translated part of the factor IX  
 RT gene responsible for mild haemophilia B.";  
 RL Thromb. Haemost. 70:370-371(1993).  
 RN [8]  
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).  
 RX MEDLINE=90078229; PubMed=2592373;  
 RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
 RA Ogata K., Kamaya T., Saito H., Niho Y., Iwanaga S.;  
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by  
 RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell  
 RT chymase.";  
 RL J. Biol. Chem. 264:21257-21265(1989).  
 RN [9]  
 RP HYDROXYLATION OF ASP-110.  
 RX MEDLINE=83308813; PubMed=6688526;  
 RA McMullen B.A., Fujikawa K., Kistiel W.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
 RT K-dependent blood coagulation zymogens.";  
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
 RN [10]  
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=78194509; PubMed=659613;  
 RA di Scipio R.G., Kurachi K., Davie E.W.;  
 RT "Activation of human factor IX (Christmas factor).";  
 RL J. Clin. Invest. 61:1528-1538(1978).  
 RN [11]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185715; PubMed=6425296;  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RT "Derivatives of blood coagulation factor IX contain a high affinity  
 RT Ca<sup>2+</sup>-binding site that lacks gamma-carboxyglutamic acid.";  
 RL J. Biol. Chem. 259:5698-5704(1984).  
 RN [12]  
 RP ERRATUM.  
 RX Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RL J. Biol. Chem. 260:2583-2583(1985).  
 RN [13]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE.  
 RX MEDLINE=86189947; PubMed=3009023;  
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
 RT "Defective propeptide processing of blood clotting factor IX caused  
 RT by mutation of arginine to glutamine at position -4.";  
 RL Cell 45:343-348(1986).  
 RN [14]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimomishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [15]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [16]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-107.  
 RX MEDLINE=92388094; PubMed=1517205;  
 RA Nishimura H., Takao T., Hase S., Shimomishi Y., Iwanaga S.;  
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
 RT serine 61 through the fucose residue.";  
 RL J. Biol. Chem. 267:17520-17525(1992).  
 RN [17]  
 RP PHOSPHORYLATION OF SER-114.  
 RA Harris R.J., Papac D.I., Triuong L., Smith K.J.;  
 RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";  
 RL (in) Abstracts of 11th international conference on methods in protein  
 RL structure analysis, pp.50-50, Annecy (1996).  
 RN [18]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=20575397; PubMed=1113752;  
 RA Arruda V.R., Hagstrom J.N., Deitch J., Heiman-Patterson T.,  
 RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
 RA Larson P.J., High K.A.;  
 RT "Posttranslational modifications of recombinant myotube-synthesized  
 RT human factor IX.";  
 RL Blood 97:130-138(2001).  
 RN [19]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=95229607; PubMed=7713897;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
 RT binding region of factor IX by two-dimensional NMR spectroscopy.";  
 RL J. Biol. Chem. 270:7980-7987(1995).  
 RN [20]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96032604; PubMed=7547952;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
 RT domain of factor IX.";  
 RL Biochemistry 34:12126-12137(1995).  
 RN [21]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96279169; PubMed=8663165;  
 RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
 RA Furie B.;  
 RT "Identification of the phospholipid binding site in the vitamin K-  
 RT dependent blood coagulation protein factor IX.";  
 RL J. Biol. Chem. 271:16227-16236(1996).  
 RN [22]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=97199336; PubMed=9047312;  
 RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,  
 RA Smith H., Hickey R.G., Pedersen L.G.;  
 RT "Refinement of the NMR solution structure of the  
 RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
 RT molecular dynamics simulation with initial Ca<sup>2+</sup> positions determined  
 RT by a genetic algorithm.";  
 RL Biochemistry 36:2132-2138(1997).  
 RN [23]  
 RP STRUCTURE BY NMR OF 91-133.  
 RX MEDLINE=91308127; PubMed=1854745;  
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;  
 RT "Sequence-specific 1H NMR assignments, secondary structure, and  
 RT location of the calcium binding site in the first epidermal growth  
 RT factor like domain of blood coagulation factor IX.";  
 RL Biochemistry 30:7402-7409(1991).  
 RN [24]  
 RP STRUCTURE BY NMR OF 92-130.  
 RX MEDLINE=93284090; PubMed=1304885;  
 RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,

RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;  
 RT "The three-dimensional structure of the first EGF-like module of  
 RL human factor IX: comparison with EGF and TGF-alpha.";   
 RN Protein Sci. 1:81-90(1992).  
 RN (25)  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
 RX MEDLINE=95330802; PubMed=7606779;  
 RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;  
 RT "The structure of a Ca(2+)-binding epidermal growth factor-like  
 RL domain: its role in protein-protein interactions.";   
 RN Cell 82:131-141(1995).  
 RN (26)  
 RP MOLECULAR PATHOLOGY OF HEMOPHILIA B.  
 QY Query Match 47.4%; Score 90; DB 1; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 1.3e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 DB 49 SGLLEFVQGNLERECMEKCSFEAREVENTERTTEFWKQY 91  
 2 NGFLXXLRQSLKRCXKXLCSPFXAPXIPRNXXRTQFWVSY 44  
 RESULT 15  
 PRTC HUMAN STANDARD; PRT; 461 AA.  
 ID P04070; Q16001; Q15190; Q15189;  
 AC P04070; Q16001; Q15190; Q15189;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoprothombin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 DE PROC.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85270390; PubMed=2991887;  
 RA Foster D.C., Yoshitake S., Davie E.W.;  
 RT "The nucleotide sequence of the gene for human protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85269639; PubMed=2991859;  
 RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,  
 RL Long G.L.;  
 RT "The structure and evolution of a 461 amino acid human protein C  
 RT precursor and its messenger RNA, based upon the DNA sequence of  
 RL cloned human liver cDNAs.";   
 RN Nucleic Acids Res. 13:5233-5247(1985).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86120978; PubMed=3511471;  
 RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;  
 RT "Evolution and organization of the human protein C gene";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Pool C.L., Yi Q.,  
 RL Nickerson D.A.;  
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN (5)  
 RP SEQUENCE OF 106-461 FROM N.A.  
 RX MEDLINE=84272714; PubMed=6589623;  
 RA Foster D.C., Davie E.W.;  
 RT "Characterization of a cDNA coding for human protein C.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).  
 RN (6)  
 RP CARBOHYDRATE-LINKAGE SITE ASN-371.  
 RX MEDLINE=90293094; PubMed=1694179;

RA Miletich J.P., Broze G.J., Jr.;  
 RT "Beta protein C is not glycosylated at asparagine 329. The rate of  
 RT translation may influence the frequency of usage at asparagine-X-  
 RT cysteine sites.";   
 RL J. Biol. Chem. 265:11397-11404(1990).  
 RN (7)  
 RP HYDROXYLATION.  
 RX MEDLINE=92184750; PubMed=1544894;  
 RA Harris R.J., Ling V.T., Spellman M.W.;  
 RT "O-linked fucose is present in the first epidermal growth factor  
 RT domain of factor XII but not protein C";   
 RL J. Biol. Chem. 267:5102-5107(1992).  
 RN (8)  
 RP 3D-STRUCTURE MODELING OF 175-450.  
 RX MEDLINE=94272342; PubMed=8003977;  
 RA Fisher C.L., Greenberg J.S., Griffin J.H.;  
 RT "Models of the serine protease domain of the human antithrombotic  
 RT plasma factor activated protein C and its zymogen.";   
 RL Protein Sci. 3:588-599(1994).  
 RN (9)  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.  
 RX MEDLINE=97157472; PubMed=9003757;  
 RA Mather T., Oganeseyan V., Hof P., Huber R., Foundling S., Esmen C.,  
 RA Bode W.;  
 RT "The 2.8 A crystal structure of Gla-domainless activated protein C";  
 RL EMBO J. 15:6822-6831(1996).  
 RN (10)  
 RP REVIEW ON PROC VARIANTS.  
 RX MEDLINE=93190290; PubMed=8446940;  
 RA Reltama P.H., Poort S.R., Bernardi F., Gandille S., Long G.L.,  
 RA Sala N., Cooper D.N.;  
 RT "Protein C deficiency: a database of mutations. For the Protein C & S  
 RT Subcommittee of the Scientific and Standardization Committee of the  
 RT International Society on Thrombosis and Haemostasis";   
 RL Thromb. Haemost. 69:77-84(1993).  
 RN (11)  
 RP VARIANT CYS-444.  
 RX MEDLINE=87204221; PubMed=2437584;  
 RA Romeo G., Hassan H.U., Straampfl S., Roncuzzi L., Cianetti L.,  
 RA Leonard A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,  
 RA Cortese R.;  
 RT "Hereditary thrombophilia: identification of nonsense and missense  
 RT mutations in the protein C gene";   
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).  
 RN (12)  
 RP VARIANT TRP-211 (LONDON-1).  
 RX MEDLINE=90098906; PubMed=2602169;  
 RA Grundy C.B., Chitollie A., Talbot S., Bevan D., Kakkar V.V.,  
 RA Cooper D.N.;  
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG->TGG) in  
 RT the protein C gene causing thrombosis";   
 RL Nucleic Acids Res. 17:10513-10513(1989).  
 RN (13)  
 RP VARIANT CYS-272.  
 RX MEDLINE=91329836; PubMed=1868249;  
 RA Reltama P.H., Poort S.R., Allaart C.F., Brier E., Bertina R.M.;  
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with  
 RT symptomatic protein C deficiency type I: heterogeneity and founder  
 RT effects.";   
 RL Blood 78:890-894(1991).  
 RN (14)  
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.  
 RX MEDLINE=92190481; PubMed=13447706;  
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,  
 RA Rainville I.R., Long G.L.;  
 RT "Protein C Vermont: symptomatic type II protein C deficiency  
 RT associated with two Gla domain mutations.";   
 RL Blood 79:1456-1465(1992).  
 RN (15)  
 RP VARIANT ASP-418 (HONG KONG-2).  
 RX MEDLINE=92305321; PubMed=1611081;  
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;  
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C



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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(without alignments)  
196.288 Million cell updates/sec

Title: 10Gln28PHE\_4  
Perfect score: 190  
Sequence: 1 ANGFLXLRQGSGLKRXCRX.....XXAFXIFRNXXRTQFWVS 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 120   | 63.2        | 701    | 4 Q96PQ8  | Q96PQ8 homo sapien |
| 2          | 104   | 54.7        | 460    | 11 Q91WN8 | Q91WN8 mus musculu |
| 3          | 103   | 54.2        | 446    | 11 Q61109 | Q61109 mus musculu |
| 4          | 98    | 51.6        | 460    | 11 Q99PC6 | Q99PC6 mus musculu |
| 5          | 96    | 50.5        | 456    | 6 Q9TTR0  | Q9TTR0 canis famli |
| 6          | 93    | 48.9        | 482    | 11 Q63207 | Q63207 rattus norv |
| 7          | 90    | 47.4        | 456    | 4 Q14316  | Q14316 homo sapien |
| 8          | 90    | 47.4        | 461    | 6 Q95ND7  | Q95ND7 pan troglod |
| 9          | 90    | 47.4        | 461    | 6 Q95ND6  | Q95ND6 pan troglod |
| 10         | 90    | 47.4        | 481    | 11 Q54740 | Q54740 mus musculu |
| 11         | 90    | 47.4        | 481    | 11 Q99L32 | Q99L32 mus musculu |
| 12         | 90    | 47.4        | 481    | 11 Q88947 | Q88947 mus musculu |
| 13         | 87    | 45.8        | 100    | 4 Q15253  | Q15253 homo sapien |
| 14         | 87    | 45.8        | 608    | 13 Q9PTW7 | Q9PTW7 struthio ca |
| 15         | 86    | 45.3        | 49     | 6 Q95WE8  | Q95WE8 bos taurus  |
| 16         | 86    | 45.3        | 469    | 6 Q9GMD9  | Q9GMD9 orithorhyn  |

|    |      |      |     |           |                     |
|----|------|------|-----|-----------|---------------------|
| 17 | 79   | 41.6 | 138 | 6 Q28994  | Q28994 sus scrofa   |
| 18 | 77   | 40.5 | 433 | 13 Q90YK1 | Q90YK1 brachydanio  |
| 19 | 77   | 40.5 | 648 | 6 Q29094  | Q29094 sus scrofa   |
| 20 | 76   | 40.0 | 399 | 11 Q9COW3 | Q9COW3 mus musculu  |
| 21 | 75   | 39.5 | 607 | 13 Q91001 | Q91001 gallus gall  |
| 22 | 73.5 | 38.7 | 542 | 5 Q8T613  | Q8T613 halocynthia  |
| 23 | 72   | 37.9 | 650 | 4 Q9NSD0  | Q9NSD0 homo sapien  |
| 24 | 72   | 37.9 | 650 | 4 Q16519  | Q16519 homo sapien  |
| 25 | 68   | 35.8 | 179 | 4 Q8TAS3  | Q8TAS3 homo sapien  |
| 26 | 68   | 35.8 | 198 | 11 Q8R182 | Q8R182 mus musculu  |
| 27 | 61   | 32.1 | 678 | 4 Q14393  | Q14393 homo sapien  |
| 28 | 60   | 31.6 | 673 | 11 Q61592 | Q61592 mus musculu  |
| 29 | 60   | 31.6 | 674 | 11 Q99K57 | Q99K57 mus musculu  |
| 30 | 58   | 30.5 | 25  | 11 Q9QVH6 | Q9QVH6 rattus sp.   |
| 31 | 58   | 30.5 | 674 | 11 Q93772 | Q93772 rattus sp.   |
| 32 | 54   | 28.4 | 98  | 13 P82807 | P82807 notechis sc  |
| 33 | 51   | 26.8 | 130 | 12 Q9DUB8 | Q9DUB8 ct vtrus. o  |
| 34 | 50   | 26.3 | 184 | 10 Q9LVF1 | Q9LVF1 arabidopsis  |
| 35 | 47.5 | 25.0 | 575 | 10 Q94E17 | Q94E17 oryza sativ  |
| 36 | 47.5 | 25.0 | 608 | 10 Q9XE36 | Q9XE36 medicago sa  |
| 37 | 47   | 24.7 | 174 | 2 Q93FY1  | Q93FY1 bruceella ab |
| 38 | 46.5 | 24.5 | 196 | 10 Q04284 | Q04284 selaginella  |
| 39 | 46.5 | 24.5 | 567 | 10 Q8W432 | Q8W432 arabidopsis  |
| 40 | 46.5 | 24.5 | 603 | 10 Q9LP67 | Q9LP67 arabidopsis  |
| 41 | 46.5 | 24.5 | 606 | 10 Q9SUG9 | Q9SUG9 arabidopsis  |
| 42 | 46.5 | 24.5 | 651 | 10 Q8S218 | Q8S218 oryza sativ  |
| 43 | 46   | 24.2 | 249 | 5 Q9VYS0  | Q9VYS0 drosophila   |
| 44 | 45.5 | 23.9 | 431 | 10 Q94EY5 | Q94EY5 arabidopsis  |
| 45 | 45.5 | 23.9 | 492 | 10 Q9SM07 | Q9SM07 cicer ariet  |

## ALIGNMENTS

|          |  |   |              |      |         |
|----------|--|---|--------------|------|---------|
| RESULT 1 | ID   | SEQUENCE FROM N.A.                                | PRELIMINARY; | PRT; | 701 AA. |
| Q96PQ8   | Q96PQ8   | 01-DEC-2001 (TREMBLrel. 19, Created)              |              |      |         |
| AC       | Q96PQ8   | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) |              |      |         |
| DT       | 01-DEC-2001 (TREMBLrel. 19, Last sequence update)                      |   |              |      |         |
| DT       | 01-MAR-2002 (TREMBLrel. 20, Last annotation update)                    |   |              |      |         |
| DE       | Factor VII active site mutant immunoglobulin.                          |   |              |      |         |
| OS       | Homo sapiens (Human).  |   |              |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |   |              |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.              |   |              |      |         |
| OX       | NCBI_TaxID=9606;   |   |              |      |         |
| RN       | [1]  |   |              |      |         |
| RP       | SEQUENCE FROM N.A.   |   |              |      |         |
| RX       | MEDLINE=21477448; PubMed=11593034;                                     |   |              |      |         |
| RA       | Hu Z., Garen A.;   |   |              |      |         |
| RT       | "Targeting tissue factor on tumor vascular endothelial cells and tumor |   |              |      |         |
| RT       | cells for immunotherapy in mouse models of prostatic cancer.";         |   |              |      |         |
| RT       | Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).                    |   |              |      |         |
| DR       | EMBL; AF272774; AAKS686.1; -.  |   |              |      |         |
| DR       | InterPro; IPR000152; Asx hydroxyl.                                     |   |              |      |         |
| DR       | InterPro; IPR000561; EGF-like.   |   |              |      |         |
| DR       | InterPro; IPR000742; EGF-2.  |   |              |      |         |
| DR       | InterPro; IPR001881; EGF-Ca.   |   |              |      |         |
| DR       | InterPro; IPR003006; IG_MHC.   |   |              |      |         |
| DR       | InterPro; IPR001254; Ser protease_Try.                                 |   |              |      |         |
| DR       | InterPro; IPR000294; VltK_dep_GLA.                                     |   |              |      |         |
| DR       | Pfam; PF00008; EGF; 2.   |   |              |      |         |
| DR       | Pfam; PF00594; gla; 1.   |   |              |      |         |
| DR       | Pfam; PF00047; ig; 2.  |   |              |      |         |
| DR       | Pfam; PF00089; trypsin; 1.   |   |              |      |         |
| DR       | SMART; SMO0181; EGF; 2.  |   |              |      |         |
| DR       | PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.                             |   |              |      |         |
| DR       | PROSITE; PS01186; EGF_2; UNKNOWN_1.                                    |   |              |      |         |
| DR       | PROSITE; PS01187; EGF_CA; UNKNOWN_1.                                   |   |              |      |         |
| DR       | PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.                        |   |              |      |         |
| DR       | PROSITE; PS00290; IG_MHC; UNKNOWN_1.                                   |   |              |      |         |
| DR       | PROSITE; PS00240; TRYPSIN_DOM; 1.                                      |   |              |      |         |

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CBB42CC92F CRC64;

Query Match 63.2%; Score 120; DB 4; Length 701;  
 Best Local Similarity 52.3%; Pred. No. 1.7e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQGLRXKCRXXLCSPFXAFXIFRNXXRTROGFWSY 44  
 Db 61 ANAFLEELRPGSLERCKEBCQCSFEAREIFKDAERTKLFWISY 104

## RESULT 2

Q91WN8 PRELIMINARY; PRT; 460 AA.  
 ID Q91WN8;  
 AC Q91WN8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Similar to protein C.  
 GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCB1\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013896; AAH13896.1; -.  
 DR MGD; MGI:97771; Proc.  
 DR InterPro; IPR00152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
 DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FC274 CRC64;

Query Match 54.7%; Score 104; DB 11; Length 460;  
 Best Local Similarity 45.5%; Pred. No. 1e-10;

Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQGLRXKCRXXLCSPFXAFXIFRNXXRTROGFWSY 44  
 Db 42 ANSFLLEMRPGSLERCKMEICDFEEAQEIFQVEDTLAWIKY 85

## RESULT 3

Q61109 PRELIMINARY; PRT; 446 AA.  
 ID Q61109;  
 AC Q61109;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Coagulation factor VII.  
 GN F7 OR FVII.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCB1\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=96276538; PubMed=8701412;  
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";

CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 TRYPSIN FAMILY.  
 DR EMBL; U44795; AAC52570.1; -.  
 DR HSSP; P08709; 1PAK.

DR MEROPS; S01.215; -.  
 DR MGD; MGI:109325; F7.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001064; Crystallin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_1like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TYP\_Spc; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAAMMA; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;  
 KW Serine protease.  
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 54.2%; Score 103; DB 11; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 1.5e-10;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQGLRXKCRXXLCSPFXAFXIFRNXXRTROGFWSY 44  
 Db 42 ANSLLELWPGSLERCKNEBCQCSFEAREIFKSPERTKQFVIVY 85

## RESULT 4

Q99PC6 PRELIMINARY; PRT; 460 AA.  
 ID Q99PC6;  
 AC Q99PC6;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Anticoagulant protein C.  
 GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCB1\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/  
 RA Korf I.;

"Complete sequence of UC72A01.";  
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY  
 DR EMBL; AF318182; AAK07918.1; --  
 DR HSSP; P04070; 1PCU.  
 DR MEROPS; S01.218; --  
 DR MGD; MGI:97771; Proc.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00001; EGF\_1like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRY\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KW Hydroxylation; Repeat; Serine protease.  
 SQ SEQUENCE 460 AA; 51784 MW; 0293BC2589D3ED16 CRC64;  
 Query Match 51.6%; Score 98; DB 11; Length 460;  
 Best Local Similarity 43.2%; Pred. No. 1.3e-09;  
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRQGSILKRXCRXXLCSFYXAFIRNXXRTQGFVWSY 44  
 Db 42 ANSFLEMRPQSLERECEMEICDLEAQEIFQNVEDTLAFWIKY 85  
 RESULT 5  
 Q9TTR0 PRELIMINARY; PRT; 456 AA.  
 AC Q9TTR0;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Protein C precursor.  
 GN PROC.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Leeb T., Kopp T., Deppe A., Breen M., Matlis U., Brunberg L.,  
 RA Brenig B.;  
 RT "Molecular characterization and chromosomal assignment of the canine  
 RT protein C gene."  
 RL Mamm. Genome 10:135-139(1999).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99371952; PubMed=10443005;  
 RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;  
 RT "Analysis of canine protein C gene polymorphisms."  
 RL Anim. Genet. 30:237-238(1999).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.

DR EMBL; AJ001979; CAA05126.1; --  
 DR HSSP; P04070; 1PCU.  
 DR MEROPS; S01.218; --  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00001; EGF\_1like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRY\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KW Hydroxylation; Repeat; Serine protease; Signal.  
 FT SIGNAL 1  
 FT CHAIN 43  
 FT CHAIN 193  
 FT CHAIN 195  
 FT CHAIN 456  
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C3459FF CRC64;  
 Query Match 50.5%; Score 96; DB 6; Length 456;  
 Best Local Similarity 43.2%; Pred. No. 3.1e-09;  
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRQGSILKRXCRXXLCSFYXAFIRNXXRTQGFVWSY 44  
 Db 43 ANSFLEIRAGSLERECEMEICDFEAKEIFQNVDDTLAWISKY 86  
 RESULT 6  
 O63207 PRELIMINARY; PRT; 482 AA.  
 AC O63207;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Factor X.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=96093366; PubMed=8578539;  
 RA Stanton C., Ross R.P., Hutson S., Wallin R.;  
 RT "Evidence for competition between vitamin K-dependent clotting factors  
 RT for intracellular processing by the vitamin K-dependent gamma-  
 RT carboxylase."  
 RL Thromb. Res. 80:63-73(1995).  
 RL [2]  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 CC EMBL; X79807; CAA56202.1; --  
 DR HSSP; P00742; 1XKA.  
 DR MEROPS; S01.216; --  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00001; EGF\_1like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRY\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KW Hydroxylation; Repeat; Serine protease; Signal.  
 FT SIGNAL 1  
 FT CHAIN 43  
 FT CHAIN 193  
 FT CHAIN 195  
 FT CHAIN 456  
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C3459FF CRC64;

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DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.9%; Score 93; DB 11; Length 482;
Best Local Similarity 36.4%; Pred. No. 1.2e-08;
Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXRCRXKXLCSPFXAFIFRNXXRTRQFWVS 44
Db 41 ANSFEEIKKGNLRECEVEICSFEEAREVFEDNEKTEFTWNNY 84

RESULT 7
ID 014316 PRELIMINARY; PRT; 456 AA.
AC 014316;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-1999 (TrEMBLrel. 11, Last sequence update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas
disease HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=88327116; PubMed=3416069;
RA Reicema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
Brice E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AL033403; CAA21954.1; -.
DR EMBL: X55008; CAB38245.2; -.
DR HSSP: P00740; ICFH.
DR MEROPS: S01.214; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001438; EGF_1I.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
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DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 47.4%; Score 90; DB 4; Length 456;
Best Local Similarity 41.9%; Pred. No. 3.9e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXXLRGSLRXRCRXKXLCSPFXAFIFRNXXRTRQFWVS 44
Db 44 SGLLEEFVQGNLERCEMEKCSFEAREVFENTERITTEFTWKQY 86

RESULT 8
ID 095ND7 PRELIMINARY; PRT; 461 AA.
AC 095ND7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=504;
RC Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Gene Genet. Syst. 0:0-0(2001).
DR EMBL: AB062470; BAB58885.1; -.
DR EMBL: AB062458; BAB58885.1; JOINED.
DR EMBL: AB062460; BAB58885.1; JOINED.
DR EMBL: AB062462; BAB58885.1; JOINED.
DR EMBL: AB062464; BAB58885.1; JOINED.
DR EMBL: AB062466; BAB58885.1; JOINED.
DR EMBL: AB062468; BAB58885.1; JOINED.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; gla; 1.
DR Pfam: PF00594; gla; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_2.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
```

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SO SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 47.4%; Score 90; DB 6; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 4e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NGFLXXLRQGLXRXCRXXLCSPFXAFIFRNXXRTROPFWVSY 44  
 Db 49 SGKLEFPVQGNLERECMEKCSFEERAREVFENTERTEFWKQY 91

## RESULT 9

O95ND6 PRELIMINARY; PRT; 461 AA.

AC O95ND6; 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Coagulation factor XI.  
 GN F9.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=505;  
 RA Sacta Y.;

RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees";  
 RL Genes Genet. Syst. 0:0-0(2001).

DR EMBL; AB062471; BAB58886.1; -.  
 DR EMBL; AB062459; BAB58886.1; JOINED.  
 DR EMBL; AB062461; BAB58886.1; JOINED.  
 DR EMBL; AB062463; BAB58886.1; JOINED.  
 DR EMBL; AB062465; BAB58886.1; JOINED.  
 DR EMBL; AB062467; BAB58886.1; JOINED.  
 DR EMBL; AB062469; BAB58886.1; JOINED.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF\_1like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00094; Gla; 2.  
 DR Pfam; PF00089; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
 DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
 KW Hydrolyase; Serine protease.  
 SO SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 47.4%; Score 90; DB 6; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 4e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NGFLXXLRQGLXRXCRXXLCSPFXAFIFRNXXRTROPFWVSY 44  
 Db 49 SGKLEFPVQGNLERECMEKCSFEERAREVFENTERTEFWKQY 91

RESULT 10  
 O54740 PRELIMINARY; PRT; 481 AA.

AC O54740;  
 DT 01-JUN-1998 (TRENBLrel. 06, Created)  
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6).

GN F10 OR F10.  
 OS Mus musculus (Mouse).  
 OC Plasmid pluscript.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;  
 RX MEDLINE=98454993; PubMed=9783672;  
 RA Heidtmann H.H., Kontermann R.E.;  
 RT Thromb. Res. 92:33-41(1998).  
 RL "Cloning and recombinant expression of mouse coagulation factor X";  
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL; AJ222677; CAA10933.1; -.  
 DR HSSP; P00742; IYKA.  
 DR MEROPS; S01.216; -.  
 DR MGD; MGI:103107; F10.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF\_1like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00094; Gla; 2.  
 DR Pfam; PF00089; Gla; 1.

DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_1like; 1.  
 DR SMART; SM00059; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Plasmid;  
 KW Repeat; Serine protease; Signal.  
 FT SIGNAL 1 40 POTENTIAL.  
 FT CHAIN 1 481 COAGULATION FACTOR X.  
 SO SEQUENCE 481 AA; 53986 MW; CF702DE5BF9D97AE CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;  
 Best Local Similarity 31.8%; Pred. No. 4.1e-08;  
 Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRQGLXRXCRXXLCSPFXAFIFRNXXRTROPFWVSY 44  
 Db 41 ANSFEEBKGNLERECMEKCSFEERAREVFEDDEKTEWYTKY 84

## RESULT 11

O99L32 PRELIMINARY; PRT; 481 AA.

AC O99L32;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Coagulation factor X.  
 GN F10.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strubeberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AAH03877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ
SEQUENCE 481 AA; 54004 MW; BD88B96C8A0B7E7F CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 4,1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXKRCRXKLCGFXXAFXIFRNXXRTROFWVS 44
Db 41 ANSFFEEFKGNLERECMEICSYEEVREIFEDDEKTEKWTXY 84

RESULT 12
088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
DE F10.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; Pubmed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
Castellino F.J., Rosen E.D.;

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RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129Sj;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC6345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ
SEQUENCE 481 AA; 54018 MW; 8AC09D5E9D271E CRC64;

Query Match 47.4%; Score 90; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 4,1e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLXKRCRXKLCGFXXAFXIFRNXXRTROFWVS 44
Db 41 ANSFFEEFKGNLERECMEICSYEEVREIFEDDEKTEKWTXY 84

RESULT 13
015253 PRELIMINARY; PRT; 100 AA.
AC 015253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
DE F2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; Pubmed=3471151;
RA McGallivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;

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RT "Recombinant genetic approaches to functional mapping of thrombin."  
RL Ann. N. Y. Acad. Sci. 485:73-79 (1986).  
DR EMBL; M33011; AAA60220.1; -  
DR HSSP; P00735; 2PPI.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00069; GLA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
KM Signal.  
FT SIGNAL 1 43 POTENTIAL.  
FT CHAIN 44 >100 POTENTIAL.  
FT NON\_TER 100 100  
SQ SEQUENCE 100 AA; 11302 MW; FDESD0174E1F6FE CRC64;  
Query Match 45.8%; Score 87; DB 4; Length 100;  
Best Local Similarity 38.6%; Pred. No. 3.4e-08;  
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;  
QY 1 ANGFLXXLRQGSILRXCRXXLCSPXXAFXIFRNXXRTROPWVS 44  
Db 44 ANTFLEEVKGNLRRECKVEETCYEEAFALSSSTATDVFWMY 87  
RESULT 14  
O9PTW7 PRELIMINARY; PRT; 608 AA.  
AC O9PTW7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Prothrombin.  
GN OSPT.  
OS Struthio camelus (Ostrich).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;  
OC Struthio.  
OX NCBI\_TaxId=6801;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20579470; PubMed=1137455;  
RA Frost C., Naudé R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;  
RT "Purification and characterization of ostrich prothrombin.";  
RL Int. J. Biochem. Cell Biol. 32:1151-1159 (2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
CC EMBL; AB028871; BAA89046.1; -  
DR HSSP; P00734; 1UUS.  
DR MEROPS; S01.217; -  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000001; Kingle.  
DR InterPro; IPR001254; Ser protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00051; kingle; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR PRINTS; PR00018; KRINGLE.  
DR PRODOM; PD000395; Kingle; 2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00130; KR; 2.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 2.  
DR PROSITE; PS00070; KRINGLE\_2; 2.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.

SQ SEQUENCE 608 AA; 69392 MW; 11B974B9AE54EA2 CRC64;  
Query Match 45.8%; Score 87; DB 13; Length 608;  
Best Local Similarity 35.7%; Pred. No. 1.8e-07;  
Matches 15; Conservative 7; Mismatches 20; Indels 0; Gaps 0;  
QY 3 GFLXXLRQGSILRXCRXXLCSPXXAFXIFRNXXRTROPWVS 44  
Db 47 GFLXEMLKGNLRRECKVEETCYEEAFALSSSTATDVFWMY 88  
RESULT 15  
O9SME8 PRELIMINARY; PRT; 49 AA.  
AC O9SME8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Coagulation factor IX (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxId=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mizlata M.N., Amaral E.J.;  
RT "Partial sequence of bovine F9 coding gene.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF394598; AAK77556.1; -  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
FT NON\_TER 1 49  
FT NON\_TER 49 49  
SQ SEQUENCE 49 AA; 6023 MW; D1SC6DE9CCBA4A14 CRC64;  
Query Match 45.3%; Score 86; DB 6; Length 49;  
Best Local Similarity 37.2%; Pred. No. 2.6e-08;  
Matches 16; Conservative 7; Mismatches 20; Indels 0; Gaps 0;  
QY 2 NGFLXXLRQGSILRXCRXXLCSPXXAFXIFRNXXRTROPWVS 44  
Db 6 SGKLEFVAVGNLRRECKVEETCYEEAFALSSSTATDVFWMY 48

Search completed: March 19, 2003, 15:13:40  
Job time : 48.3125 secs

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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using bw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10Gln28PHE\_4  
Perfect score: 190  
Sequence: 1 ANGFLXLRPGSLKRXCRX.....XXAFXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
|------------|-------|-------------|--------|----|------------------|
| 1          | 155   | 81.6        | 44     | 3  | US-08-955-636-4  |
| 2          | 129   | 67.9        | 44     | 3  | US-08-955-636-28 |
| 3          | 124   | 65.3        | 44     | 3  | US-08-955-636-30 |
| 4          | 123   | 64.7        | 44     | 3  | US-08-955-636-26 |
| 5          | 121   | 63.7        | 44     | 3  | US-08-955-636-27 |
| 6          | 120   | 63.2        | 44     | 3  | US-08-955-636-3  |
| 7          | 120   | 63.2        | 406    | 1  | US-08-293-778-24 |
| 8          | 120   | 63.2        | 406    | 1  | US-08-295-411-5  |
| 9          | 120   | 63.2        | 406    | 2  | US-08-955-471-5  |
| 10         | 120   | 63.2        | 406    | 5  | PCT-US92-10242-5 |
| 11         | 120   | 63.2        | 444    | 1  | US-08-475-845-2  |
| 12         | 120   | 63.2        | 444    | 2  | US-08-327-690-2  |
| 13         | 120   | 63.2        | 444    | 2  | US-08-660-289-2  |
| 14         | 120   | 63.2        | 444    | 2  | US-08-537-807-2  |
| 15         | 120   | 63.2        | 444    | 2  | US-08-871-003-2  |
| 16         | 120   | 63.2        | 444    | 3  | US-08-464-233-2  |
| 17         | 120   | 63.2        | 444    | 4  | US-08-189-607-2  |
| 18         | 120   | 63.2        | 444    | 4  | US-09-378-907-2  |
| 19         | 120   | 63.2        | 444    | 5  | PCT-US94-05779-2 |
| 20         | 120   | 63.2        | 466    | 1  | US-07-882-202A-4 |
| 21         | 120   | 63.2        | 466    | 1  | US-08-021-615A-4 |
| 22         | 120   | 63.2        | 466    | 1  | US-08-321-777-4  |
| 23         | 120   | 63.2        | 466    | 4  | US-09-009-217-14 |
| 24         | 120   | 63.2        | 466    | 4  | US-09-009-656-14 |
| 25         | 120   | 63.2        | 466    | 5  | PCT-US93-04493-4 |
| 26         | 116   | 61.1        | 44     | 3  | US-08-955-636-29 |
| 27         | 106   | 55.8        | 41     | 1  | US-08-229-280-4  |

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|----|----|------|-----|---|------------------|--------------------|
| 28 | 98 | 51.6 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appli  |
| 29 | 98 | 51.6 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appli  |
| 30 | 98 | 51.6 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appli  |
| 31 | 98 | 51.6 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appli  |
| 32 | 98 | 51.6 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appli  |
| 33 | 98 | 51.6 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appli  |
| 34 | 98 | 51.6 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appli  |
| 35 | 95 | 50.0 | 44  | 3 | US-08-955-636-23 | Sequence 23, Appli |
| 36 | 95 | 50.0 | 45  | 3 | US-08-955-636-33 | Sequence 33, Appli |
| 37 | 94 | 49.5 | 44  | 3 | US-08-955-636-2  | Sequence 2, Appli  |
| 38 | 94 | 49.5 | 44  | 3 | US-08-955-636-24 | Sequence 24, Appli |
| 39 | 93 | 48.9 | 448 | 1 | US-08-295-411-3  | Sequence 3, Appli  |
| 40 | 93 | 48.9 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appli  |
| 41 | 93 | 48.9 | 448 | 5 | PCT-US92-10068-1 | Sequence 1, Appli  |
| 42 | 93 | 48.9 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appli  |
| 43 | 92 | 48.4 | 44  | 3 | US-08-955-636-25 | Sequence 25, Appli |
| 44 | 92 | 48.4 | 487 | 1 | US-08-469-468-53 | Sequence 53, Appli |
| 45 | 92 | 48.4 | 487 | 2 | US-08-469-658-53 | Sequence 53, Appli |

## ALIGNMENTS

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RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      81.6%; Score 155; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 2.9e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANGFLXLRPGSLKRXCRXLCFFXXAFXIFRNXXRTQFWVSY 44
DB 1 ANGFLXLRPGSLKRXCRXLCFFXXAFXIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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Best Local Similarity  /5.0%;  Pred. NO. 1.1e-14;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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US-V8-255-118-24  
; Sequence 24, Appli  
; Patent No. 5590560

GENERAL INFORMATION:  
APPLICANT: Nicolaesen, Else M.  
APPLICANT: Bjorn, Soren E.  
APPLICANT: Wiberg, Finn C.  
APPLICANT: Woodbury, Richard  
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.  
STREET: 405 Lexington Avenue, 62nd floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,778  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,509  
FILING DATE:  
APPLICATION NUMBER: DK 3235/87  
FILING DATE: 25-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/434,149  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129,224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 63.2%; Score 120; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No.3.8e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILKRXCRXKLCSPFXAXIFRNXXRTQFWVSY 44  
Db 1 ANAFLYLRPGSLVRYRCYKQCSFYARYIFMDAVRTKLFWISY 44

RESULT 8  
US-08-295-411-5  
Sequence 5, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Meesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5679639ch Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI263,0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-295-411-5

Query Match 63.2%; Score 120; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No.3.8e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILKRXCRXKLCSPFXAXIFRNXXRTQFWVSY 44  
Db 1 ANAFLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 9  
US-08-955-471-5  
Sequence 5, Application US/08955471  
Patent No. 5968751  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Meesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,471  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/295,411  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSH1263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-955-471-5

Query Match 63.2%; Score 120; DB 2; Length 406;  
Best Local Similarity 52.3%; Pred. No. 3.8e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLRXRCRXLCSPFXAFLFRNXXTRQFWWSY 44  
DB 1 ANAFLELRPGSLERCKEQCSFEERARLFKDAERTKLFWISY 44

RESULT 10  
PCT-US92-10242-5  
Sequence 5, Application PC/TUS9210242  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: For Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10666 North Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR0472P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
PCT-US92-10242-5

Query Match 63.2%; Score 120; DB 5; Length 406;  
Best Local Similarity 52.3%; Pred. No. 3.8e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRGSLRXRCRXLCSPFXAFLFRNXXTRQFWWSY 44  
DB 1 ANAFLELRPGSLERCKEQCSFEERARLFKDAERTKLFWISY 44

RESULT 11  
US-08-475-845-2  
Sequence 2, Application US/08475845  
Patent No. 5788965  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,845  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,690  
FILING DATE: 24-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725

;; FILING DATE: 21-MAY-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/662,920  
;; FILING DATE: 28-FEB-1991  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 13952-8-4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 206-467-9600  
;; TELEFAX: 415-543-5043  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 444 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-475-845-2

Query Match 63.2%; Score 120; DB 1; Length 444;  
Best Local Similarity 52.3%; Pred. No. 4.2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLROGSLXRCXRLCSFXXAFXIFRNXXRTROFWVS 44  
DB 39 ANAFLELRPGSLERECKEQCSFEAREIFPDARTKLFWISY 82

RESULT 12  
US-08-327-690-2  
; Sequence 2, Application US/08327690  
; Patent No. 5817788  
; GENERAL INFORMATION:  
; APPLICANT: Berkner, Kathleen L.  
; APPLICANT: Petersen, Lars C.  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Hedner, Ulla  
; APPLICANT: Bregengaard, Claus  
; TITLE OF INVENTION: Modified Factor VII  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Hourie and Crew  
; STREET: One Market Plaza, Stuart Street Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/327,690  
; FILING DATE: 24-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/065,725  
; FILING DATE: 21-MAY-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/662,920  
; FILING DATE: 28-FEB-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 13952-8-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-467-9600  
; TELEFAX: 415-543-5043

;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 444 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-327-690-2

Query Match 63.2%; Score 120; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 4.2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLROGSLXRCXRLCSFXXAFXIFRNXXRTROFWVS 44  
DB 39 ANAFLELRPGSLERECKEQCSFEAREIFPDARTKLFWISY 82

RESULT 13  
US-08-660-289-2  
; Sequence 2, Application US/08660289  
; Patent No. 5833982  
; GENERAL INFORMATION:  
; APPLICANT: Berkner, Kathleen L.  
; APPLICANT: Petersen, Lars C.  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Hedner, Ulla  
; APPLICANT: Bregengaard, Claus  
; TITLE OF INVENTION: Modified Factor VII  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Hourie and Crew  
; STREET: One Market Plaza, Stuart Street Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,289  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/475,845  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: 08/327,690  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/065,725  
; FILING DATE: 21-MAY-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/662,920  
; FILING DATE: 28-FEB-1991  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 13952-8-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-467-9600  
; TELEFAX: 415-543-5043  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 444 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-660-289-2

Query Match 63.2%; Score 120; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 4, 2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXCRXXLCSPXXAFXIFRNXXRTROPFWSY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14  
US-08-537-807-2  
; Sequence 2, Application US/08537807  
; Patent No. 5861374  
; GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,807  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05779  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 08/065,725  
FILING DATE: 21-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 63.2%; Score 120; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 4, 2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXCRXXLCSPXXAFXIFRNXXRTROPFWSY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15  
US-08-871-003-2  
; Sequence 2, Application US/08871003  
; Patent No. 5937864  
; GENERAL INFORMATION:

APPLICANT: Hart, Charles E.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle

STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 63.2%; Score 120; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 4, 2e-13;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRGSLRXCRXXLCSPXXAFXIFRNXXRTROPFWSY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEAREIFKDAERTKLFWISY 82

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

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Title: 10Gln28PHE\_4  
Perfect score: 190  
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

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Published Applications AA:\*  
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7: /cgn2\_6/ptodata/2/pubpaa/PCTUS PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09 NEW PUB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10 NEW PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10 PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60 NEW PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                 | Description       |
|------------|-------|-------------|--------|----|--------------------|-------------------|
| 1          | 120   | 63.2        | 406    | 9  | US-10-109-498-1    | Sequence 1, Appl1 |
| 2          | 94    | 49.5        | 419    | 9  | US-10-182-263-6    | Sequence 6, Appl1 |
| 3          | 90    | 47.4        | 415    | 10 | US-09-118-748-2    | Sequence 2, Appl2 |
| 4          | 90    | 47.4        | 461    | 9  | US-10-132-829-5    | Sequence 5, Appl1 |
| 5          | 90    | 47.4        | 461    | 10 | US-09-884-901-3    | Sequence 3, Appl1 |
| 6          | 89    | 46.8        | 419    | 9  | US-10-182-263-1    | Sequence 1, Appl1 |
| 7          | 89    | 46.8        | 419    | 9  | US-10-182-263-3    | Sequence 3, Appl1 |
| 8          | 89    | 46.8        | 419    | 9  | US-10-182-263-4    | Sequence 4, Appl1 |
| 9          | 89    | 46.8        | 419    | 9  | US-10-182-263-5    | Sequence 5, Appl1 |
| 10         | 89    | 46.8        | 419    | 9  | US-09-978-917A-4   | Sequence 4, Appl1 |
| 11         | 89    | 46.8        | 461    | 9  | US-10-182-263-2    | Sequence 2, Appl1 |
| 12         | 89    | 46.8        | 461    | 9  | US-09-578-917A-2   | Sequence 2, Appl1 |
| 13         | 67    | 35.3        | 96     | 9  | US-09-759-130B-313 | Sequence 313, App |
| 14         | 67    | 35.3        | 209    | 9  | US-09-759-130B-312 | Sequence 312, App |
| 15         | 67    | 35.3        | 226    | 9  | US-09-759-130B-310 | Sequence 310, App |
| 16         | 50    | 26.3        | 95     | 9  | US-09-759-130B-356 | Sequence 356, App |
| 17         | 50    | 26.3        | 208    | 9  | US-09-759-130B-355 | Sequence 355, App |
| 18         | 50    | 26.3        | 225    | 9  | US-09-759-130B-353 | Sequence 353, App |
| 19         | 41    | 21.6        | 1438   | 12 | US-10-006-091-1    | Sequence 1, Appl1 |

|    |    |      |      |    |                    |                    |
|----|----|------|------|----|--------------------|--------------------|
| 20 | 41 | 21.6 | 1438 | 12 | US-10-047-257-1    | Sequence 1, Appli  |
| 21 | 41 | 21.6 | 1471 | 12 | US-10-095-718-2    | Sequence 2, Appli  |
| 22 | 41 | 21.6 | 2332 | 9  | US-09-957-641-2    | Sequence 4, Appli  |
| 23 | 41 | 21.6 | 2351 | 9  | US-10-132-829-4    | Sequence 334, App  |
| 24 | 40 | 21.1 | 484  | 10 | US-09-801-368-334  | Sequence 516, App  |
| 25 | 39 | 20.5 | 197  | 9  | US-10-076-622-516  | Sequence 517, App  |
| 26 | 39 | 20.5 | 197  | 12 | US-10-007-805-516  | Sequence 517, App  |
| 27 | 39 | 20.5 | 232  | 9  | US-10-076-622-517  | Sequence 1024, App |
| 28 | 39 | 20.5 | 232  | 12 | US-10-007-805-517  | Sequence 7, Appli  |
| 29 | 39 | 20.5 | 233  | 10 | US-09-867-550-1024 | Sequence 4, Appli  |
| 30 | 39 | 20.5 | 243  | 9  | US-09-938-418-7    | Sequence 122, App  |
| 31 | 39 | 20.5 | 243  | 9  | US-10-045-992-4    | Sequence 122, App  |
| 32 | 39 | 20.5 | 243  | 9  | US-10-063-547-122  | Sequence 366, App  |
| 33 | 39 | 20.5 | 243  | 9  | US-10-174-590-366  | Sequence 366, App  |
| 34 | 39 | 20.5 | 243  | 9  | US-10-176-758-366  | Sequence 127, App  |
| 35 | 39 | 20.5 | 243  | 9  | US-10-063-616-122  | Sequence 366, App  |
| 36 | 39 | 20.5 | 243  | 9  | US-10-175-737-366  | Sequence 366, App  |
| 37 | 39 | 20.5 | 243  | 9  | US-10-175-737-366  | Sequence 366, App  |
| 38 | 39 | 20.5 | 243  | 9  | US-10-063-502-122  | Sequence 366, App  |
| 39 | 39 | 20.5 | 243  | 9  | US-10-173-706-366  | Sequence 366, App  |
| 40 | 39 | 20.5 | 243  | 9  | US-10-175-738-366  | Sequence 366, App  |
| 41 | 39 | 20.5 | 243  | 9  | US-10-175-752-366  | Sequence 366, App  |
| 42 | 39 | 20.5 | 243  | 9  | US-10-176-482-366  | Sequence 366, App  |
| 43 | 39 | 20.5 | 243  | 9  | US-10-176-757-366  | Sequence 366, App  |
| 44 | 39 | 20.5 | 243  | 9  | US-10-176-913-366  | Sequence 366, App  |
| 45 | 39 | 20.5 | 243  | 9  | US-10-180-552-366  | Sequence 366, App  |

#### ALIGNMENTS

RESULT 1  
US-10-109-498-1  
; Sequence 1, Application US/10109498  
; Publication No. US20030044908A1  
; GENERAL INFORMATION:  
; APPLICANT: Persson, Egon  
; TITLE OF INVENTION: Coagulation Factor VII Derivatives  
; FILE REFERENCE: 6286.200-US  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/281,261  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: PA 2001 00477  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(406)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-109-498-1  
Query Match 63.2%; Score 120; DB 9; Length 406;  
Best Local Similarity 75.0%; Pred. No. 3.7e-13;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
CY 1 ANGFLLXLRPGSLKRXCRXXLCSPFXAXIFRNXXRTQFWVSY 44  
DB 1 ANAFLLXLRPGSLKRXCRXXCSPFXAXIFRNXXRTQFWVSY 44  
RESULT 2  
US-10-182-263-6  
; Sequence 6, Application US/10182263  
; Publication No. US20030022354A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlitz, Bruce E  
; APPLICANT: Jones, Bryan E

```

; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          49.5%; Score 94; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1,3e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANGFLXXLRQGSIXRCXKXLCSPFXAIFYIRNXXRTROFWY 41
DB 1 ANSFLEELRQGSIERCEIEICDFEBAKEIFEDVDTLAFW 41

RESULT 3
US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, Jinli
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,571
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-118-748-2

Query Match          47.4%; Score 90; DB 10; Length 415;
Best Local Similarity 41.9%; Pred. No. 6,6e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXXLRQGSIXRCXKXLCSPFXAIFYIRNXXRTROFWY 44
DB 3 SCKLEEFVQGNLERECMEBKCSFEERAEVFNTERTEFTFWKY 45

RESULT 4
US-10-132-829-5
; Sequence 5, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; FILE REFERENCE: 6627-PA1170
; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          47.4%; Score 90; DB 9; Length 461;
Best Local Similarity 41.9%; Pred. No. 7,4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXXLRQGSIXRCXKXLCSPFXAIFYIRNXXRTROFWY 44
DB 49 SCKLEEFVQGNLERECMEBKCSFEERAEVFNTERTEFTFWKY 91

RESULT 5
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: USFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match          47.4%; Score 90; DB 10; Length 461;
Best Local Similarity 41.9%; Pred. No. 7,4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXXLRQGSIXRCXKXLCSPFXAIFYIRNXXRTROFWY 44
DB 49 SCKLEEFVQGNLERECMEBKCSFEERAEVFNTERTEFTFWKY 91

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
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Qy 1 ANGFLXLLRQGSILXRCXRXLCSPXAXFIFRNXXRTROFW 41
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Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 7
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match 46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLLRQGSILXRCXRXLCSPXAXFIFRNXXRTROFW 41
    |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 8
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match 46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLLRQGSILXRCXRXLCSPXAXFIFRNXXRTROFW 41
    |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 9
US-10-182-263-5
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; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match 46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLLRQGSILXRCXRXLCSPXAXFIFRNXXRTROFW 41
    |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 10
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match 46.8%; Score 89; DB 9; Length 419;
Best Local Similarity 46.3%; Pred. No. 1e-07;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGFLXLLRQGSILXRCXRXLCSPXAXFIFRNXXRTROFW 41
    |||||
Db 1 ANSFLEELRHGSLERECIEICDFEAKEIFQNVDDTLAFW 41

RESULT 11
US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
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; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match
Best Local Similarity 46.8%; Score 89; DB 9; Length 461;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCXXLCSEFXAXFIFRNXXRTROFW 41
DB 43 ANSFLELRHRSLSRECEIEICDFEEXKEIFQVVDTLAFW 83

RESULT 12
US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(42)
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2

Query Match
Best Local Similarity 46.8%; Score 89; DB 9; Length 461;
Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCXXLCSEFXAXFIFRNXXRTROFW 41
DB 43 ANSFLELRHRSLSRECEIEICDFEEXKEIFQVVDTLAFW 83

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match
Best Local Similarity 35.3%; Score 67; DB 9; Length 96;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSIXRCXXLCSEFXAXFIFRNXXRTROFWYSY 44
DB 46 GNIRECNEELCNVEAREIFVDEDXTIAFQOEY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match          35.3%; Score 67; DB 9; Length 209;
Best Local Similarity 38.2%; Pred. No. 0.00035;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLXRXCRXXLCSPYXAFIFRNXXRTROFWVS 44
DB 46 GNLRRCNEELCNVEAREIFVDEDKTIAFWQRY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-5350NMTM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match          35.3%; Score 67; DB 9; Length 226;
Best Local Similarity 38.2%; Pred. No. 0.00038;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 11 GSLXRXCRXXLCSPYXAFIFRNXXRTROFWVS 44
DB 63 GNLRRCNEELCNVEAREIFVDEDKTIAFWQRY 96

Search completed: March 20, 2003, 13:30:18
Job time : 9.375 secs
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|          |   |
|----------|---|
| DR       | WP1; 1999-288309/24.  |
| XX       | Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic   |
| PT       | acid domain, useful for treating clotting disorders   |
| XX       |   |
| PS       | Disclosure; Page 80; 86pp; English.   |
| XX       |   |
| CC       | This sequence represents a modified GLA (gamma-carboxyglutamic acid)  |
| CC       | domain. The invention relates to a vitamin K-dependent polypeptide  |
| CC       | comprising a modified GLA domain containing an amino acid substitution  |
| CC       | which enhances membrane binding of the modified polypeptide as compared   |
| CC       | to the native polypeptide. The polypeptide is used to treat a clotting  |
| CC       | disorder by decreasing or increasing clot formation. Modification of the  |
| CC       | GLA domain results in a protein which has enhanced membrane binding   |
| CC       | affinity as compared to the native protein.   |
| XX       |   |
| SQ       | Sequence 44 AA;   |
| OY       | Query Match 84.3%; Score 161; DB 20; Length 44;<br>Best Local Similarity 95.5%; Pred. No. 1e-19; Mismatches 0; Gaps 0<br>Matches 42; Conservative 1; Indels 1 |
| Dd       | 1 ANAFPLXLLRNGSLRXCKKXCSPFXAXEYIFPDAXRTKLFWISY 44<br>1 ANAFPLXLLRNGSLRXCKKXCSPFXAXEYIFPDAXRTKLFWISY 44  |
| RESULT 2 |   |
| ID       | AAV18310 standard; peptide; 44 AA.  |
| AC       | AAV18310,   |
| XX       |   |
| DT       | 17-AUG-1999 (first entry)   |
| DE       | Modified GLA domain of vitamin K-dependent protein.   |
| XX       |   |
| KW       | GLA domain; mutein; vitamin K-dependent protein; clotting disorder;   |
| KW       | therapy.  |
| XX       |   |
| OS       | Homo sapiens.   |
| OS       | Synthetic.  |
| XX       |   |
| FH       | Key Location/Qualifiers   |
| FT       | Misc-difference 1..44   |
| FT       | /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  |
| FT       | acid"   |
| XX       |   |
| PN       | WO9920767-A1.   |
| XX       |   |
| PD       | 29-APR-1999.  |
| XX       |   |
| PF       | 20-OCT-1998; 98WO-US22152.  |
| XX       |   |
| PR       | 23-OCT-1997; 97US-0955636.  |
| PA       | (MINN ) UNIV MINNESOTA.   |
| XX       |   |
| PI       | Nelaeetuen GL;  |
| XX       |   |
| DR       | WP1; 1999-288309/24.  |
| XX       |   |
| PT       | Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic   |
| PT       | acid domain, useful for treating clotting disorders   |
| XX       |   |
| PS       | Disclosure; Page 80; 86pp; English.   |
| XX       |   |
| CC       | This sequence represents a modified GLA (gamma-carboxyglutamic acid)  |
| CC       | domain. The invention relates to a vitamin K-dependent polypeptide  |
| CC       | comprising a modified GLA domain containing an amino acid substitution  |
| CC       | which enhances membrane binding of the modified polypeptide as compared   |
| CC       | to the native polypeptide. The polypeptide is used to treat a clotting  |
| CC       | disorder by decreasing or increasing clot formation. Modification of the  |
| CC       | disorder by decreasing or increasing clot formation. Modification of the  |

|   |  |   |
|---|--|---|
| CC  |  | GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein. |
| XX  |  |   |
| XX  |  |   |
| SQ  | Sequence   | 44 AA;  |
| Query Match 83.8%; Score 160; DB 20; Length 44;<br>Best Local Similarity 95.5%; Pred. No. 1.5e-19;<br>Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |  |   |
| Oy  | 1 ANAFLLRLNGSLKRXCKXQCSPFXAXEIFPDARTLFWISY   | 44<br>     <br>   |
| Db  | 1 ANAFLLRLNGSLKRXCKXQCSPFXAXIRFDARTLFWISY  | 44<br>     <br>   |
| <b>RESULT 3</b><br><b>AAYI8305</b><br><b>ID AAYI8305 standard; peptide: 44 AA.</b>  |  |   |
| XX  | AAYI8305;  |   |
| AC  |  |   |
| DT  | 17-AUG-1999 (first entry)  |   |
| XX  |  |   |
| DE  | Human factor VII GLA domain.   |   |
| KW  | GLA domain; vitamin K-dependent protein; clotting disorder;  |   |
| KM  | therapy.   |   |
| XX  |  |   |
| OS  | Homo sapiens.  |   |
| XX  |  |   |
| FH  | Key Location/Qualifiers  |   |
| FT  | Misc-difference 1..44 /note= "Xaa= gamma-carboxylglutamic acid, or glutamic acid"  |   |
| FT  |  |   |
| XX  |  |   |
| PV  | WO9920767-A1.  |   |
| XX  |  |   |
| PD  | 29-APR-1999.   |   |
| XX  |  |   |
| PF  | 20-OCT-1998; 98WO-US22152.   |   |
| XX  |  |   |
| PR  | 23-OCT-1997; 97US-0955636.   |   |
| XX  |  |   |
| PA  | (MINU ) UNIV MINNESOTA.  |   |
| XX  |  |   |
| PI  | Nelaeuten GL;  |   |
| DR  | WPJ; 1999-286309/24.   |   |
| XX  |  |   |
| PT  | Vitamin K-dependent polypeptide with modified gamma-carboxylglutamic acid domain, useful for treating clotting disorders   |   |
| XX  |  |   |
| PS  | Disclosure: Page 15; 86pp; English.  |   |
| XX  |  |   |
| CC  | This sequence is the factor VII GLA (gamma-carboxylglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the CC GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein. |   |
| CC  |  |   |
| CC  |  |   |
| SQ  | Sequence   | 44 AA;  |
| Query Match 82.7%; Score 158; DB 20; Length 44;<br>Best Local Similarity 95.5%; Pred. No. 3.3e-19;<br>Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |  |   |
| Oy  | 1 ANAFLLRLNGSLKRXCKXQCSPFXAXEIFDARTLFWISY  | 44<br>     <br>   |
| Db  | 1 ANAFLLRLNGSLKRXCKXQCSPFXAKIRFDARTLFWISY  | 44<br>     <br>   |

```

RESULT 4
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
XX AAB36395;
AC
XX 27-FEB-2001 (first entry)
DT
XX
XX Human factor VII gamma-carboxylglutamic acid domain SEQ ID NO:3.
DE
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxylglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Homo sapiens.
OS
XX MO20006753-A2.
PN
XX
XX 09-NOV-2000.
PD
XX
XX 28-APR-2000; 2000WO-US11416.
PF
XX
XX 29-APR-1999; 99US-0302239.
PR
XX
XX (MINU ) UNTV MINNESOTA.
PA
XX
XX Nelsestuen GL;
PI
XX
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot
XX formation in a mammal, a factor VII or factor IX containing a modified
XX GLA domain is useful for increasing clot formation and for treating a
XX bleeding disorder, including thrombosis and clotting disorders such as
XX haemophilia A, haemophilia B and liver disease. The present sequence
XX represents a wild type human factor VII GLA domain sequence, given in
XX the exemplification of the present invention.
XX
XX Sequence 44 AA;
SQ
Query Match 82.7%; Score 158; DB 22; Length 44;
Best Local Similarity 95.3%; Pred. No. 3.3e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ANAFLELXLRGSLRCKXKQCSFXXAEXIFKDXRTKLFWISY 44
DB 1 ANAFLELXLRGSLRCKXKQCSFXXAEXIFKDXRTKLFWISY 44

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DE Mutant blood coagulant factor VII (FVII-31).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 311..317
FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
PD
XX
XX 24-AUG-1999; 99JP-0237610.
PF
XX
XX 24-AUG-1999; 99JP-0237610.
PR
XX
XX (KAGA ) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
PA
XX
XX WPI; 2001-310677/33.
DR
XX
XX N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
XX Claim 14; Page 20-21; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 82.7%; Score 158; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 3.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1 ANAFLELXLRGSLRCKXKQCSFXXAEXIFKDXRTKLFWISY 44
DB 1 ANAFLELXLRGSLRCKXKQCSFXXAEXIFKDXRTKLFWISY 44

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RESULT 6
AAB84871
ID AAB84871 standard; protein; 401 AA.
XX
XX AAB84871;
AC
XX 31-JUL-2001 (first entry)
DT
XX
XX Mutant blood coagulant factor VII (FVII-39).
DE
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 235..239
FT /note="Wild-type Val-Pro-Gly-Thr-Thr substituted by
FT Asp-Arg-Lys-Thr-Leu"
FT Misc-difference 311..317
FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX

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PD 13-MAR-2001.  
 XX 24-AUG-1999; 99JP-0237610.  
 XX 24-AUG-1999; 99JP-0237610.  
 XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 XX WPI; 2001-310677/33.  
 DR N-PSDB; AAH19464.  
 XX  
 PT Mutant of blood coagulant factor VII, used for substitution therapy in  
 the treatment of hemophilia -  
 XX  
 PS Claim 16; Page 23-24; 29pp; Japanese.  
 XX  
 CC The present invention relates to mutants of blood coagulant factor VII  
 (FVII) or activated blood coagulant factor VII (FVIIa). The present  
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an  
 CC agent for the substitution therapy of haemophilia inhibitor patients.  
 XX  
 SQ Sequence 401 AA;  
 Query Match 82.7%; Score 158; DB 22; Length 401;  
 Best Local Similarity 72.7%; Pred. No. 3,2e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
 DB 1 ANAFLLELRPGSLRECKEQCSEFARERIFKDAERTKLFWISY 44

RESULT 7  
 AAR35764  
 ID AAR35764 standard; protein; 406 AA.  
 XX  
 AC AAR35764;  
 XX  
 DT 24-SEP-1993 (first entry)  
 XX  
 DE Factor VII (VII).  
 XX  
 PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;  
 KM Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;  
 KM exosite; catalytic activity.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..152  
 FT /note= "Factor VII light chain"  
 FT 153..406  
 FT /note= "Factor VII heavy chain"  
 FT 374..388  
 FT /note= "exosite 1"  
 FT 290..310  
 FT /note= "exosite 2"  
 FT 290..310  
 FT /note= "pref. PC polypeptide; claim 2, page 136"  
 FT 374..388  
 FT /note= "pref. PC polypeptide; claim 2, page 136"  
 FT 289..304  
 FT /note= "pref. PC polypeptide; claim 4, page 137"  
 FT 290..304  
 FT /note= "pref. PC polypeptide; claim 4, page 137"  
 FT 245..266  
 FT /note= "claim 9, page 138-139 describes an antibody  
 that reacts with Factor VII; fragments  
 289-304, 290-304, 290-310, 374-388 and  
 400-414 but not with fragment 245-266"  
 XX  
 PN WO9309804-A.  
 XX

PD 27-MAY-1993.  
 XX 18-NOV-1992; 92WO-US10242.  
 XX 18-NOV-1991; 91US-0793989.  
 XX (SCRI ) SCRIPPS RES INST.  
 XX Griffen JH, Meesters RM;  
 PI WPI; 1993-182244/22.  
 DR  
 XX  
 PT Serine protease derived polypeptide(s) and anti-peptide  
 PT antibodies - for inhibiting coagulation and assaying for the  
 PT presence of serine protease in fluid samples  
 XX  
 PS Disclosure; Page 133-135; 149pp; English.  
 XX  
 CC The PC polypeptides indicated in the Features Table inhibit  
 CC coagulation (they prevent binding of serine protease to natural  
 CC substrates), esp. when admin. to give an intravascular blood  
 CC concn. of 0.1-100 (pref. 0.5-10) microm.  
 CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described  
 CC in the specification but have not yet been added to the SEQUENCE  
 CC LISTING.  
 XX  
 SQ Sequence 406 AA;  
 Query Match 82.7%; Score 158; DB 14; Length 406;  
 Best Local Similarity 72.7%; Pred. No. 3,2e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
 DB 1 ANAFLLELRPGSLRECKEQCSEFARERIFKDAERTKLFWISY 44

RESULT 8  
 AAM14509  
 ID AAM14509 standard; protein; 406 AA.  
 XX  
 AC AAM14509;  
 XX  
 DT 14-MAY-1997 (first entry)  
 XX  
 DE Modified blood coagulation Factor VII (R290S).  
 XX  
 KM Blood coagulation; factor 7; murein; mutation; modification;  
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 6  
 FT /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 7  
 FT /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 14  
 FT /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 16  
 FT /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 19  
 FT /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 20  
 FT /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 17..22  
 FT Disulfide-bond





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FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33
FT /note= "proteolytic site"
FT Modified-site 35
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 38..39
FT /note= "proteolytic site"
FT Cleavage-site 42..43
FT /note= "proteolytic site"
FT Cleavage-site 44..45
FT /note= "proteolytic site"
FT Disulfide-bond 50..61
FT Disulfide-bond 55..70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72..81
FT Disulfide-bond 91..102
FT Disulfide-bond 98..112
FT Disulfide-bond 114..127
FT Disulfide-bond 135..162
FT Cleavage-site 143..144
FT /note= "proteolytic site"
FT Modified-site 145
FT /note= "glycosylation site"
FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note= "proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 315
FT /note= "native Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide
FT bond"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393
FT /note= "proteolytic site"
FT Cleavage-site 396..397
FT /note= "proteolytic site"
FT Cleavage-site 402..403
FT /note= "proteolytic site"
FT US5580560-A.
FT EN
FT 03-DEC-1996.
FT PD
FT 13-NOV-1989; 89US-0434149.
FT PE
FT 09-AUG-1993; 93US-0104509.
FT 13-NOV-1989; 89US-0434149.
FT 12-JUN-1992; 92US-0898248.
FT 22-AUG-1994; 94US-0293778.
FT XX
FT (NOVO ) NOVO-NORDISK AS.
FT PA
FT Bjoern SE, Nicolaisen EM, Wiberg FC, Woodbury R;
FT WPI, 1997-033523/03.
FT DR
FT Mutated human factor VII or VIIa proteins - with amino acid
FT substitutions to improve proteolytic stability

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XX XX
XX Example 4; Page -; 28pp; English.
XX PS
XX Modified human factor VII or VIIa proteins are stabilised against
CC proteolytic cleavage by substitution of one of the residues Lys32,
CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
CC Lys341 by an amino acid that provides a proteolytically more stable
CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC bleeding disorders such as thrombocytopenia and von Willebrand's
CC disease. They are also suitable for addition to plasma substitutes.
CC The present sequence is a specific example of a modified factor VII
CC protein.
XX XX
XX Sequence 406 AA;
SQ
Query Match 82.7%; Score 158; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 3.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAPLXIRNGSLXRXCKXKXOCFFXAXEKFQDXRRTLFWISY 44
Db 1 ANAFLELRPGSLERBECKEQQCFEAREIFQDAERTLFWISY 44

RESULT 10
AAU7745
ID AAU7745 standard; protein; 406 AA.
AC AAU7745;
XX
XX 05-JUN-2002 (first entry)
DE Human factor VIIa active site mutant.
KW Factor VIIa; human; shock heat treatment; protein stability;
KW protein manufacture; protein conformation; mutant; muten.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Active-site 193
FT Active-site /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242
FT Active-site /note= "Member of the factor VIIa catalytic triad"
FT Active-site 344
FT Active-site /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344
FT /label= Gly, Met, Thr
FT /note= "Preferably Ala, wild type Ser"
FT WO200177141-A1.
XX
XX 18-OCT-2001.
XX PD
XX 06-APR-2001; 2001WO-DK00234.
XX PF
XX 06-APR-2000; 2000DK-0000573.
XX PR
XX 17-APR-2000; 2000US-197650P.
XX XX
XX (NOVO ) NOVO NORDISK AS.
XX PA
XX Mathiesen F;
XX XX
XX WPI; 2001-657162/75.
XX DR
XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
PT involves a shock heat treatment -
XX XX
XX Disclosure; Page -; 22pp; English.
XX PS
XX The invention describes a method of stabilising a polypeptide involving
CC

```



|  |   |  |
|--|---|--|
| KW   |   | cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease;  |
| KM   |   | myocardial infarction; thrombotic stroke; deep-vein thrombosis.  |
| XX   |   |  |
| OS   | Homo sapiens.   |  |
| XX   |   |  |
| FT   | Key   | Location/Qualifiers  |
| FT   | Modified-site   | 52 /note= "O-glycosylated"   |
| FT   | Modified-site   | 60 /note= "O-glycosylated"   |
| FT   | Modified-site   | 145 /note= "N-glycosylated"  |
| FT   | Cleavage-site   | 152..153 /note= "proteolytic cleavage site converting FVII zymogen<br>to an activated form, comprising two chains<br>linked by a single disulphide bridge" |
| FT   | Modified-site   | 322 /note= "N-glycosylated"  |
| XX   |   |  |
| PN   | WO200158935-A2.   |  |
| PD   | 16-AUG-2001.  |  |
| XX   |   |  |
| PF   | 12-FEB-2001; 2001WO-DK00094.  |  |
| XX   |   |  |
| PR   | 11-FEB-2000; 2000DK-0000218.  |  |
| PR   | 18-OCT-2000; 2000DK-0001558.  |  |
| PA   | (MAXY-) MAXYGEN APS.  |  |
| PI   | Anderseen KV, Pedersen AH, Bornaes C,   |  |
| XX   |   |  |
| DR   | WPI; 2001-581807/65.  |  |
| N-PSDB:  | AAI99983.   |  |
| XX   |   |  |
| PT   | New conjugate, useful for treating Factor VIIA related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group - |  |
| XX   |   |  |
| PS   | Disclosure; Page 85-86; 89pp; English.  |  |
| XX   |   |  |
| CC   | The invention relates to novel Factor VII (FVIII) or Factor VIIA (FVIIA)  |  |
| CC   | polypeptide conjugates, comprising at least one non-polypeptide group   |  |
| CC   | covalently attached to a polypeptide, where the amino acid sequence of  |  |
| CC   | polypeptide differs from that of the wildtype FVIIA (AAM52171) in that at   |  |
| CC   | least one amino acid residue containing an attachment group for the   |  |
| CC   | non-polypeptide group has been introduced or removed. The FVIIA   |  |
| CC   | conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  |  |
| CC   | cerebroprotective activity and are useful for treating FVIIA/TF-related   |  |
| CC   | diseases or disorders such as haemophilia, liver disease, myocardial  |  |
| CC   | infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  |  |
| CC   | have increased functional in vivo half life and/or increased plasma half  |  |
| CC   | life, increased bioavailability and or reduced sensitivity to proteolytic   |  |
| CC   | degradation. Consequently medical treatment using the conjugates has a  |  |
| CC   | number of advantages over currently available such as longer duration   |  |
| CC   | between injections.   |  |
| XX   |   |  |
| SQ   | Sequence 406 AA;  |  |
| Query Match  | 82.7%; Score 159; DB 22; Length 406;  |  |
| Best Local Similarity  | 72.7%; Pred. No. 3.2e-18;   |  |
| Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0; |   |  |
| OY   | 1 ANAFLLXLRNGSLKRYCKKKQCSFFXAEXIFKDAKTKFWISY 44   |  |
| DB   | 1 ANAFLEELRPGSLERCKEKCQCSFEAREIFFKDAERTKLFWISY 44   |  |
| RESULT 13  |   |  |
| ID   | AAM52181 standard; Protein; 406 AA.   |  |
| XX   |   |  |

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| AC  | AAM52181;   |               |
| XX  |   |               |
| DT  | 07-FEB-2002   | (first entry) |
| XX  |   |               |
| DE  | Human FVII mutant T106N.  |               |
| XX  |   |               |
| KM  | Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  |               |
| KM  | cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;   |               |
| KM  | myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;   |               |
| XX  | muteln.   |               |
| OS  | Homo sapiens.   |               |
| XX  | Synthetic.  |               |
| FH  |   |               |
| Key | Location/Qualifiers   |               |
| FT  | Misc-difference   | 6             |
| FT  | /label= Glu, OTHER  |               |
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| FT  | /label= Glu, OTHER  |               |
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| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
| FT  | Misc-difference   | 19            |
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| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
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| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
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| FT  | /label= Glu, OTHER  |               |
| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
| FT  | Misc-difference   | 26            |
| FT  | /label= Glu, OTHER  |               |
| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
| FT  | Misc-difference   | 29            |
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| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
| FT  | Misc-difference   | 35            |
| FT  | /label= Glu, OTHER  |               |
| FT  | /note= "OTHER = gamma carboxyglutamic acid"   |               |
| FT  | Modified-site   | 52            |
| FT  | /note= "O-glycosylated"   |               |
| FT  | Modified-site   | 60            |
| FT  | /note= "O-glycosylated"   |               |
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| FT  | /note= "wild-type Thr substituted by Asn"   |               |
| FT  | Modified-site   | 145           |
| FT  | /note= "N-glycosylated"   |               |
| FT  | Cleavage-site   | 152, 153      |
| FT  | /note= "proteolytic cleavage site converting FVII zymogen<br>to an activated form, comprising two chains<br>linked by a single disulphide bridge" |               |
| FT  | Modified-site   | 322           |
| FT  | /note= "N-glycosylated"   |               |
| XX  |   |               |
| PN  | WO200158935-A2.   |               |
| XX  |   |               |
| PD  | 16-AUG-2001.  |               |
| XX  |   |               |
| PF  | 12-FEB-2001; 2001WO-DK00094.  |               |
| XX  |   |               |
| PR  | 11-FEB-2000; 2000DK-0000218.  |               |
| PR  | 18-OCT-2000; 2000DK-0001558.  |               |
| XX  |   |               |
| PA  | (MAXY-) MAXYGEN APS.  |               |
| XX  |   |               |
| PI  | Andersen KV, Pedersen AH, Bornaaes C;   |               |
| XX  |   |               |

DR WPI, 2001-581807/65.  
 XX New conjugate, useful for treating Factor VIIa related diseases or  
 PT disorders such as haemophilia, liver disease, myocardial infarction and  
 PT deep-vein thrombosis, comprises non-polypeptide group covalently  
 PT attached to polypeptide group -  
 XX  
 PS Example 3; Page -; 89pp; English.  
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
 CC polypeptide conjugates, comprising at least one non-polypeptide group  
 CC covalently attached to a polypeptide, where the amino acid sequence of  
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
 CC least one amino acid residue containing an attachment group for the  
 CC non-polypeptide group has been introduced or removed. The FVIIa  
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
 CC cerebroprotective activity and are useful for treating FVIIa/Ff-related  
 CC diseases or disorders such as haemophilia, liver disease, myocardial  
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
 CC have increased functional in vivo half life and/or increased plasma half  
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
 CC degradation. Consequently medical treatment using the conjugates has a  
 CC number of advantages over currently available such as longer duration  
 CC between injections. The present sequence is that of a human FVII mutant,  
 CC having an addition in vivo glycosylation site and tested for its  
 CC amidolytic activity.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1  
 CC (AAM52171).  
 CC  
 SQ Sequence 406 AA;  
 Query Match 82.7%; Score 158; DB 22; Length 406;  
 Best Local Similarity 95.5%; Pred. No. 3.2e-18;  
 Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ANAFLLXRLNGSLRXCKXQCSFXAXEIXFKDAXRTKLFMISY 44  
 Db 1 ANFLXLRGSLRXCKXQCSFXAXEIXFKDAXRTKLFMISY 44  
 RESULT 14  
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 ID AAM52182 standard; Protein; 406 AA.  
 XX  
 AC AAM52182;  
 XX  
 DT 07-FEB-2002 (first entry)  
 XX  
 DE Human FVII mutant K143N/N145T.  
 XX  
 KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
 KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;  
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;  
 KW mutin.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT MISC-difference 6 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT MISC-difference 7 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT MISC-difference 14 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT MISC-difference 16 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT MISC-difference 19 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
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FT /label= Glu, OTHER  
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 FT MISC-difference 20 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT MISC-difference 25 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
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 FT /note= "OTHER = gamma carboxyglutamic acid"  
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 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT MISC-difference 35 /label= Glu, OTHER  
 FT /note= "OTHER = gamma carboxyglutamic acid"  
 FT Modified-site 52 /note= "O-glycosylated"  
 FT Modified-site 60 /note= "O-glycosylated"  
 FT MISC-difference 143 /note= "Wild-type Lys substituted by Asn"  
 FT MISC-difference 145 /note= "Wild-type Asn substituted by Thr"  
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen  
 FT to an activated form, comprising two chains  
 FT linked by a single disulphide bridge"  
 FT Modified-site 322 /note= "N-glycosylated"  
 FT  
 PN MO200158935-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 12-FEB-2001; 2001WO-DK00094.  
 XX  
 PR 11-FEB-2000; 2000DK-0000218.  
 PR 18-OCT-2000; 2000DK-0001558.  
 XX  
 PA (MAXY-) MAXYGEN APS.  
 XX  
 PI Andersen KV, Pedersen AH, Bornaaes C;  
 XX  
 DR WPI, 2001-581807/65.  
 XX  
 XX New conjugate, useful for treating Factor VIIa related diseases or  
 PT disorders such as haemophilia, liver disease, myocardial infarction and  
 PT deep-vein thrombosis, comprises non-polypeptide group covalently  
 PT attached to polypeptide group -  
 XX  
 PS Example 3; Page -; 89pp; English.  
 XX  
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
 CC polypeptide conjugates, comprising at least one non-polypeptide group  
 CC covalently attached to a polypeptide, where the amino acid sequence of  
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
 CC least one amino acid residue containing an attachment group for the  
 CC non-polypeptide group has been introduced or removed. The FVIIa  
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
 CC cerebroprotective activity and are useful for treating FVIIa/Ff-related  
 CC diseases or disorders such as haemophilia, liver disease, myocardial  
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
 CC have increased functional in vivo half life and/or increased plasma half  
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
 CC degradation. Consequently medical treatment using the conjugates has a  
 CC number of advantages over currently available such as longer duration  
 CC between injections. The present sequence is that of a human FVII mutant,  
 CC having an addition in vivo glycosylation site and tested for its  
 CC amidolytic activity.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1



GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10ASN28GLU  
Perfect score: 191  
Sequence: 1 ANAFLLXLRNGSLRXCKXX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
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| 1          | 161   | 84.3        | 44     | 3     | US-08-955-636-27 |
| 2          | 160   | 83.8        | 44     | 3     | US-08-955-636-26 |
| 3          | 158   | 82.7        | 44     | 3     | US-08-955-636-3  |
| 4          | 158   | 82.7        | 406    | 1     | US-08-293-778-24 |
| 5          | 158   | 82.7        | 406    | 1     | US-08-295-411-5  |
| 6          | 158   | 82.7        | 406    | 2     | US-08-955-471-5  |
| 7          | 158   | 82.7        | 406    | 5     | PCT-US92-10242-5 |
| 8          | 158   | 82.7        | 444    | 1     | US-08-475-845-2  |
| 9          | 158   | 82.7        | 444    | 2     | US-08-327-690-2  |
| 10         | 158   | 82.7        | 444    | 2     | US-08-660-289-2  |
| 11         | 158   | 82.7        | 444    | 2     | US-08-537-807-2  |
| 12         | 158   | 82.7        | 444    | 2     | US-08-871-003-2  |
| 13         | 158   | 82.7        | 444    | 3     | US-08-464-233-2  |
| 14         | 158   | 82.7        | 444    | 4     | US-09-189-607-2  |
| 15         | 158   | 82.7        | 444    | 4     | US-09-378-907-2  |
| 16         | 158   | 82.7        | 444    | 5     | PCT-US94-05779-2 |
| 17         | 158   | 82.7        | 446    | 1     | US-07-882-202A-4 |
| 18         | 158   | 82.7        | 446    | 1     | US-08-021-615A-4 |
| 19         | 158   | 82.7        | 466    | 1     | US-08-321-777-4  |
| 20         | 158   | 82.7        | 466    | 4     | US-09-009-217-14 |
| 21         | 158   | 82.7        | 466    | 4     | US-09-009-656-14 |
| 22         | 158   | 82.7        | 466    | 5     | PCT-US93-04493-4 |
| 23         | 156   | 81.7        | 44     | 3     | US-08-955-636-30 |
| 24         | 155   | 81.2        | 44     | 3     | US-08-955-636-28 |
| 25         | 152   | 79.6        | 44     | 3     | US-08-955-636-29 |
| 26         | 143   | 74.9        | 41     | 1     | US-08-229-280-4  |
| 27         | 122   | 63.9        | 44     | 3     | US-08-955-636-4  |

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| 28 | 107 | 56.0 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appl  |
| 29 | 107 | 56.0 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appl  |
| 30 | 107 | 56.0 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appl  |
| 31 | 107 | 56.0 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appl  |
| 32 | 107 | 56.0 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appl  |
| 33 | 107 | 56.0 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appl  |
| 34 | 107 | 56.0 | 488 | 1 | US-08-487-037-1  | Sequence 3, Appl  |
| 35 | 98  | 51.3 | 448 | 1 | US-08-295-411-3  | Sequence 3, Appl  |
| 36 | 98  | 51.3 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appl  |
| 37 | 98  | 51.3 | 448 | 5 | PCT-US92-10068-1 | Sequence 3, Appl  |
| 38 | 98  | 51.3 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appl  |
| 39 | 97  | 50.8 | 44  | 3 | US-08-955-636-18 | Sequence 18, Appl |
| 40 | 97  | 50.8 | 487 | 2 | US-08-469-486-53 | Sequence 53, Appl |
| 41 | 97  | 50.8 | 487 | 2 | US-08-469-658-53 | Sequence 53, Appl |
| 42 | 97  | 50.8 | 492 | 1 | US-08-469-486-2  | Sequence 2, Appl  |
| 43 | 97  | 50.8 | 492 | 2 | US-08-469-658-2  | Sequence 2, Appl  |
| 44 | 96  | 50.3 | 44  | 3 | US-08-955-636-24 | Sequence 24, Appl |
| 45 | 96  | 50.3 | 44  | 3 | US-08-955-636-35 | Sequence 35, Appl |

## ALIGNMENTS

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RESULT 1
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisseuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27

Query Match      84.3%; Score 161; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 7.2e-20;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXCKXXQCSFXXAEXIFKDXRTKLFWISY 44
DB 1 ANAFLLXLRNGSLRXCKXXQCSFXXAEXIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisseuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-26

Query Match 83.8%; Score 160; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 1.1e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFYXAEIIFDAXRTKLFWISY 44  
Db 1 ANAFLXLRBGLXRXCKXQCSFYXARXIFDAXRTKLFWISY 44

## RESULT 3

US-08-955-636-3  
Sequence 3, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
TITLE OF INVENTION: POLYPEPTIDES  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955.636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-3

Query Match 82.7%; Score 158; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2.3e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFYXAEIIFDAXRTKLFWISY 44  
Db 1 ANAFLXLRPGSLXRXCKXQCSFYXARXIFDAXRTKLFWISY 44

## RESULT 4

US-08-293-778-24  
Sequence 24, Application US/08293778  
Patent No. 5580560  
GENERAL INFORMATION:  
APPLICANT: Nicolaissen, Elise M.  
APPLICANT: Bjorn, Soren E.  
APPLICANT: Wibergh, Finn C.  
APPLICANT: Woodbury, Richard  
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5580560 No. 5580560disk of No. 5580560th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,778  
FILING DATE:  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/104,509  
FILING DATE:  
APPLICATION NUMBER: DK 3235/87  
FILING DATE: 25-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/434,149  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129, 224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 82.7%; Score 158; DB 1; Length 406;  
Best Local Similarity 72.7%; Pred. No. 2.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFYXAEIIFDAXRTKLFWISY 44  
Db 1 ANAFLYLRPGSLYRCKYQCSFYXARXIFDAXRTKLFWISY 44

## RESULT 5

US-08-295-411-5  
Sequence 5, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Masters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas



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/
/   REGISTRATION NUMBER: 34,163
/   REFERENCE/DOCKET NUMBER: TSRI263.0C1
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 619-554-2937
/   TELEFAX: 619-554-6312
/   INFORMATION FOR SEQ ID NO: 5:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 406 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   HYPOTHETICAL: NO
/   ANTI-SENSE: NO
/   FEATURE:
/   NAME/KEY: Region
/   LOCATION: 1..152
/   OTHER INFORMATION: /note= "Factor VII Light Chain"
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/   US-08-295-411-5
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/   Query Match      82.7%; Score 158; DB 1; Length 406;
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/   Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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/   QY 1 ANAFLLXLRNGSLXRXCKXXQCSFFXAXEYFKDAXRTKLFWISY 44
/   DB 1 ANAFLEELRPGSLRECKEKCQSFEEAREIFKDAERTKLFWISY 44
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/   RESULT 6
/   US-08-955-471-5
/   Sequence 5, Application US/08955471
/   Patent No. 5968751
/   GENERAL INFORMATION:
/   APPLICANT: Griffin, John H.
/   APPLICANT: Meesters, Rolf M.
/   TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
/   TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
/   NUMBER OF SEQUENCES: 10
/   CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Office of Patent Counsel, The Scripps
/   ADDRESSEE: Research Institute
/   STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
/   CITY: La Jolla
/   STATE: CA
/   COUNTRY: USA
/   ZIP: 92037
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: PatentIn Release #1.0, Version #1.25
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/955,471
/   FILING DATE:
/   CLASSIFICATION:
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: 08/295,411
/   FILING DATE:
/   CLASSIFICATION:
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Fitting, Thomas
/   REGISTRATION NUMBER: 34,163
/   REFERENCE/DOCKET NUMBER: TSRI263.0C1
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 619-554-2937
/   TELEFAX: 619-554-6312
/   INFORMATION FOR SEQ ID NO: 5:
/   SEQUENCE CHARACTERISTICS:
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/
/   LENGTH: 406 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   HYPOTHETICAL: NO
/   ANTI-SENSE: NO
/   FEATURE:
/   NAME/KEY: Region
/   LOCATION: 1..152
/   OTHER INFORMATION: /note= "Factor VII Light Chain"
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/   US-08-955-471-5
/
/   Query Match      82.7%; Score 158; DB 2; Length 406;
/   Best Local Similarity 72.7%; Pred. No. 2.3e-18;
/   Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
/
/   QY 1 ANAFLLXLRNGSLXRXCKXXQCSFFXAXEYFKDAXRTKLFWISY 44
/   DB 1 ANAFLEELRPGSLRECKEKCQSFEEAREIFKDAERTKLFWISY 44
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/   RESULT 7
/   PCT-US92-10242-5
/   Sequence 5, Application PC/TUS9210242
/   GENERAL INFORMATION:
/   APPLICANT: Griffin, John H.
/   APPLICANT: Meesters, Rolf
/   TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
/   TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
/   NUMBER OF SEQUENCES: 10
/   CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Office of Patent Counsel, The Scripps
/   ADDRESSEE: Research Institute
/   STREET: 10666 North Torrey Pines Road, TPC 8
/   CITY: La Jolla
/   STATE: CA
/   COUNTRY: USA
/   ZIP: 92037
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: PatentIn Release #1.0, Version #1.25
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: PCT/US92/10242
/   FILING DATE: 19921118
/   CLASSIFICATION:
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 07/793,989
/   FILING DATE: 18-NOV-1991
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Fitting, Thomas
/   REGISTRATION NUMBER: 34,163
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 619-554-2937
/   TELEFAX: 619-554-6312
/   INFORMATION FOR SEQ ID NO: 5:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 406 amino acids
/   TYPE: AMINO ACID
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   HYPOTHETICAL: NO
/   ANTI-SENSE: NO
/   FEATURE:
/   NAME/KEY: Region
/   LOCATION: 1..152
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OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
PCT-US92-10242-5

Query Match 82.7%; Score 158; DB 5; Length 406;  
Best Local Similarity 72.7%; Pred. No. 2,3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFPLXLRNGSLRXKCKXQCSFYXAEIFKDAARTKLFWISY 44  
Db 1 ANAFLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 44

RESULT 8  
US-08-475-845-2  
Sequence 2, Application US/08475845  
Patent No. 5788965  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,845  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-475-845-2

Query Match 82.7%; Score 158; DB 1; Length 444;  
Best Local Similarity 72.7%; Pred. No. 2,5e-18;

Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 ANAFPLXLRNGSLRXKCKXQCSFYXAEIFKDAARTKLFWISY 44  
Db 39 ANAFLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 82

RESULT 9  
US-08-327-690-2  
Sequence 2, Application US/08327690  
Patent No. 5817788  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-327-690-2

Query Match 82.7%; Score 158; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 2,5e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFPLXLRNGSLRXKCKXQCSFYXAEIFKDAARTKLFWISY 44  
Db 39 ANAFLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 82

RESULT 10  
US-08-660-289-2  
Sequence 2, Application US/08660289  
Patent No. 5833982  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.

```

; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
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; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match      82.7%; Score 158; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 2.5e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLKRCXKXCSFYXAEIIFKDXRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEKCQCSFEAREIFKDAERTKLFWISY 82

RESULT 11
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
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; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match      82.7%; Score 158; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 2.5e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLKRCXKXCSFYXAEIIFKDXRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEKCQCSFEAREIFKDAERTKLFWISY 82

RESULT 12
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-871-003-2

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|                       |              |                    |                | Gaps 0;     |

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QY      1 ANAFLLXLRNGSLRXCRXXQCSFXAEXIFKDAERTKLFWISY 44
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      39 ANAFLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 82

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1      RESULT 13
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3      : Sequence 2, Application US/08464233
4      : Patent No. 6039944
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Berkner, Kathleen L.
8      : APPLICANT: Petersen, Lars C.
9      : APPLICANT: Hart, Charles E.
10     : APPLICANT: Hedner, Ulla
11     : APPLICANT: Bregensgaard, Claus
12     : TITLE OF INVENTION: Modified Factor VII
13     :
14     : NUMBER OF SEQUENCES: 4
15     :
16     : CORRESPONDENCE ADDRESS:
17     : ADDRESS: Townsend and Townsend Kourile and Crew
18     : STREET: One Market Plaza, Stewart Street Tower
19     : CITY: San Francisco
20     : STATE: CA
21     : COUNTRY: U.S.A.
22     :
23     : ZIP: 94105-1492
24     :
25     : COMPUTER READABLE FORM:
26     : MEDIUM TYPE: Floppy disk
27     : COMPUTER: IBM PC compatible
28     : OPERATING SYSTEM: PC-DOS/MS-DOS
29     : SOFTWARE: Patentin Releasee #1.24
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33     :
34     : FILING DATE:
35     : CLASSIFICATION:
36     : PRIOR APPLICATION DATA:
37     : APPLICATION NUMBER: US/08/327,690
38     : FILING DATE: 24-OCT-1994
39     : APPLICATION NUMBER: 08/065,725
40     : FILING DATE: 21-MAY-1993
41     : CLASSIFICATION:
42     : PRIOR APPLICATION DATA:
43     : APPLICATION NUMBER: 07/662,920
44     : FILING DATE: 28-FEB-1991
45     : CLASSIFICATION:
46     : ATTORNEY/AGENT INFORMATION:
47     : NAME: Parmelee, Steven W.
48     : REGISTRATION NUMBER: 31,990
49     : REFERENCE/DOCKET NUMBER: 13952-8-3
50     : TELECOMMUNICATION INFORMATION:
51     : TELEPHONE: 206-467-9600
52     : TELEFAX: 415-543-5043
53     : INFORMATION FOR SEQ ID NO: 2:
54     : SEQUENCE CHARACTERISTICS:
55     : LENGTH: 444 amino acids
56     : TYPE: amino acid
57     : TOPOLOGY: linear
58     :
59     : MOLECULE TYPE: protein
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61     : US-08-464-233-2

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| Matches               | 32;    | Conservative       | 0;     | Mismatches 12; |
|                       |        |                    | Indels | 0;             |
|                       |        |                    | Gaps   | 0;             |

QY 1 ANAFLXXLRNCSLXRCKXQCSFXAEXIFKDAKRTKLFWISY 44  
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Db 39 ANAFLEELRPGSLERECKEEQCSFEAREIFKDAERTKLFWISY 82

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1      RESULT 14
2      US-09-189-607-2
3      Sequence 2, Application US/09189607
4      Patent No. 6168789
5      GENERAL INFORMATION:
6      APPLICANT: Berkner, Kathleen L.
7      APPLICANT: Petersen, Lars C.
8      APPLICANT: Hart, Charles E.
9      APPLICANT: Hedner, Ulla
10     APPLICANT: Bregengard, Claus
11     TITLE OF INVENTION: Modified Factor VII
12     NUMBER OF SEQUENCES: 4
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Townsend and Townsend Khourie and Crew
15     STREET: One Market Plaza, Steuart Street Tower
16     CITY: San Francisco
17     STATE: CA
18     COUNTRY: U.S.A.
19     ZIP: 94105-1492
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patentin Release #1.24
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/09/189,607
27     FILING DATE:
28     CLASSIFICATION:
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: 08/660,289
31     FILING DATE:
32     PRIOR APPLICATION DATA:
33     APPLICATION NUMBER: 08/327,690
34     FILING DATE:
35     PRIOR APPLICATION DATA:
36     APPLICATION NUMBER: 08/065,725
37     FILING DATE: 21-MAY-1993
38     CLASSIFICATION:
39     PRIOR APPLICATION DATA:
40     APPLICATION NUMBER: 07/662,920
41     FILING DATE: 28-FEB-1991
42     CLASSIFICATION:
43     ATTORNEY/AGENT INFORMATION:
44     NAME: Parmelee, Steven W.
45     REGISTRATION NUMBER: 31,990
46     REFERENCE/DOCKET NUMBER: 13952-8-4
47     TELECOMMUNICATION INFORMATION:
48     TELEPHONE: 206-467-9600
49     TELEFAX: 415-543-5043
50     INFORMATION FOR SEQ ID NO: 2:
51     SEQUENCE CHARACTERISTICS:
52     LENGTH: 444 amino acids
53     TYPE: amino acid
54     TOPOLOGY: linear
55     MOLECULE TYPE: protein
56     US-09-189-607-2

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| Query Match              | 82.7% | Score 158;         | DB 4;     | Length 444; |
| Best Local Similarity    | 72.7% | Pred. No. 2.5e-18; |           |             |
| Matches 32; Conservative | 0;    | Mismatches 12;     | Indels 0; | Gaps 0;     |

QY 1 ANAFLXXLRNGSLXRXCXXQCSFXXAEXIFKDAKRTKLFWISY 44  
39 ANAFLBELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 82  
Db

RESULT 15  
US-09-378-907-2  
; Sequence 2, Application US/09378907  
; Patent No. 6183743

/ GENERAL INFORMATION:  
/ APPLICANT: Hart, Charles E.  
/ APPLICANT: Petersen, Lars C.  
/ APPLICANT: Hedner, Ulla  
/ APPLICANT: Rasmussen, Mirella E.  
/ TITLE OF INVENTION: Modified Factor VII  
/ NUMBER OF SEQUENCES: 4  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Zymogenetics, Inc.  
/ STREET: 1201 Eastlake Avenue East  
/ CITY: Seattle  
/ STATE: WA  
/ COUNTRY: USA  
/ ZIP: 98102  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.24  
/ CURRENT APPLICATION DATA:  
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/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/871,003  
/ FILING DATE:  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Sawislak, Deborah A  
/ REGISTRATION NUMBER: 37,438  
/ REFERENCE/DOCKET NUMBER: 90-07C7  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 444 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-09-378-907-2

Query Match 82.7%; Score 158; DB 4; Length 444;  
Best Local Similarity 72.7%; Pred. No. 2.5e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXRLRNGSLKRXCKXXCSFXXAEXIFKDXARTLFWISY 44  
Db 39 ANAFLELRPGSLERBECKEQQCSFEAREIFKDXARTLFWISY 82

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Job time : 10.75 secs

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10ASN28GLU  
Perfect score: 191  
Sequence: 1 ANAFLXLLRNGSLRXCKXX.....XXAEXIFKDXRKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR 73: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
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| 5          | 100   | 52.4        | 461    | 1 S18994 | protein C (activat  |
| 6          | 98    | 51.3        | 488    | 1 EXHU   | coagulation factor  |
| 7          | 97    | 50.8        | 482    | 1 EXBO   | coagulation factor  |
| 8          | 92    | 48.2        | 482    | 1 EXRT   | coagulation factor  |
| 9          | 90    | 47.1        | 456    | 1 KXBO   | protein C (activat  |
| 10         | 87    | 45.5        | 475    | 1 EXCH   | coagulation factor  |
| 11         | 86    | 45.0        | 461    | 1 KXHU   | coagulation factor  |
| 12         | 84    | 44.0        | 632    | 1 TBHU   | thrombin (EC 3.4.2  |
| 13         | 81    | 42.4        | 416    | 1 KFB0   | coagulation factor  |
| 14         | 80    | 41.9        | 617    | 2 S10511 | thrombin (EC 3.4.2  |
| 15         | 80    | 41.9        | 618    | 2 A35827 | thrombin (EC 3.4.2  |
| 16         | 78    | 40.8        | 461    | 1 KFHU   | coagulation factor  |
| 17         | 73    | 38.2        | 452    | 1 A30351 | coagulation factor  |
| 18         | 73    | 38.2        | 459    | 2 J00419 | coagulation factor  |
| 19         | 69    | 34.0        | 642    | 2 S53433 | plasma protein S p  |
| 20         | 65    | 33.5        | 625    | 1 TBBO   | thrombin (EC 3.4.2  |
| 21         | 62    | 32.5        | 675    | 1 KXBO   | plasma protein S p  |
| 22         | 60    | 31.4        | 642    | 2 S53434 | plasma protein S p  |
| 23         | 60    | 31.4        | 646    | 2 S38819 | plasma protein S -  |
| 24         | 60    | 31.4        | 676    | 1 KXHU   | plasma protein S p  |
| 25         | 59    | 30.9        | 396    | 1 KXBO   | plasma protein Z -  |
| 26         | 59    | 30.9        | 675    | 1 KXRT   | plasma protein S p  |
| 27         | 57.5  | 30.1        | 576    | 2 G96763 | probable MAP kinase |
| 28         | 54    | 28.3        | 422    | 1 KXHU   | plasma protein Z p  |
| 29         | 52.5  | 27.5        | 594    | 2 D84859 | probable MAP kinase |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 52.5 | 27.5 | 603  | 2 C96575 | probable MAP kinase |
| 31 | 52   | 27.2 | 675  | 1 KXMS   | plasma protein S p  |
| 32 | 51   | 26.7 | 673  | 2 A48089 | growth arrest-spec  |
| 33 | 49   | 25.7 | 674  | 2 I55476 | growth potentialin  |
| 34 | 49   | 25.7 | 678  | 2 B48089 | growth arrest-spec  |
| 35 | 48   | 25.1 | 671  | 2 D96996 | uncharacterized lo  |
| 36 | 45   | 23.6 | 879  | 2 S55864 | hypothetical prote  |
| 37 | 44.5 | 23.3 | 1217 | 2 T21403 | hypothetical prote  |
| 38 | 44   | 23.0 | 413  | 1 VHVNH  | nucleoprotein - in  |
| 39 | 44   | 23.0 | 455  | 2 C81494 | probable 2-isoprop  |
| 40 | 43   | 22.5 | 1321 | 2 S27337 | multidrug resistan  |
| 41 | 43   | 22.5 | 1321 | 2 T23476 | hypothetical prote  |
| 42 | 42.5 | 22.3 | 319  | 2 T15137 | hypothetical prote  |
| 43 | 42.5 | 22.3 | 322  | 2 T20272 | hypothetical prote  |
| 44 | 42.5 | 22.3 | 410  | 2 T25574 | hypothetical prote  |
| 45 | 42.5 | 22.3 | 907  | 2 T15792 | hypothetical prote  |

#### ALIGNMENTS

##### RESULT 1

KFHU7  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1989 #sequence revision 19-May-1994 #text\_change 08-Dec-2000  
C:Accession: A28322; A23819; A31186; B31186; S63524  
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insoley, M.Y.; Hagen, F.S.; Murri  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A>Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende  
A:Reference number: A28322; PMID:87260948; PMID:3037537  
A:Accession: A28322  
A:Molecule type: DNA  
A:Residues: 1-466 <OH>  
A:Cross-references: GB:002933; NID:6180333; PIDN:AA51983.1; PID:6180334  
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A>Title: Characterization of a cDNA coding for human factor VII.  
A:Reference number: A23819; PMID:86205965; PMID:3486420  
A:Accession: A23819  
A:Molecule type: mRNA  
A:Residues: 1-466 <HAG>  
A:Cross-references: GB:M13232; NID:6182799; PIDN:AA88040.1; PID:6182801  
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.  
Biochemistry 27, 7785-7793, 1988  
A>Title: Amino acid sequence and posttranslational modifications of human factor VII-a fr  
A:Reference number: A90539; PMID:89088153; PMID:3264725  
A:Accession: A31186  
A:Molecule type: protein  
A:Residues: 213-466 <THI>  
A:Molecule type: protein  
A:Residues: 213-466 <THI>  
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wibeberg, F.C.; Christensen, M.; Komiyama, Y.; Peders  
J. Biol. Chem. 266, 11051-11057, 1991  
A>Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at  
A:Reference number: A40529; PMID:91250411; PMID:1304059  
R:Persson, E.; Petersen, L.C.  
Eur. J. Biochem. 234, 293-300, 1995  
A>Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy  
A:Reference number: S63524; PMID:96096752; PMID:8529655  
A:Accession: S63524  
A:Molecule type: protein  
A:Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>  
C:Genetics:  
A:Gene: GDB:F7  
A:Cross-references: GDB:119897; OMIM:227500  
A:Map position: 13q34-13q34  
A:Functions: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen  
coagulation factor IX in the presence of calcium and tissue factor

A;Pathway: blood coagulation extrinsic pathway  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-60/Domain: propeptide #status predicted <PRO>  
 F;45-104/Domain: Gla domain homology <GLA>  
 F;61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>  
 F;110-141/Domain: EGF homology <EG1>  
 F;151-187/Domain: EGF homology <EG2>  
 F;213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
 F;213-447/Domain: trypsin homology <TRY>  
 F;66-67-74-76-79-80-85-86-89-95/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F;77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,  
 F;112,120/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
 F;205,382/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F;212-213/Cleavage site: Arg-Tle (coagulation factor XIla) #status experimental  
 F;253,302,404/Active site: His, Asp, Ser #status predicted  
 F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 82.7%; Score 158; DB 1; Length 466;  
 Best Local Similarity 72.7%; Pred. No. 3.1e-19;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXKXCKXQCSFYXAEIFPDAXRTKLFWISY 44  
 Db 61 ANAFLEELRPGSLRECKEELCSFEAREIFPDARTKLFWISY 104

## RESULT 2

coagulation factor VII - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
 C;Accession: I46932  
 R;Brothers: A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.  
 Thromb. Res. 69, 231-238, 1993  
 A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
 A;Reference number: I46932; MUID:93190306; PMID:8383365  
 A;Accession: I46932  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-443 <BRO>  
 A;Cross-references: GB:S56300; NID:9266294; PID:9266295  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 F;24-83/Domain: Gla domain homology <GLA>  
 F;89-120/Domain: EGF homology <EG1>  
 F;130-166/Domain: EGF homology <EG2>  
 F;192-425/Domain: trypsin homology <TRY>

Query Match 64.9%; Score 124; DB 2; Length 443;  
 Best Local Similarity 54.5%; Pred. No. 2.2e-13;  
 Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXKXCKXQCSFYXAEIFPDAXRTKLFWISY 44  
 Db 40 ANAFLEELRPGSLRECKEELCSFEAREVFOSTERTKQFWISY 83

## RESULT 3

coagulation factor VIIa (EC 3.4.21.21) - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
 C;Accession: A31979; C20274  
 R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
 J. Biol. Chem. 263, 1868-1877, 1988  
 A;Title: Bovine factor VII. Its purification and complete amino acid sequence.  
 A;Reference number: A31979; MUID:89008362; PMID:3049594  
 A;Accession: A31979  
 A;Molecule type: protein  
 A;Residues: 1-407 <TAK>  
 R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1993  
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe  
 A;Reference number: A20274; MUID:83308813; PMID:6688526  
 A;Accession: C20274

A;Molecule type: protein

A;Residues: 58-62, 'X', 64-68 <MCM>

A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.

J. Biochem. 104, 867-868, 1988

A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagu

A;Reference number: A44566; MUID:89213999; PMID:3149637

A;Contents: annotation

A;Note: structure and location of covalently bound carbohydrate

C;Function:

A;Description: catalyzes the proteolytic activation of coagulation factor X in the preser

gulation factor IX in the presence of calcium and tissue factor

A;Pathway: blood coagulation extrinsic pathway

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F;1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F;50-81/Domain: EGF homology <EG1>

F;91-127/Domain: EGF homology <EG2>

F;153-387/Domain: trypsin homology <TRY>

F;6-7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F;17-22,50-61,55-61,55-70,72-81,91-102,99-112,114-127,135-262,159-164,178-194,310-329,340-368/I

F;52/Binding site: carboxylate (Ser) (covalent) #status experimental

F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental

F;145,203/Binding site: carboxylate (Asn) (covalent) #status experimental

F;152-153/Cleavage site: Arg-Tle (coagulation factor XIla) #status experimental

F;193,242,344/Active site: His, Asp, Ser #status predicted

F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 59.7%; Score 114; DB 1; Length 407;  
 Best Local Similarity 50.0%; Pred. No. 1.1e-11;  
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXKXCKXQCSFYXAEIFPDAXRTKLFWISY 44  
 Db 1 ANGFLEELRPGSLRECKEELCSFEAREIFRNERTRQFWISY 44

## RESULT 4

protein C (activated) (EC 3.4.21.69) precursor - mouse  
 N;Alternate names: vitamin K-dependent serine proteinase  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C;Accession: UX0210  
 R;Tada, N.; Sato, M.; Tanjima, A.; Iwase, R.; Hashimoto-Gotoh, T.  
 J. Biochem. 111, 491-495, 1992  
 A;Title: Isolation and characterization of a mouse protein C cDNA.  
 A;Reference number: UX0210; MUID:92316897; PMID:1618739  
 A;Accession: UX0210  
 A;Molecule type: mRNA  
 A;Residues: 1-461 <TAD>  
 A;Cross-references: GB:D10445; NID:9220385; PIDN:BA401235.1; PID:9220386  
 A;Experimental source: liver  
 A;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg  
 B.  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F;1-33/Domain: signal sequence #status predicted <SIG>  
 F;27-85/Domain: Gla domain homology <GLA>  
 F;334-41/Domain: propeptide #status predicted <PRO>  
 F;42-196,199-461/Product: protein C #status predicted <PRC>  
 F;91-130/Domain: EGF homology <EG1>  
 F;139-174/Domain: EGF homology <EG2>  
 F;199-461/Domain: heavy chain #status predicted <PCH>  
 F;199-211/Domain: activation peptide #status predicted <ACT>  
 F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>



F:212-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,166-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
 F:214,290,355/Binding site: carbonyl (Asn) (covalent) #status predicted  
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 52.9%; Score 101; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 2,2e-09;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRXCCKXXQCSEFXAEXIFKDXARTLFWISY 44  
 Db 42 ANSFLFEMRPGSLERECMEICDFEAEQEIFQNVEDTLAFWIKY 85

RESULT 5  
 S18994  
 protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
 C:Accession: S18994; S24312  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 submitted to the EMBL Data Library, February 1992  
 A:Description: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S18994

A:Accession: S18994  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OKA>  
 A:Cross-references: EMBL:X64336; NID:956962; PIDN:CAA5617.1; PID:956963  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 Biochim. Biophys. Acta 1131, 329-332, 1992  
 A:Title: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OKA2>  
 A:Cross-references: EMBL:X64336; NID:956962; PIDN:CAA5617.1; PID:956963  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:37-85/Domain: Gla domain homology <GLA>  
 F:33-42/Domain: propeptide #status predicted <PRO>  
 F:43-461/Product: protein C #status predicted <PRC>  
 F:91-130/Domain: EGF homology <EG1>  
 F:139-174/Domain: EGF homology <EG2>  
 F:213-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat  
 F:215,291,355/Binding site: carbonyl (Asn) (covalent) #status predicted  
 F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 52.4%; Score 100; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 3,2e-09;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRXCCKXXQCSEFXAEXIFKDXARTLFWISY 44  
 Db 42 ANSFLFEMRPGSLERECMEICDFEAEQEIFQNVEDTLAFWIKY 85

RESULT 6  
 EXHU  
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

C:Species: Homo sapiens (man)  
 N:Alternate names: Stuart factor  
 C:Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
 C:Accession: A24478; J00917; A24453; A25853; A22208; A21284; A20362; S39415; I54051; A00  
 R:Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
 Biochemistry 25, 5098-5102, 1986

A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization is

A:Reference number: A24478; MUID:87026600; PMID:3768336

A:Accession: A24478

A:Molecule type: DNA

A:Residues: 1-488 <LEY>

A:Cross-references: GB:I29433; GB:M14327; NID:945809; PIDN:AA52764.1; PID:9182831

R:Meslier, T.L.; Piltman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag

A:Reference number: J00917; MUID:91216473; PMID:1802434

A:Accession: J00917

A:Molecule type: mRNA

A:Residues: 1-488 <MES>

A:Cross-references: GB:M57285; NID:9182389; PIDN:AA52421.1; PID:9182390

R:Mao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A:Title: Liver-specific expression of the gene coding for human factor X, a blood coagul

A:Reference number: A42485; MUID:92218390; PMID:1313796

A:Accession: A42485

A:Molecule type: DNA

A:Residues: 1-15 <MA>

A:Experimental source: liver

A:Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)

R:Xu, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A:Reference number: A25853; MUID:86221713; PMID:3011603

A:Accession: A25853

A:Molecule type: mRNA

A:Residues: 19-284, E', 289-488 <XAU>

A:Cross-references: GB:M2613; NID:9180335; PIDN:AA51984.1; PID:9180336

R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulat

A:Reference number: A22208; MUID:85216545; PMID:2582420

A:Accession: A22208

A:Molecule type: mRNA

A:Residues: 13-441, S', 443-488 <FUN>

A:Cross-references: GB:K03194; NID:9182840; PIDN:AA52490.1; PID:9182841

R:Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A:Title: Characterization of a cDNA coding for human factor X.

A:Reference number: A21284; MUID:84222026; PMID:6587384

A:Accession: A21284

A:Molecule type: mRNA

A:Residues: 13-284, E', 289-488 <LE2>

A:Cross-references: GB:K0186

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Saeagawa, T.; Howald, W.N.; Kwa, E.Y.; Weinstein

Biochemistry 22, 2875-2884, 1983

A:Title: Complete amino acid sequence of the light chain of human blood coagulation fact

A:Reference number: A20362; MUID:83257207; PMID:6871167

A:Accession: A20362

A:Molecule type: protein

A:Residues: 41-179 <MCM>

A:Note: glycosylation sites

A:Note: identification and characterization of beta-hydroxyaspartic acid

R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabunham, K.; Lyman, G.

Gene 84, 517-519, 1989

A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human

A:Reference number: I54051; MUID:90128299; PMID:2612918

A:Accession: I54051

A:Status: translation not shown; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-23 <RBS>

A:Cross-references: GB:M33297; NID:918360; PIDN:AA52636.1; PID:9553330

R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blau

J. Mol. Biol. 232, 947-966, 1993  
 A:Title: Structure of human des(1-45) Factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A49458; PMID:93360277; PMID:8355279  
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 C:Genetics:  
 A:Gene: GDB:F10  
 A:Cross-references: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A>Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:41-179/Domain: Gla domain homology <Gla>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:235-234/Domain: activation peptide #status experimental <APT>  
 F:235-462/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
 F:57-62/Disulfide bonds: #status predicted  
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:224-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 51.3%; Score 98; DB 1; Length 488;  
 Best Local Similarity 38.6%; Pred. No. 7.5e-09;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLRNGSLXRXKXQCSFYXAEKIFDKARXKLFWISY 44  
 Db 41 ANSFLBKKKGLHRECMETCSYEBARVEFDSKTFEWMKY 84

RESULT 7  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; MUID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FUN>  
 A:Cross-references: CB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Tiliat, K.  
 Biochemistry 19, 659-667, 1980  
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, N, 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:8330813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Tiliat, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:7605069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-282,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKRG', 446-492 <T  
 A>Note: carbohydrate binding sites and disulfide bonds were determined  
 R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; MUID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A>Note: beta-hydroxyaspartic acid site  
 R:Pinou, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196,199-209,216-233 <INO>  
 A>Note: carbohydrate binding sites  
 R:Tiliat, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; De  
 Biochemistry 11, 4899-4903, 1972  
 A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
 A:Reference number: A12453; MUID:79053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Tiliat, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to f  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Sugo, T.; Björk, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic  
 A:Reference number: A38024; MUID:84185716; PMID:6546930  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of two  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), or  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stron  
 C:Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin  
 C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:41-84/Domain: Gla domain homology <Gla>  
 F:91-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:235-233/Domain: activation peptide #status experimental <APT>  
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:234-461/Domain: trypsin homology <TRY>  
 F:46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #s  
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status p  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:208,485/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat

F:240-245,260-276,389-403,414-442/Dileulfide bonds: #status experimental  
F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 50.8%; Score 97; DB 1; Length 492;  
Best Local Similarity 40.9%; Pred. No. 1,1e-08;  
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLKRXCKXQCSFXXAEXIFPKDARTKLFWISY 44  
Db 41 ANSFLEEVKQGNLERECLEBACSLFEARVEFEDAEQTDERSKY 84

## RESULT 8

EXRT  
coagulation factor Xa (EC 3.4.21.6) precursor - rat

C/Species: Rattus norvegicus (Norway rat)  
C/Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #text\_change 08-Dec-2000  
C/Accession: S49075; J04670; PS0191; PS0190; I62745  
R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Thromb. Res. 80, 63-73, 1995

A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra

A/Reference number: A58498; M0ID:96093366; PMID:8578539

A/Accession: S49075

A/Molecule type: mRNA

A/Residues: 1-482 <STA1>

A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAAS6202.1; PID:G506601

A/Note: Submitted to the EMBL Data Library, June 1994

A/Note: neither the complete nucleic acid sequence nor the complete translation are shown

R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Gene 169, 269-273, 1996

A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.

A/Reference number: J04670; M0ID:96194815; PMID:8647460

A/Accession: J04670

A/Molecule type: mRNA

A/Residues: 1-482 <STA2>

A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAAS6202.1; PID:G506601

A/Experimental source: Cos-1 cell

R/Enjyoji, K.; Miyazaki, K.; Kato, H.

A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma

A/Reference number: PS0190; M0ID:92041742; PMID:1718949

A/Accession: PS0191

A/Molecule type: protein

A/Residues: 41-58 'X', 60-65 <ENJ1>

A/Accession: PS0190

A/Molecule type: protein

A/Residues: 183-186, 'X', 188-207 <ENJ2>

R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Nihou, Y.  
Eur. J. Haematol. 52, 162-168, 1994

A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of

A/Reference number: I46196; M0ID:94222160; PMID:8168596

A/Accession: I62745

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 295-383, 'G', 385-455 <MUR>

A/Cross-references: GB:D21215; NID:G415309; PIDN:BA04756.1; PID:G455336

C/Function:

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic

F:1-23/Domain: signal sequence #status predicted <PRO>

F:24-40/Domain: propeptide #status predicted <PRO>

F:41-179/Domain: Gla domain homology <GLA>

F:183-482/Domain: EGF homology <EGF>

F:129-164/Domain: EGF homology <EG2>

F:183-482/Domain: coagulation factor X heavy chain #status predicted <HCN>

F:183-482/Domain: activation peptide #status predicted <ACT>

F:232-482/Domain: coagulation factor Xa heavy chain #status predicted <ACT>

F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:187/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted  
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 48.2%; Score 92; DB 1; Length 482;  
Best Local Similarity 38.6%; Pred. No. 8e-08;  
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLKRXCKXQCSFXXAEXIFPKDARTKLFWISY 44  
Db 41 ANSFLEEVKQGNLERECLEBACSLFEARVEFEDAEQTDERSKY 84

## RESULT 9

KXBO

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N/Alternate names: autoprothrombin IIA; plasma protein C

C/Species: Bos primigenius taurus (cattle)

C/Date: 30-Nov-1980 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999

C/Accession: A26250; A18385; A18386; A00928

R/Long, G.L.; Balagaje, R.M.; Macgillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A/Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A/Reference number: A26250; M0ID:85014826; PMID:6091100

A/Accession: A26250

A/Molecule type: mRNA

A/Residues: 1-456 <LON>

R/Fernlund, P.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982

A/Title: Amino acid sequence of the light chain of bovine protein C.

A/Reference number: A18385; M0ID:83007325; PMID:6696876

A/Accession: A18385

A/Molecule type: protein

A/Residues: 40-194 <FER>

A/Note: 82-Lys was also found

R/Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A/Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.

A/Reference number: A19316; M0ID:83169769; PMID:6572939

A/Contents: annotation; revision to residue 110

R/Stenflo, J.; Fernlund, P.

J. Biol. Chem. 257, 12180-12190, 1982

A/Title: Amino acid sequence of the heavy chain of bovine protein C.

A/Reference number: A18386; M0ID:83007326; PMID:6696877

A/Accession: A18386

A/Molecule type: protein

A/Residues: 197-454, 'PV' <STE>

R/Beson, N.L.; DeBault, L.B.; Beson, C.T.

J. Biol. Chem. 258, 5548-5553, 1983

A/Title: Proteolytic formation and properties of gamma-carboxylglutamic acid-domainless protein C

A/Reference number: A37541; M0ID:83213513; PMID:6404092

A/Contents: annotation; activation; calcium binding

R/Johnson, A.B.; Beson, N.L.; Laue, T.M.; Beson, C.T.

J. Biol. Chem. 258, 5554-5560, 1983

A/Title: Structural changes required for activation of protein C are induced by Ca2+ and

A/Reference number: A37542; M0ID:83213514; PMID:6406503

A/Contents: annotation; activation; calcium binding

C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

B/Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved

C/Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with strong

C/Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding;

F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>

F:24-83/Domain: Gla domain homology <GLA>

F:30-39/Domain: propeptide #status predicted <PRO>

F:40-194/Product: protein C light chain #status experimental <LCH>

```
F;98-128/Domain: EGF homology <EG1>
F;137-172/Domain: EGF homology <EG2>
F;197-456/Product: protein C heavy chain #status experimental <HCH>
F;197-210/Domain: activation peptide #status experimental <APr>
F;211-440/Domain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;119-128,137-148,144-157,180-318,237-253,368-382,393-421/Disulfide bonds: #stat
F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222,298,397/Active site: His, Asp, Ser #status predicted
F;366/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match          47.1% Score 90; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 1.7e-07;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRNGSLRXKCKXKXCFXKXAEIPKDAKRTKLFWISY 44
Db 40 ANSFLEELRPGNVERECSEVECFEAREIFONTEDTMAFWISFY 83

RESULT 10
EXCH
Coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N/Alternate names: virus-activating proteinase
C/Species: Gallus gallus (chicken)
C/Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
C/Accession: S15838; S20380; S20381
R/Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotch, B.; Ogasawara, T.; Na
FEBS Lett. 283, 281-285, 1991
A/Title: Primary structure of the virus activating protease from chick embryo. Its ident
A/Reference number: S15838; MUID:91257322; PMID:2044767
A/Accession: S15838
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-475 <SUZ>
A/Cross-references: DDBJ:D00844; NID:G222869; PIDN:BA00724.1; PID:G222870
R/Gotch, B.; Yamachi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A/Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A/Reference number: S20380; MUID:92164779; PMID:1537403
A/Accession: S20380
A/Molecule type: protein
A/Residues: 41-55 <GOZ>
A/Accession: S20381
A/Molecule type: protein
A/Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
C/Function:
A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A/Pathway: blood coagulation
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan
F;1-20/Domain: signal sequence #status predicted <PRO>
F;21-40/Domain: propeptide #status predicted
F;25-84/Domain: Gla domain homology <GLA>
F;41-181/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-167/Domain: EGF homology <EG2>
F;166-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F;186-240/Domain: activation peptide #status predicted <APr>
F;241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;241-468/Domain: trypsin homology <TRY>
F;46,47,54,55,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #
F;57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;281,328,425/Active site: His, Asp, Ser #status predicted

Query Match          45.5% Score 87; DB 1; Length 475;
Best Local Similarity 36.4%; Pred. No. 5.8e-07;
Matches 16; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRNGSLRXKCKXKXCFXKXAEIPKDAKRTKLFWISY 44
```

```
Db 41 ANSFLEEMKQNIERECNEERCSKEAREATEDNEKTEEFNNITY 84

RESULT 11
KXHU
protein C (activated) (EC 3.4.21.69) precursor - human
N/Alternate names: autoprothrombin IIa; plasma protein C
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C/Accession: A22311; A25426; A21781; A23789; A00927
R/Foster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A/Title: The nucleotide sequence of the gene for human protein C.
A/Reference number: A22311; MUID:85270390; PMID:2991887
A/Accession: A22311
A/Molecule type: DNA
A/Residues: 1-461 <FOS1>
A/Cross-references: GB:M1228; NID:G190333; PIDN:AAA60166.1; PID:G190334
R/Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A/Title: Evolution and organization of the human protein C gene.
A/Reference number: A25426; MUID:86120978; PMID:3511471
A/Accession: A25426
A/Molecule type: DNA
A/Residues: 1-445, 'L', 446-461 <PLU>
A/Cross-references: GB:M12712; NID:G190330; PIDN:AAA60165.1; PID:G190332
R/Foster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A/Title: Characterization of a cDNA coding for human protein C.
A/Reference number: A21781; MUID:84272714; PMID:6589623
A/Accession: A21781
A/Molecule type: mRNA
A/Residues: 'Q', 107-461 <FOS2>
A/Cross-references: GB:X02059; NID:G190322; PIDN:AAA60164.1; PID:G190323
R/Beckmann, R.J.; Schmidt, R.J.; Senterre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A/Title: The structure and evolution of a 461 amino acid human protein C precursor and it
A/Reference number: A23789; MUID:85269639; PMID:2991859
A/Accession: A23789
A/Molecule type: protein
A/Residues: 1-461 <BEC>
A/Cross-references: GB:X02750; NID:G35689; PIDN:CAA26528.1; PID:G763120
R/Miletiich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A/Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
A/Reference number: A44605; MUID:90293094; PMID:1694179
A/Contents: annotation; carbohydrate binding sites; activation peptide
A/Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R/Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A/Title: O-linked fucose is present in the first epidermal growth factor domain of factor
A/Reference number: A44606; MUID:92184750; PMID:1544894
A/Contents: annotation; beta-hydroxyaspartic acid
C/Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that in
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also it
C/Comment: protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C/Genetics:
A/Gene: GDB:PROC
A/Cross-references: GDB:120317; OMIM:176860
A/Map position: 2q13-q21
A/Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C/Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F;1-32/Domain: signal sequence #status predicted <PRO>
F;127-86/Domain: propeptide #status predicted <APr>
F;33-42/Domain: Gla domain homology <GLA>
F;43-197/Product: protein C light chain #status predicted <LCH>
F;92-131/Domain: EGF homology <EG1>
F;140-175/Domain: EGF homology <EG2>
F;200-461/Product: protein C heavy chain #status predicted <HCH>
F;200-211/Domain: activation peptide #status experimental <APr>
```

F:212-445/Domain: trypsin homology <TRY>  
 F:48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D  
 F:106-111/Disulfide bonds: #status predicted  
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent  
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
 F:253,299,402/Active site: His, Asp, Ser #status predicted  
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 45.0%; Score 86; DB 1; Length 461;  
 Best Local Similarity 43.9%; Pred. No. 8,4e-07;  
 Matches 18; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFXXLRNGSLXRXKXQCSFXAXEIPKDXRKLFW 41  
 DB 43 ANSFLELRHSLRECEIEICDFEAKEIFQNVDDTLAFW 83

RESULT 12

thrombin (EC 3.4.21.5) precursor [validated] - human  
 N:Alternate names: coagulation factor II  
 N:Contains: prothrombin  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000  
 C:Accession: A29351, A00914, B00914; A37549; A37550; I51952  
 R:Degen, S.J.F.; Davie, E.W.  
 Biochemistry 26, 6165-6177, 1987  
 A>Title: Nucleotide sequence of the gene for human prothrombin.  
 A:Reference number: A29351; MUID:88077877; PMID:2825773  
 A:Accession: A29351  
 A:Molecule type: DNA  
 A:Residues: 1-622 <DEG>  
 A:Cross-references: GB:M17262; GB:M33691; NID:G558069; PIDN:CAAC63054.1; PID:G339641  
 R:Degen, S.J.F.; Macgillivray, R.T.A.; Davie, E.W.  
 Biochemistry 22, 2087-2097, 1983  
 A>Title: Characterization of the complementary deoxyribonucleic acid and gene coding for  
 A:Reference number: A00914; MUID:83231465; PMID:6305407  
 A:Molecule type: mRNA  
 A:Residues: 8-163, 'N', 165-622 <DEG>  
 A:Cross-references: GB:V00595; GB:J00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344  
 A:Accession: B00914  
 A:Molecule type: DNA  
 A:Residues: 188-311 <DE3>  
 R:Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.  
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977  
 A:Reference number: A37549; MUID:77193964; PMID:266717  
 A:Accession: A37549  
 A:Molecule type: protein  
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'W', 196-308,  
 R:Butkowsk, R.U.; Elion, J.; Downing, M.R.; Mann, K.G.  
 J. Biol. Chem. 252, 4942-4957, 1977  
 A>Title: Primary structure of human prothrombin 2 and alpha-thrombin.  
 A:Reference number: A37550; MUID:77207112; PMID:873923  
 A:Accession: A37550  
 A:Molecule type: protein  
 A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-  
 R:Rabiet, M.J.; Blaisbail, A.; Furie, B.; Furie, B.C.  
 J. Biol. Chem. 261, 13210-13215, 1986  
 A:Reference number: A37551; MUID:87008532; PMID:3759958  
 A:Content: annotation; activation cleavages  
 R:Macgillivray, R.T.; Irwin, D.M.; Guinot, E.R.; Stone, J.C.  
 Ann. N.Y. Acad. Sci. 485, 73-79, 1986  
 A>Title: Recombinant genetic approaches to functional mapping of thrombin.  
 A:Reference number: I51952; MUID:87182874; PMID:3471151  
 A:Accession: I51952  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2, 'R', 5-100 <RES>  
 A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724

C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds  
 C:Comment: can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain  
 ter 314-Arg, are released in natural blood clotting.  
 C:Comment: The cleavage after Arg-199, observed in vitro, does not occur in plasma.  
 C:Comment: The gamma-carboxyglutamy 1 residues bind calcium ions, result from the carboxy)  
 ent interaction with the negatively charged phospholipid membrane surface.  
 C:Comment: The prothrombin precursor is synthesized in the liver.  
 C:Genetic:  
 A:Gene: GDB:F2  
 A:Cross-references: GDB:119894; OMIM:176930  
 A:Map position: 11p11-11q12  
 A:Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplic  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-43/Domain: propeptide #status predicted <PRO>  
 F:44-622/Domain: Gla domain homology <Gla>  
 F:44-622/Product: prothrombin #status experimental <MAT>  
 F:108-186/Domain: activation peptide #status experimental <AP>  
 F:213-291/Domain: kringle homology <KR1>  
 F:328-363/Product: thrombin light chain #status experimental <LCH>  
 F:364-622/Product: thrombin heavy chain #status experimental <HCH>  
 F:364-613/Domain: trypsin homology <TRY>  
 F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status  
 F:121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:336-482,536-550,564-594/Disulfide bonds: #status predicted  
 F:331-407/Disulfide bonds: #status experimental  
 F:406,462/Active site: His, Asp #status predicted  
 F:416/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:568/Active site: Ser #status experimental

Query Match 44.0%; Score 84; DB 1; Length 622;  
 Best Local Similarity 36.4%; Pred. No. 2,5e-06;  
 Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANAFXXLRNGSLXRXKXQCSFXAXEIPKDXRKLFWISY 44  
 DB 44 ANTFLEVRKGNLRECEVETCSYEAFEALESSTATVPMWAKY 87

RESULT 13

KFBO  
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
 N:Alternate names: Christmas factor  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999  
 C:Accession: A14757; B20274; I45891; A00923  
 R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neutath, H.; Davie, E.W.; Tit  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
 A>Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac  
 A:Reference number: A14757; MUID:80056619; PMID:291916  
 A:Accession: A14757  
 A:Molecule type: protein  
 A:Residues: 1-63, 'T', 65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6588526  
 A:Accession: B20274  
 A:Molecule type: protein  
 A:Residues: 59-63, 'X', 65-69 <MCM>  
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
 Nature 299, 178-180, 1982  
 A>Title: Molecular cloning of the gene for human anti-haemophilic factor IX.  
 A:Reference number: I45891; MUID:82272386; PMID:6287289  
 A:Accession: I45891  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 52-139 <CHO>  
 A:Cross-references: GB:J00007; NID:G163053; PIDN:AAA30520.1; PID:G163054

R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988  
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag  
 A:Reference number: A44556; MUID:89213999; PMID:3149637  
 A:Contents: annotation  
 A:Note: structure and location of a carbohydrate covalently bound to Ser  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
 A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan  
 F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:1-45/Domain: Gla domain homology (fragment) <GLA>  
 F:51-82/Domain: EGF homology <EG1>  
 F:88-124/Domain: EGF homology <EG2>  
 F:147-181/Domain: activation peptide #status experimental <AP1>  
 F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:182-409/Domain: trypsin homology <TRY>  
 F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #sta  
 F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide  
 F:53/Binding site: carbonyl-ate (Ser) (covalent) #status experimental  
 F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:158,168,173,261/Binding site: carbonyl-ate (Asn) (covalent) #status experimental  
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 42.4%; Score 81; DB 1; Length 416;  
 Best Local Similarity 41.2%; Pred. No. 5.5e-06;  
 Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSIXRCKXKXQCSFXAXEYFDKARTKLFWISY 44  
 Db 12 GNLEBECKEKCSFEARVFEKTEKTFMCOY 45

RESULT 14

S10511  
 Chrombin (EC 3.4.21.5) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-May-1993 #sequence revision 07-May-1993 #text\_change 03-May-2002  
 C:Accession: S10511; A60576; B42696  
 R:Dihaich, M.; Monard, D.  
 Nucleic Acids Res. 18, 4251, 1990  
 A:Title: cDNA sequence of rat prothrombin.  
 A:Reference number: S10511; MUID:90332426; PMID:2377469  
 A:Accession: S10511  
 A:Molecule type: mRNA  
 A:Residues: 1-617 <DIR>  
 A:Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970  
 R:Henrikson, K.P.; Jasin, E.E.; Greenwood, J.A.; Dickerman, H.W.  
 Endocrinology 126, 167-175, 1990  
 A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.  
 A:Reference number: A60576; MUID:90091942; PMID:2293980  
 A:Accession: A60576  
 A:Molecule type: protein  
 A:Residues: 44-58 <HEN>  
 A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute  
 R:Banfield, D.K.; Macgillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: B42696  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 383-617, 'E', <BAN>  
 A:Cross-references: GB:M81397  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:125-43/Domain: signal sequence #status predicted <PRO>  
 F:128-88/Domain: Gla domain homology <GLA>

F:44-617/Product: prothrombin #status experimental <PMAT>  
 F:109-187/Domain: kringle homology <KR1>  
 F:215-292/Domain: kringle homology <KR2>  
 F:360-609/Domain: trypsin homology <TRY>  
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status i  
 F:61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5  
 F:402,458,564/Active site: His, Asp, Ser #status predicted

Query Match 41.9%; Score 80; DB 2; Length 617;  
 Best Local Similarity 37.2%; Pred. No. 1.2e-05;  
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

OY 2 NAFLLXNLNGSLXKXKXQCSFXAXEYFDKARTKLFWISY 44  
 Db 46 SGFLERKGNLRECVBEQCSYBEAFALSPQDTDFVMKX 88

RESULT 15

Chrombin (EC 3.4.21.5) precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text\_change 03-May-2002  
 C:Accession: A35827; A42696; S12081  
 R:Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J.A.,  
 DNA Cell Biol. 9, 487-498, 1990  
 A:Title: Characterization of the cDNA coding for mouse prothrombin and localization of tr  
 A:Reference number: A35827; MUID:91025551; PMID:2222810  
 A:Accession: A35827  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-618 <DSG>  
 A:Cross-references: GB:X53308; NID:953813; PIDN:CAA36548.1; PID:953814  
 A:Experimental source: strain C57BL/6  
 A:Note: the data were obtained from females resulting from the cross of M. domesticus and  
 R:Banfield, D.K.; Macgillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: A42696  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 384-618, 'E', <BAN>  
 A:Cross-references: GB:M81394  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:125-43/Domain: propeptide #status predicted <PRO>  
 F:128-88/Domain: Gla domain homology <GLA>  
 F:44-618/Product: prothrombin B #status predicted <MAT>  
 F:109-187/Domain: kringle homology <KR1>  
 F:215-293/Domain: kringle homology <KR2>  
 F:361-610/Domain: trypsin homology <TRY>  
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status i  
 F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5  
 F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 41.9%; Score 80; DB 2; Length 618;  
 Best Local Similarity 37.2%; Pred. No. 1.2e-05;  
 Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

OY 2 NAFLLXNLNGSLXKXKXQCSFXAXEYFDKARTKLFWISY 44  
 Db 46 SGFLERKGNLRECVBEQCSYBEAFALSPQDTDFVMKX 88

Search completed: March 19, 2003, 15:00:49  
 Job time : 31.125 secs

GenCore version 5.1.4 p5.4578  
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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)  
328.082 Million cell updates/sec

Title: 10ASN28GLU  
Perfect score: 191  
Sequence: 1 ANAFLLXLRNGSLXRXCKXX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 158   | 82.7        | 466    | FA7_HUMAN  | P08709 homo sapien |
| 2          | 124   | 64.9        | 444    | FA7_RABIT  | P08139 oryctolagus |
| 3          | 114   | 59.7        | 407    | FA7_BOVIN  | P22457 bos taurus  |
| 4          | 113   | 59.2        | 446    | FA7_MOUSE  | P70375 mus musculu |
| 5          | 101   | 52.9        | 461    | PRTC_MOUSE | P3587 mus musculu  |
| 6          | 100   | 52.4        | 459    | PRTC_PIG   | Q93162 sus scrofa  |
| 7          | 100   | 52.4        | 461    | PRTC_RAT   | P31394 rattus norv |
| 8          | 98    | 51.3        | 488    | FA10_HUMAN | P00742 homo sapien |
| 9          | 98    | 51.3        | 490    | FA10_RABIT | O19045 oryctolagus |
| 10         | 97    | 50.8        | 492    | FA10_BOVIN | P00743 bos taurus  |
| 11         | 95    | 49.7        | 218    | TMG1_HUMAN | O14668 homo sapien |
| 12         | 90    | 47.1        | 456    | PRTC_BOVIN | P00745 bos taurus  |
| 13         | 88    | 46.1        | 231    | TMG3_HUMAN | Q92427 homo sapien |
| 14         | 87    | 45.5        | 475    | FA10_CHICK | P25155 gallus gall |
| 15         | 86    | 45.0        | 461    | PRTC_HUMAN | P04070 homo sapien |
| 16         | 84    | 44.0        | 458    | PRTC_RABIT | O28661 oryctolagus |
| 17         | 84    | 44.0        | 622    | THRB_HUMAN | P00734 homo sapien |
| 18         | 81    | 42.4        | 416    | FA9_BOVIN  | P00741 bos taurus  |
| 19         | 80    | 41.9        | 617    | THRB_RAT   | P18232 rattus norv |
| 20         | 80    | 41.9        | 618    | THRB_MOUSE | P19221 mus musculu |
| 21         | 78    | 40.8        | 376    | FA10_TROCA | P14488 tropidochis |
| 22         | 78    | 40.8        | 461    | FA9_HUMAN  | P00740 homo sapien |
| 23         | 75    | 39.3        | 202    | TMG2_HUMAN | O14669 homo sapien |
| 24         | 73    | 38.2        | 452    | FA9_CANFA  | P19540 canis fami  |
| 25         | 73    | 38.2        | 459    | FA9_MOUSE  | P16294 mus musculu |
| 26         | 69    | 36.1        | 226    | TMG4_HUMAN | Q92426 homo sapien |
| 27         | 64    | 33.5        | 625    | THRB_BOVIN | P00735 bos taurus  |
| 28         | 62    | 32.5        | 675    | PRTC_BOVIN | P07224 bos taurus  |
| 29         | 60    | 31.4        | 646    | PRTC_RABIT | P08118 oryctolagus |
| 30         | 60    | 31.4        | 649    | PRTC_MACMU | Q28520 macaca mula |
| 31         | 60    | 31.4        | 676    | PRTC_HUMAN | P07225 homo sapien |
| 32         | 59    | 30.9        | 396    | PRT2_BOVIN | P00744 bos taurus  |
| 33         | 59    | 30.9        | 675    | PRTS_RAT   | P53813 rattus norv |

|    |      |      |      |   |            |                    |
|----|------|------|------|---|------------|--------------------|
| 34 | 54   | 28.3 | 400  | 1 | PRTZ_HUMAN | P22891 homo sapien |
| 35 | 52   | 27.2 | 675  | 1 | PRTS_MOUSE | Q08761 mus musculu |
| 36 | 45   | 23.6 | 353  | 1 | MLJA_CHICK | P49285 gallus gall |
| 37 | 45   | 23.0 | 879  | 1 | YN65_YEAST | P42837 saccharomyc |
| 38 | 44   | 23.0 | 413  | 1 | NCAP_HINV  | P19691 infectious  |
| 39 | 43   | 22.5 | 1321 | 1 | MDR1_CAEEL | P34712 caenorhabdi |
| 40 | 42.5 | 22.3 | 322  | 1 | YQJ3_CAEEL | Q09292 caenorhabdi |
| 41 | 42   | 22.0 | 263  | 1 | PFJA_STRMU | O68575 streptococc |
| 42 | 42   | 22.0 | 818  | 1 | CD81_HUMAN | Q9Y5F3 homo sapien |
| 43 | 41.5 | 21.7 | 1290 | 1 | BXB_CLOBO  | P10844 clostridium |
| 44 | 40.5 | 21.2 | 356  | 1 | MURB_BUCAL | P57153 buchnera ap |
| 45 | 40   | 20.9 | 341  | 1 | MURB_PASMU | P57952 pasteurella |

## ALIGNMENTS

RESULT 1  
ID FA7\_HUMAN STANDARD; PRT; 466 AA.  
AC P08709; Q14339;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
conversion accelerator) (Eptacog alfa).  
GN F7.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86205965; PubMed=3486420;  
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
RA Woodbury R.G., Hart C.E., Insley M.Y., Kissel W., Kurachi K.,  
RA Davie E.W.;  
RT "Characterization of a cDNA coding for human factor VII";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87260948; PubMed=3037537;  
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
RA Hagen F.S., Murray M.J.;  
RT "Nucleotide sequence of the gene coding for human factor VII, a  
vitamin K-dependent protein participating in blood coagulation";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.  
RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
RA Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=89088153; PubMed=3264725;  
RA Thim L., Bjern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
RA Pedersen A.H., Hedner U.;  
RT "Amino acid sequence and posttranslational modifications of human  
factor VIIa from plasma and transfected baby hamster kidney cells";  
RL Biochemistry 27:7785-7793(1988).  
RN [5]  
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
RX MEDLINE=91250411; PubMed=1904059;  
RA Bjorn S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,  
RA Komiyama Y., Pedersen A.H., Kissel W.;  
RT "Human plasma and recombinant factor VII. Characterization of O-  
glycosylations at serine residues 52 and 60 and effects of site-  
directed mutagenesis of serine 52 to alanine";  
RL J. Biol. Chem. 266:11051-11057(1991).  
RN [6]  
RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
RX MEDLINE=9062160; PubMed=2511201;



RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [17]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=8598903; Winkler F.K., Guha A.,  
 RA Banner D.W., D'Arcy A., Chene C., Kirchofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RL Nature 380:41-46(1996).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=9925787;  
 RA Zhang B., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPTI mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=96367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gipeert G.P., Forsen S., Steinflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Mede T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patraccini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferrati M., Patraccini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 RT (115His and 333Ser) in the human coagulation factor VII gene.";  
 RL Hum. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lunley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;  
 RA Chating S., Clarke B., Sridhara S., Chu K., Friedman P., Vanhusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MET HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";  
 RL Thromb. Haemost. 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arfani A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferrarese P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,  
 RA Zatzov R., Seligsohn U.;  
 RT "A1a244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN [21]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:5189-5191(1998).  
 CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR Xa, FACTOR XIa, FACTOR IXa, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to  
 CC form factor Xa.  
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -I- TISSUE SPECIFICITY: PLASMA.  
 CC -I- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -I- PHARMACEUTICAL: Available under the names Niasase or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in



Query Match 82.7%; Score 158; DB 1; Length 466;  
Best Local Similarity 72.7%; Pred. No. 4.1e-20;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRXCKXXQCSFXXAEXIFKDXRTKLFMISY 44  
Db 61 ANAFLELRPGSLERCKEKCQSFEBAREIFKDXRTKLFMISY 104

RESULT 2  
FA7\_RABIT STANDARD; PRT; 444 AA.  
AC P98139; P79224;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_Taxid=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93190306; PubMed=8383365;  
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";  
RT Thromb. Res. Suppl. 69:231-238(1993).  
RL [2]  
RN REVISION TO 395.  
RC TISSUE=Liver;  
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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CC  
CC EMBL; U77477; AAB37326.1; -.  
CC HESP; P08709; 1FAK.  
DR MEROPS; S01.215; -.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR005561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PRO0089; trypsin\_1.  
DR Pfam; PRO0594; gla\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PRO0001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
KW EGF-like domain; Repeat; Signal; Hydroxylation.  
FT SIGNAL 1 21  
FT PROPEP 22 39  
FT CHAIN 40 191  
FT CHAIN 192 444  
FT DOMAIN 45 74  
FT DOMAIN 85 121  
FT DOMAIN 126 167  
FT DOMAIN 192 444  
FT SITE 191 192  
FT ACT\_SITE 232 232  
FT ACT\_SITE 281 281  
FT ACT\_SITE 383 383  
FT BINDING 377 377  
FT DISULFID 56 61  
FT DISULFID 89 100  
FT DISULFID 94 109  
FT DISULFID 111 120  
FT DISULFID 130 141  
FT DISULFID 137 151  
FT DISULFID 153 166  
FT DISULFID 174 301  
FT DISULFID 198 203  
FT DISULFID 217 233  
FT DISULFID 349 368  
FT DISULFID 379 407  
FT MOD\_RES 45 45  
FT MOD\_RES 46 46  
FT MOD\_RES 53 53  
FT MOD\_RES 55 55  
FT MOD\_RES 58 58  
FT MOD\_RES 59 59  
FT MOD\_RES 64 64  
FT MOD\_RES 65 65  
FT MOD\_RES 68 68  
FT MOD\_RES 74 74  
FT MOD\_RES 102 102  
FT MOD\_RES 211 211  
FT MOD\_RES 242 242  
FT CARBOHYD 306 306  
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 64.9%; Score 124; DB 1; Length 444;  
Best Local Similarity 54.5%; Pred. No. 3.8e-14;  
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRXCKXXQCSFXXAEXIFKDXRTKLFMISY 44  
Db 40 ANAFLELRPGSLERCKEKLCSFEBARVFOSTERTKOFMITY 83

RESULT 3

FA7\_BOVIN  
ID -FA7\_BOVIN STANDARD; PRT; 407 AA.  
AC P22457;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
F7.  
GN Bos taurus (Bovine).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
OX [1]  
RN [1]  
RP MEDLINE=89008362; PubMed=3049594;  
RX Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;  
RA "Bovine factor VII. Its purification and complete amino acid sequence.";  
RT J. Biol. Chem. 263:14868-14877(1988).  
RL [2]  
RN [2]  
RP MEDLINE=89213999; PubMed=3149637;  
RX Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;  
RA "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX.";  
RT J. Biochem. 104:867-868(1988).  
RL [3]  
RN [3]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-I-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
DR PIR: A31979; A31979.  
DR HSSP: P08709; 1BF9.  
DR MEROPS: S01.215; -;  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR001438; EGF\_II.  
DR InterPro: IPR002383; GLA blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00089; trypsin\_1.  
DR Pfam: PF00594; gla; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR0010; EGFBLD.  
DR PRINTS: PR00001; GLABLD.  
DR SMART: SM00179; EGF\_CA; 1.  
DR SMART: SM00001; EGF\_like; 1.

DR SMART: SM00069; GLA; 1.  
DR SMART: SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_CA; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.  
KM EGF-like domain; Repeat.  
FT CHAIN 1 152  
FT CHAIN 153 407  
FT DOMAIN 6 35  
FT DOMAIN 46 82  
FT DOMAIN 87 128  
FT DOMAIN 153 407  
FT SITE 152 153  
FT ACT\_SITE 193 193  
FT ACT\_SITE 242 242  
FT ACT\_SITE 344 344  
FT BINDING 338 338  
FT DISULFID 17 22  
FT DISULFID 50 61  
FT DISULFID 72 81  
FT DISULFID 91 102  
FT DISULFID 98 112  
FT DISULFID 114 127  
FT DISULFID 135 262  
FT DISULFID 159 164  
FT DISULFID 178 194  
FT DISULFID 310 329  
FT DISULFID 340 368  
FT MOD\_RES 6 7  
FT MOD\_RES 7 6  
FT MOD\_RES 14 14  
FT MOD\_RES 16 16  
FT MOD\_RES 19 19  
FT MOD\_RES 20 20  
FT MOD\_RES 25 25  
FT MOD\_RES 26 26  
FT MOD\_RES 29 29  
FT MOD\_RES 35 35  
FT MOD\_RES 52 52  
FT CARBOHYD 145 145  
FT CARBOHYD 203 203  
FT SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;  
Query Match 59.7%; Score 114; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 2e-12;  
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;  
Oy 1 ANAFLLXLRNGSLKRXCKXQCSPFXAEXIFKDAKRYLFWISY 44  
DB 1 ANGFLLEILLPSLRECRREELCSFEAEHIFRNERTRQFWVSY 44  
RESULT 4  
FA7\_MOUSE  
ID -FA7\_MOUSE STANDARD; PRT; 446 AA.  
AC P70375;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
F7 OR CF7.  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97127167; PubMed=8972017;  
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine blood  
 coagulation factor VII gene."  
 RL Thromb. Haemost. 76:957-964(1996).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWMOGEN FORM. FACTOR VII IS  
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR  
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U66079; AAC33796.1; -.  
 DR HSSP; P08709; 1BF9.  
 DR MEROPS; S01.215; -.  
 DR MGD; MGI:109325; P7.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF\_1like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; trypsin\_1.  
 DR Pfam; PF00594; gla\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA\_1.  
 DR SMART; SM00001; EGF\_1like\_1.  
 DR SMART; SM00069; GLA\_1.  
 DR SMART; SM00020; TRYP\_SPC\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS01187; EGF\_CA\_1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM\_1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER\_1.  
 KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 193  
 FT CHAIN 194 446  
 FT DOMAIN 47 76  
 FT DOMAIN 87 123  
 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 128 169 EGF-LIKE 2.  
 FT DOMAIN 194 446 SERINE PROTEASE.  
 FT SITE 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,  
 FT ACT\_SITE 234 234 FACTOR IXa, OR THROMBIN) (BY SIMILARITY).  
 FT ACT\_SITE 283 283 BY SIMILARITY.  
 FT ACT\_SITE 385 385 BY SIMILARITY.  
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 96 111 BY SIMILARITY.  
 FT DISULFID 113 122 BY SIMILARITY.  
 FT DISULFID 132 143 BY SIMILARITY.  
 FT DISULFID 139 153 BY SIMILARITY.  
 FT DISULFID 155 168 BY SIMILARITY.  
 FT DISULFID 176 303 BY SIMILARITY.  
 FT DISULFID 200 205 BY SIMILARITY.  
 FT DISULFID 219 235 BY SIMILARITY.  
 FT DISULFID 351 370 BY SIMILARITY.  
 FT DISULFID 381 409 BY SIMILARITY.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50276 MW; 2512B44A45CB6E CRC64;

Query Match 59.2%; Score 113; DB 1; Length 446;  
 Best Local Similarity 54.5%; Pred. No. 3, 3e-12;  
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFXXLRNGSLXKXCKXQCSFXXAEXIFKDXAKFKLWISY 44  
 Db 42 ANSLBELWPGSLERECNEQCSFEAREIFKSPERTKQPIVY 85

RESULT 5  
 ID PRTC\_MOUSE STANDARD; PRT; 461 AA.  
 AC P33587; O35498;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 factor XIV).  
 DE PROC.  
 GN Mus musculus (Mouse).  
 OS Mus musculus.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RC MEDLINE=92316897; PubMed=1618739;  
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;  
 RT "Isolation and characterization of a mouse protein C cDNA."  
 RL J. Biochem. 111:491-495(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ;  
 RX MEDLINE=98152576; PubMed=9493582;  
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine gene encoding

RT anticoagulant protein C.";  
 RL Thromb. Haemost. 79:310-316 (1998).  
 RN [3]  
 RP SEQUENCE OF 274-434 FROM N.A.  
 RC STRAIN=BAIB/c;  
 RX MEDLINE=94318474; PubMed=8043441;  
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nihō Y.;  
 RT "A comparative study of partial primary structures of the catalytic  
 RL region of mammalian protein C.";  
 RL Br. J. Haematol. 86:590-600 (1994).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D10445; BAA01235.1; -;  
 DR EMBL: AF034569; AAC33795.1; -;  
 DR EMBL: D43755; BAA07812.1; -;  
 DR PIR: JX0210; JX0210.  
 DR HSSP: P04070; 1PCU.  
 DR MEROPS: S01.218; -;  
 DR MGD: MGI:97771; PROC.  
 DR InterPro: IPR000152; AaX\_hydroxyl.  
 DR InterPro: IPR000114; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR002183; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin\_1.  
 DR Pfam: PF00594; Gla\_1.  
 DR PRINTS: PRO0722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA.1.  
 DR SMART: SM00001; EGF\_like\_1.  
 DR SMART: SM00001; EGF\_like\_1.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; Tryp\_Spc\_1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE: PS00022; EGF\_1\_1.  
 DR PROSITE: PS01186; EGF\_2\_2.  
 DR PROSITE: PS01187; EGF\_CA\_1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION\_1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM\_1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER\_1.  
 KM Blood coagulation; glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.

FT SIGNAL 1 33  
 FT PROPEP 34 41  
 FT CHAIN 42 196  
 FT CHAIN 199 461  
 FT PEPTIDE 199 212  
 FT SITE 212 213  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 213 461  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 253 253  
 FT ACT\_SITE 299 299  
 FT ACT\_SITE 402 402  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 319  
 FT DISULFID 238 254  
 FT DISULFID 373 387  
 FT DISULFID 398 426  
 FT CARBOHYD 214 214  
 FT CARBOHYD 290 290  
 FT CARBOHYD 355 355  
 FT CONFLICT 328 328  
 FT CONFLICT 393 393  
 FT SEQUENCE 461 AA; 51945 MW; 53FAAD0B5B194D5E CRC64;  
 SO  
 Query Match 52.9%; Score 101; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 4.5e-10;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;  
 Oy 1 ANAFLLXLRNLSLRKXCKXQCSFYKAXIFRKDAKRTLFNISY 44  
 Db 42 ANSFLEMRPGSLERFCMEIEICDFEAEQEIFQNVEDTLAFWIKY 85  
 RESULT 6  
 PRTC\_PIG STANDARD; PRT; 459 AA.  
 AC O9GLF2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Antiproteolysin IIR) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=21121490; PubMed=11229814;  
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,  
 RA Kim H.K.W.;  
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional  
 RT protein modeling of membrane binding sites and comparative anatomy of  
 RT domains";  
 RL Cell Mol. Life Sci. 58:148-159(2001).  
 CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that  
 CC regulates blood coagulation by inactivating factors Va and VIIIa  
 CC in the presence of calcium ions and phospholipids.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIa.  
 CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved  
 CC into a light chain and a heavy chain held together by a disulfide  
 CC bond. The enzyme is then activated by thrombin, which cleaves a  
 CC tetradecapeptide from the amino end of the heavy chain; this  
 CC reaction, which occurs at the surface of endothelial cells, is  
 CC strongly promoted by thrombomodulin.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu  
 CC residues allows the modified protein to bind calcium.  
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
 CC another site, beyond the Gla domain. This Gla-independent binding  
 CC site is necessary for the recognition of the  
 CC thrombin-thrombomodulin complex.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AF191307; AAC8380.1; -;  
 DR HSSP; P04070; 1PCU.  
 DR MEROPS; S01.218; -;  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF-like.  
 DR InterPro; IPR002383; Gla\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_Gla.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PRO0001; GLABLOOD.  
 DR SMART; SM00181; EGF\_2.  
 DR SMART; SM00001; EGF-like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPsin DOM; 1.  
 DR PROSITE; PS00134; TRYPsin HIS; 1.  
 DR PROSITE; PS00135; TRYPsin SER; 1.  
 KM blood coagulation; Glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 41 BY SIMILARITY.  
 FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.

FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY  
 FT SIMILARITY).  
 FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY  
 FT SIMILARITY).  
 FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).  
 FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY  
 FT SIMILARITY).  
 FT DOMAIN 96 131 EGF-LIKE 1.  
 FT DOMAIN 135 175 EGF-LIKE 2.  
 FT DOMAIN 214 459 SERINE PROTEASE.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 112 112 HYDROXYLATION (BY SIMILARITY).  
 FT ACT\_SITE 255 255 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 301 301 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 400 400 CHARGE RELAY SYSTEM.  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 110 BY SIMILARITY.  
 FT DISULFID 100 105 BY SIMILARITY.  
 FT DISULFID 104 119 BY SIMILARITY.  
 FT DISULFID 121 130 BY SIMILARITY.  
 FT DISULFID 139 150 BY SIMILARITY.  
 FT DISULFID 146 159 BY SIMILARITY.  
 FT DISULFID 161 174 BY SIMILARITY.  
 FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 240 256 BY SIMILARITY.  
 FT DISULFID 371 385 BY SIMILARITY.  
 FT DISULFID 396 424 BY SIMILARITY.  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;  
 Query Match 52.4%; Score 100; DB 1; Length 459;  
 Best Local Similarity 45.5%; Pred. No. 6, 7e-10;  
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 ANAFLLXLRNGSLRXCKKXQCSFXXAEXIFKDXKTKFWISY 44  
 Db 42 ANSFLELRPSLSLRBECKERTCFEERBEIRFQNTENTMFWMSY 85  
 RESULT 7  
 ID PRTC\_RAT STANDARD; PRT; 461 AA.  
 AC P11354;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=Mistat; TISSUE=Liver;  
 RC MEDLINE=92329550; PubMed=1627650;  
 RA Okafor T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C.";  
 RL Biochim. Biophys. Acta 1131:329-332(1992).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIII.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TRIDECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PFM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC -----  
 CC EMBL, X64336; CAA45617.1; -.  
 DR PIR, S18994; S18994.  
 DR PIR, S24312; S24312.  
 DR HSSP, P04070; 1PCU.  
 DR MEROPS, S01.218; -.  
 DR InterPro, IPR000152; Aex\_hydroxyl.  
 DR InterPro, IPR001314; Chymotrypsin.  
 DR InterPro, IPR000561; EGF-like.  
 DR InterPro, IPR001881; EGF\_Ca.  
 DR InterPro, IPR002383; GLA\_blood.  
 DR InterPro, IPR001254; Ser\_protease\_Try.  
 DR InterPro, IPR000294; VitK\_dep\_GLA.  
 DR Pfam, PF00008; EGF\_2.  
 DR Pfam, PF00594; trypsin\_1.  
 DR Pfam, PF00089; trypsin\_1.  
 DR PRINTS, PR00722; CHYMOTRYPSIN.  
 DR PRINTS, PR00001; GLABLOOD.  
 DR SMART, SM00179; EGF\_CA\_1.  
 DR SMART, SM00001; EGF\_Like\_1.  
 DR SMART, SM00069; GLA\_1.  
 DR SMART, SM00020; Tryp\_Spc\_1.  
 DR PROSITE, PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE, PS00022; EGF\_1\_1.  
 DR PROSITE, PS01186; EGF\_2\_2.  
 DR PROSITE, PS01187; EGF\_CA\_1.  
 DR PROSITE, PS00011; GLU\_CARBOXYLATION\_1.  
 DR PROSITE, PS00240; TRYPSIN\_DOM\_1.  
 DR PROSITE, PS00134; TRYPSIN\_HIS\_1.  
 DR PROSITE, PS00135; TRYPSIN\_SER\_1.  
 KM Blood coagulation; Glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 32  
 FT PROBE 33 41 BY SIMILARITY.  
 FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).  
 FT CHAIN 199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).  
 FT PEPTIDE 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).

FT SITE 212 213 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).  
 FT DOMAIN 96 131 EGF-LIKE 1.  
 FT DOMAIN 135 175 EGF-LIKE 2.  
 FT DOMAIN 213 461 SERINE PROTEASE.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID  
 FT MOD\_RES 112 112 HYDROXYLATION (BY SIMILARITY).  
 FT ACT\_SITE 254 254 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 300 300 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 402 402 CHARGE RELAY SYSTEM.  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 110 BY SIMILARITY.  
 FT DISULFID 100 105 BY SIMILARITY.  
 FT DISULFID 104 119 BY SIMILARITY.  
 FT DISULFID 121 130 BY SIMILARITY.  
 FT DISULFID 139 150 BY SIMILARITY.  
 FT DISULFID 146 159 BY SIMILARITY.  
 FT DISULFID 161 174 BY SIMILARITY.  
 FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 239 255 BY SIMILARITY.  
 FT DISULFID 373 387 BY SIMILARITY.  
 FT DISULFID 398 426 BY SIMILARITY.  
 FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF9364EDACD5 CRC64;  
 Query Match 52.4%; Score 100; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 6.7e-10;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;  
 Cx 1 ANAFLLXLRNGSLKRXCKXCCSFXXAEXIFKDXARTLFWISY 44  
 Db 42 ANSFLEVRAGSLERECMEICDFEEAOETFNVEDTLAFWIKY 85  
 RESULT 8  
 PA10\_HUMAN STANDARD: PRT: 488 AA.  
 AC P00742; Q14340;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91216473; PubMed=1902434;  
 RA Messier T.L., Plitman D.D., Long G.L., Kaufman R.J., Church W.R.;  
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding  
 RT human coagulation factor X.";  
 RL Gene 99:291-294(1991).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026600; PubMed=3768336;  
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;  
 RT "Gene for human factor X: a blood coagulation factor whose gene  
 RT organization is essentially identical with that of factor IX and  
 RT protein C.";  
 RL Biochemistry 25:5098-5102(1986).  
 RN [3]  
 RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McGilivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RN [4]  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA.";  
 RL Gene 41:311-314(1986).  
 RN [5]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884(1983).  
 RN [6]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [7]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [8]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Bianthenship D.T., Cardin A.D., Kistiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283962; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC -----  
 DR EMBL: K01394; AAA52490.1; -  
 DR EMBL: M57285; AAA52421.1; -  
 DR EMBL: L29433; AAA52764.1; -  
 DR EMBL: L00390; AAA52764.1; JOINED.  
 DR EMBL: L00391; AAA52764.1; JOINED.  
 DR EMBL: L00392; AAA52764.1; JOINED.  
 DR EMBL: L00393; AAA52764.1; JOINED.  
 DR EMBL: L00394; AAA52764.1; JOINED.  
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 DR EMBL: M22613; AAA51984.1; -  
 DR EMBL: K01886; AAA52486.1; -  
 DR EMBL: M33297; AAA52636.1; -  
 DR PIR: A00924; EXHU.  
 DR PIR: A25853; A25853.  
 DR PIR: A24478; A24478.  
 DR PDB: IHCG; 08-MAY-95.  
 DR PDB: IFAX; 29-OCT-97.  
 DR PDB: IFXY; 17-JUN-98.  
 DR PDB: IXXA; 23-MAR-99.  
 DR PDB: IXXB; 23-MAR-99.  
 DR MEROPS: S01.216; -  
 DR GYCSULDEB: P00742; -  
 DR Genew: HGNC:3528; F10.  
 DR MIM: 134530; -  
 DR MIM: 227600; -  
 DR InterPro: IPR000152; Abx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF-2.  
 DR InterPro: IPR001881; EGF-Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00584; gla; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_1like; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TYP\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00013; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
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 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;

KW Signal; Zymogen; EGF-like domain; Repeat; 3d-structure.  
 FT SIGNAL 1 31 POTENTIAL.  
 FT PROPEP 32 40  
 FT CHAIN 41 179 FACTOR X LIGHT CHAIN.  
 FT CHAIN 183 488 FACTOR X HEAVY CHAIN.  
 FT PROPEP 183 234 ACTIVATION PEPTIDE.  
 FT CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.  
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 125 165 EGF-LIKE 2.  
 FT DOMAIN 135 488 SERINE PROTEASE.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 103 103 HYDROXYLATION.  
 FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).  
 FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).  
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 231 231 /FTID=CAR\_000012.  
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 FT ACT\_SITE 276 276 /FTID=CAR\_000013.  
 FT ACT\_SITE 322 322 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 419 419 CHARGE RELAY SYSTEM.  
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 FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 51.3%; Score 98; DB 1; Length 488;  
 Best Local Similarity 38.6%; Pred. No. 1.6e-09;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFPLXLRNGLSRXKXKXOCFFYXAEKIFPDAXRTKLFMTSY 44  
 DB 41 ANSFLEMKGHLEKRECMETCTSYEDARVDFSDKTFNFMKY 84

RESULT 9  
 FA10\_RABIT STANDARD; PRT; 490 AA.  
 AC 019045;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97256311; PubMed=9101642;  
 RA Pendurthi U.R., Anderson K.D., James H.L.;  
 RT "Characterization of a full-length cDNA for rabbit factor X.";  
 RL Thromb. Res. 85:503-514(1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME

CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)  
 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC -----  
 CC EMBL; AF003200; AAB62542.1; -;  
 CC HSSP; P00742; IHCG.  
 CC MEROPS; S01.216; -;  
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 CC InterPro; IPR001314; Chymotrypsin.  
 CC InterPro; IPR000561; EGF-like.  
 CC InterPro; IPR000742; EGF\_2.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR002383; GLA\_blood.  
 CC InterPro; IPR001254; Ser\_protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00008; EGF\_2.  
 CC Pfam; PF00089; trypsin; 1.  
 CC Pfam; PF00594; gla; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00001; GLABLOOD.  
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 CC SMART; SM00001; EGF\_Like; 1.  
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 CC PROSITE; PS00022; EGF\_1; 1.  
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 CC PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat.  
 KW SIGNAL 1 20 POTENTIAL.  
 FT PROPEP 21 40 BY SIMILARITY.  
 FT CHAIN 41 180 FACTOR X LIGHT CHAIN.  
 FT CHAIN 184 490 FACTOR X HEAVY CHAIN.  
 FT PROPEP 184 232 ACTIVATION PEPTIDE.  
 FT CHAIN 233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.  
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 125 165 EGF-LIKE 2.  
 FT DOMAIN 233 490 SERINE PROTEASE.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY  
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 FT SIMILARITY).



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FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA; 53965 MW; 3A39PA85AF2A6D11 CRC64;
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Query Match 51.3%; Score 98; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 1.6e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
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Db 41 ANSFLEELKKGNERECMEENCSEYEALFEVDEKXTEFWNKY 84
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RESULT 10
ID FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McMillin R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor)." ;
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
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RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain." ;
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X." ;
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases." ;
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta." ;
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjorker I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region." ;
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide." ;
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X." ;
RL Biochemistry 29:8111-8116(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding." ;
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X." ;
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DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00001; GLABLOD.  
 DR SMART; SM00069; GLA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.  
 FT PROPEP 1 20  
 FT CHAIN 21 218  
 FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID  
 FT PROTEIN 1.  
 FT DOMAIN 21 83  
 FT TRANSMEMBRANE (POTENTIAL).  
 FT DOMAIN 84 106  
 FT POTENTIAL.  
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 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 24 61  
 FT GLA-RICH.  
 FT DOMAIN 131 135  
 FT POLY-PRO.  
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 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 ANAFLLXLRNGSLKRXCKXQCSFPAEXIFKDXRTKLFWSY 44  
 DB 21 ANGFEEIRGNIERBECKEFCFEAREAFENNEKTKERFWSY 64  
 RESULT 12  
 ID PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)  
 DE (Aucoproteomycin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.  
 OC NCBI\_TaxID=9913;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaya R.M., McGillivray R.T.A.;  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN (2)  
 RN SEQUENCE OF 40-194.  
 RX MEDLINE=83007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.;  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 RN (3)  
 RN REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Roestorff P., Stenflo J.;  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN (4)  
 RN SEQUENCE OF 197-456.  
 RX MEDLINE=83007326; PubMed=6896877;  
 RA Stenflo J., Fernlund P.;  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RL J. Biol. Chem. 257:12180-12190(1982).  
 RN (5)  
 RN PROCESSING, AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213513; PubMed=6304092;  
 RA Esmen N.L., Debault L.E., Esmen C.T.;  
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless protein C";  
 RL J. Biol. Chem. 258:5548-5553(1983).  
 RP PROCESSING, AND CALCIUM-BINDING DATA.

RX MEDLINE=83213514; PubMed=6406503;  
 RA Johnson A.E., Esmen N.L., Lane T.M., Esmen C.T.;  
 RT "Structural changes required for activation of protein C are induced by Ca2+ binding to a high affinity site that does not contain gamma-carboxyglutamic acid";  
 RL J. Biol. Chem. 258:5554-5560(1983).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC -----  
 DR EMBL; K02435; AAA30685.1; -.  
 DR PIR; A00928; KXBO.  
 DR HSSP; P04070; IPCU.  
 DR MEROPS; S01.218; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF-like.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Gamma-carboxyglutamic acid; Glycoprotein; Serine protease;  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydroxylase; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 29  
 FT PROPEP 30 39  
 FT CHAIN 40 194  
 FT CHAIN 197 456  
 FT PEPTIDE 197 210  
 FT DOMAIN 94 129  
 FT DOMAIN 133 173  
 FT DOMAIN 211 456  
 FT MOD\_RES 45 45  
 FT MOD\_RES 46 46  
 FT MOD\_RES 53 53  
 MOD\_RES 53 53  
 PROTEIN C LIGHT CHAIN.  
 PROTEIN C HEAVY CHAIN.  
 ACTIVATION PEPTIDE.  
 EGF-LIKE 1.  
 EGF-LIKE 2.  
 SERINE PROTEASE.  
 GAMMA-CARBOXYGLUTAMIC ACID.  
 GAMMA-CARBOXYGLUTAMIC ACID.  
 GAMMA-CARBOXYGLUTAMIC ACID.

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FT  MOD RES      55      55      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      58      58      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      59      59      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      62      62      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      64      64      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      65      65      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      68      68      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      74      74      GAMMA-CARBOXYGLUTAMIC ACID.
FT  MOD RES      110     110     HYDROXYLATION.
FT  ACT_SITE     252     252     CHARGE RELAY SYSTEM.
FT  ACT_SITE     298     298     CHARGE RELAY SYSTEM.
FT  ACT_SITE     397     397     CHARGE RELAY SYSTEM.
FT  DISULFID-     56      61      BY SIMILARITY.
FT  DISULFID      89     108      BY SIMILARITY.
FT  DISULFID      98     103      BY SIMILARITY.
FT  DISULFID     102     117      BY SIMILARITY.
FT  DISULFID     119     128      BY SIMILARITY.
FT  DISULFID     137     148      BY SIMILARITY.
FT  DISULFID     144     157      BY SIMILARITY.
FT  DISULFID     159     172      BY SIMILARITY.
FT  DISULFID     180     318      INTERCHAIN.
FT  DISULFID     237     253
FT  DISULFID     368     382
FT  DISULFID     393     421
FT  CARBOHYD      136     136      N-LINKED (GLCNAC. . .)
FT  CARBOHYD      289     289      N-LINKED (GLCNAC. . .)
FT  CARBOHYD      350     350      N-LINKED (GLCNAC. . .)
FT  CARBOHYD      366     366      N-LINKED (GLCNAC. . .)
FT  VARIANT       82      82      F -> K.
FT  CONFLICT     455     455      VP -> PV (IN REF. 4).
SQ  SEQUENCE      456 AA; 51407 MM; CAA6833F894C209 CRC64;

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Query Match      47.1%; Score 90; DB 1; Length 456;
Best Local Similarity 40.9%; Pred. No. 3.9e-08;
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

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Oy  1 ANAPLXLRNGSLKRXCKXQCSFXAXEIRFKDARLTLPWISY 44
Db  40 ANFLEELRPGNVERECSEVECFEAREIRFONTEDTMAFMSFY 83

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RESULT 13
TWG3_HUMAN STANDARD; PRT; 231 AA.
AC  Q9BZD7;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Transmembrane gamma-carboxylutamic acid protein 3 precursor.
GN  TWG3.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxId=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Spinal cord;
RX  MEDLINE=2117044; PubMed=1171957;
RA  Kulman J D., Harris J.E., Xie L., Davie E.W.;
RT  "Identification of two novel transmembrane gamma-carboxylutamic acid
RT  proteins expressed broadly in fetal and adult tissues.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC  -1- PM: Gla residues are produced after subsequent posttranslational
CC  modifications of glutamic acid by a vitamin K-dependent gamma-
CC  carboxylase.
CC  -----
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CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL; AF326350; AAC00955.1; -.
DR  HSBP; P00740; 1CFH.
DR  InterPro; IPR002383; GLA_blood.
DR  InterPro; IPR000294; VitK_dep_GLA.
DR  Pfam; PF00594; gla1.1.
DR  PRINTS; PR00001; GLABLOOD.
DR  SMART; SM00069; GLA; 1.
DR  PROSITE; PS00011; GLU CARBOXYLATION, 1.
KW  Gamma-carboxylutamic acid; Vitamin K; Transmembrane.
FT  PROPEP      1      19      POTENTIAL.
FT  CHAIN       20     231      TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT                                     PROTEIN 3.
FT  DOMAIN      20      78      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM  79     101      POTENTIAL.
FT  DOMAIN     102     231      CYTOPLASMIC (POTENTIAL).
FT  DOMAIN      23      60      GLA-RICH.
SQ  SEQUENCE     231 AA; 25948 MM; 8A373E48490D81 CRC64;

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Query Match      46.1%; Score 88; DB 1; Length 231;
Best Local Similarity 36.4%; Pred. No. 4.4e-08;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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Oy  1 ANAPLXLRNGSLKRXCKXQCSFXAXEIRFKDARLTLPWISY 44
Db  20 ANFLEELRQGTIRRECEMEICSYEVEKVEFENKEKTEFWKGY 63

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RESULT 14
FA10_CHICK STANDARD; PRT; 475 AA.
ID  FA10_CHICK
AC  P25155;
DT  01-MAY-1992 (Rel. 22, Created)
DT  01-MAY-1992 (Rel. 22, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE  (Virul activating protease) (VAP).
GN  FX.
OS  Gallus gallus (Chicken).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC  Gallus.
OX  NCBI_TaxId=9031;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Chorioallantoic membrane;
RX  MEDLINE=91257322; PubMed=2044767;
RA  Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotoh B.,
RA  Ogasawara T., Nagai Y.;
RT  "Primary structure of the virus activating protease from chick
RT  embryo. Its identity with the blood clotting factor Xa.";
RL  FEBS Lett. 283:281-285(1991).
RN  [2]
RP  SEQUENCE OF 41-55 AND 241-261.
RX  TISSUE=Allantoic fluid;
RX  MEDLINE=91065352; PubMed=2174359;
RA  Gotoh B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,
RA  Nagai Y.;
RT  "An endoprotease homologous to the blood clotting factor X as a
RT  determinant of viral tropism in chick embryo.";
RL  EMBO J. 9:4189-4195(1990).
CC  -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC  converts prothrombin to thrombin in the presence of factor Va,
CC  calcium and phospholipid during blood clotting.
CC  -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC  AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC  SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC  SAC.
CC  -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC  Arg-|-Ile bonds in prothrombin to form thrombin.
CC  -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

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CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.  
 CC -1- P.TM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- P.TM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL; D00844; BAA00724.1; -  
 CC PIR; S15838; S15838.  
 CC HSSP; P00742; 1HCG.  
 CC MEROPS; S01.216; -  
 CC Interpro; IPR000152; Asx\_hydroxyl.  
 CC Interpro; IPR001314; Chymotrypsin.  
 CC Interpro; IPR000561; EGF-like.  
 CC Interpro; IPR000742; EGF 2.  
 CC Interpro; IPR001881; EGF\_Ca.  
 CC Interpro; IPR001438; EGF\_11.  
 CC Interpro; IPR002383; GLA\_blood.  
 CC Interpro; IPR001254; Ser\_protease\_Try.  
 CC Interpro; IPR000294; Vitk\_dep\_GLA.  
 CC Pfam; PF00008; EGF\_2.  
 CC Pfam; PF00089; trypsin; 1.  
 CC Pfam; PF00594; gla; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00010; EGFBL00D.  
 CC PRINTS; PR00001; GLABLOOD.  
 CC SMART; SM00179; EGF\_CA; 1.  
 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; TRY\_Spc; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 2.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC GlycoProfile; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 CC Signal; Zymogen; EGF-like domain; Repeat.  
 CC SIGNAL; 1 20  
 FT PROPEP 21 40  
 FT CHAIN 41 180  
 FT CHAIN 186 475  
 FT PROPEP 186 241  
 FT CHAIN 242 475  
 FT DOMAIN 86 122  
 FT DOMAIN 125 168  
 FT DOMAIN 241 475  
 FT MOD\_RES 46 46  
 FT MOD\_RES 47 47  
 FT MOD\_RES 54 54  
 FT MOD\_RES 56 56  
 FT MOD\_RES 59 59  
 FT MOD\_RES 60 60

FT MOD\_RES 65 65  
 FT MOD\_RES 66 66  
 FT MOD\_RES 69 69  
 FT MOD\_RES 72 72  
 FT MOD\_RES 79 79  
 FT MOD\_RES 103 103  
 FT ACT\_SITE 282 282  
 FT ACT\_SITE 328 328  
 FT ACT\_SITE 425 425  
 FT DISULFID 90 101  
 FT DISULFID 95 110  
 FT DISULFID 112 121  
 FT DISULFID 129 140  
 FT DISULFID 136 152  
 FT DISULFID 154 167  
 FT DISULFID 175 186  
 FT DISULFID 247 252  
 FT DISULFID 267 283  
 FT DISULFID 396 410  
 FT DISULFID 421 449  
 FT CARBOHYD 196 196  
 FT CARBOHYD 207 207  
 FT CARBOHYD 228 228  
 FT CARBOHYD 285 285  
 SQ SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;  
 Query Match 45.5%; Score 87; DB 1; Length 475;  
 Best local Similarity 36.4%; Pred. No. 1.4e-07;  
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 ANAFLLXRLNGSLKRYCKXQCSFYXAEKIFKDAKRTKFWISY 44  
 Db 41 ANSFLERMKGNIERECNEBRCSEKEAREAFEDNEXTEEFWNIT 84  
 RESULT 15  
 ID PRTC\_HUMAN STANDARD; PRT; 461 AA.  
 AC P04070; Q16001; Q15190; Q15189;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=65270390; PubMed=2991887;  
 RA Foster D.C., Yoshitake S., Davie E.W.;  
 RT "The nucleotide sequence of the gene for human protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=65269639; PubMed=2991859;  
 RA Beckmann R.J., Schmidt R.J., Sautter R.F., Plutsky J., Crabtree G.R.,  
 RA Long G.L.;  
 RT "The structure and evolution of a 461 amino acid human protein C  
 RT precursor and its messenger RNA, based upon the DNA sequence of  
 RT cloned human liver cDNAs";  
 RL Nucleic Acids Res. 13:5233-5247(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86120978; PubMed=3511471;

RA Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;  
 RT "Evolution and organization of the human protein C gene."  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 106-461 FROM N.A.  
 RX MEDLINE=8427214; PubMed=6589623;  
 RA Foster D.C., Davie E.W.;  
 RT "Characterization of a cDNA coding for human protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).  
 RN [6]  
 RP CARBOHYDRATE-LINKAGE SITE ASN-371.  
 RX MEDLINE=90293094; PubMed=1694179;  
 RA Mletich J.P., Broze G.J. Jr.;  
 RT "Beta protein C is not glycosylated at asparagine 329. The rate of  
 translation may influence the frequency of usage at asparagine-X-  
 cysteine sites."  
 RL J. Biol. Chem. 265:11397-11404(1990).  
 RN [7]  
 RP HYDROXYLATION  
 RX MEDLINE=92184750; PubMed=1544894;  
 RA Harris R.J., Ling V.T., Spellman M.W.;  
 RT "O-linked fucose is present in the first epidermal growth factor  
 domain of factor XII but not protein C";  
 RL J. Biol. Chem. 267:5102-5107(1992).  
 RN [8]  
 RP 3D-STRUCTURE MODELING OF 175-450.  
 RX MEDLINE=94272342; PubMed=8003977;  
 RA Fisher C.L., Greengard J.S., Griffin J.H.;  
 RT "Models of the serine protease domain of the human antithrombotic  
 plasma factor activated protein C and its zymogen";  
 RL Protein Sci. 3:588-599(1994).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.  
 RX MEDLINE=97157472; PubMed=9003757;  
 RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Emon C.,  
 RA Bode W.;  
 RT "The 2.8 A crystal structure of Glu-domainless activated protein C";  
 RL EMBO J. 15:6822-6831(1996).  
 RN [10]  
 RP REVIEW ON PROC VARIANTS.  
 RX MEDLINE=93190290; PubMed=8446940;  
 RA Reltama P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,  
 RA Saja N., Cooper D.N.;  
 RT "Protein C deficiency: a database of mutations. For the Protein C & S  
 Subcommittee of the Scientific and Standardization Committee of the  
 International Society on Thrombosis and Haemostasis";  
 RL Thromb. Haemost. 69:77-84(1993).  
 RN [11]  
 RP VARIANT CVS-444.  
 RX MEDLINE=87204221; PubMed=2437584;  
 RA Romeo G., Haasen H.D., Staempfli S., Roncuzzi L., Cianetti L.,  
 RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,  
 RA Cortese R.;  
 RT "Hereditary thrombophilia: identification of nonsense and missense  
 mutations in the protein C gene";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).  
 RN [12]  
 RP VARIANT TRP-211 (LONDON-1).  
 RX MEDLINE=9008906; PubMed=2602169;  
 RA Grundy C.B., Chicotte A., Talbot S., Bevan D., Kakkar V.V.,  
 RA Cooper D.N.;  
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in  
 the protein C gene causing thrombosis";  
 RL Nucleic Acids Res. 17:10513-10513(1989).  
 RN [13]  
 RP VARIANT CVS-272.  
 RX MEDLINE=91329836; PubMed=1868249;  
 RA Reltama P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;

RT "The spectrum of genetic defects in a panel of 40 Dutch families with  
 RT symptomatic protein C deficiency type I: heterogeneity and founder  
 RT effects";  
 RL Blood 78:890-894(1991).  
 RN [14]  
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.  
 RX MEDLINE=92190481; PubMed=1347706;  
 RA Boylil E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,  
 RA Rainville I.R., Long G.L.;  
 RT "Protein Vermont: symptomatic type II protein C deficiency  
 associated with two GLA domain mutations";  
 RL Blood 79:1456-1465(1992).  
 RN [15]  
 RP VARIANT ASP-418 (HONG KONG-2).  
 RX MEDLINE=92305321; PubMed=1611081;  
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;  
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C  
 deficiency caused by two mutant alleles, a 5-nucleotide deletion and  
 a missense mutation";  
 RL Blood 80:126-133(1992).  
 RN [16]  
 RP VARIANT LEU-289.  
 RX MEDLINE=92380660; PubMed=1511988;  
 RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;  
 RT "A novel homozygous missense mutation in the protein C (PROC) gene  
 causing recurrent venous thrombosis";  
 RL Hum. Genet. 89:683-684(1992).  
 RN [17]  
 RP VARIANTS GLN-220 AND TRP-220.  
 RX MEDLINE=92380661; PubMed=1511989;  
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;  
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)  
 gene causing recurrent venous thrombosis";  
 RL Hum. Genet. 89:685-686(1992).  
 RN [18]  
 RP VARIANT GLN-220.  
 RX MEDLINE=93250852; PubMed=1301959;  
 RA Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,  
 RA Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens W.;  
 RT "Two novel mutations responsible for hereditary type I protein C  
 deficiency: characterization by denaturing gradient gel  
 electrophoresis";  
 RL Hum. Mutat. 1:491-500(1992).  
 RN [19]  
 RP VARIANT SER-334.  
 RX MEDLINE=92276939; PubMed=1593215;  
 RA Yamamoto K., Matsumita T., Sugita I., Takamatsu J., Iwasaki E.,  
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;  
 RT "Homozygous protein C deficiency: identification of a novel missense  
 mutation that causes impaired secretion of the mutant protein C";  
 RL J. Lab. Clin. Med. 119:682-689(1992).  
 RN [20]  
 RP VARIANTS TRP-38; CVS-42; HIS-42; GLN-271 AND ASN-294.  
 RX MEDLINE=93313192; PubMed=8324221;  
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Allaud M.-F., Dupuy E.,  
 RA Juhani-Vague I., Alach M.;  
 RT "Five novel mutations located in exons III and IX of the protein C  
 gene in patients presenting with defective protein C anticoagulant  
 activity";  
 RL Blood 82:159-168(1993).  
 RN [21]  
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND  
 RP V-388.  
 RX MEDLINE=93271391; PubMed=8499565;  
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reltama P.H.,  
 RA Bertina R.M.;  
 RT "Twelve novel and two recurrent mutations in 14 Austrian families  
 with hereditary protein C deficiency";  
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).  
 RN [22]  
 RP VARIANT TRP-57.  
 RX MEDLINE=93271396; PubMed=8499568;  
 RA Millar D.S., Grundy C.B., Bignelli P., Moffat E.H., Martin R.,

RP Kakkat V.V., Cooper D.N.;  
RT "A Glia domain mutation (Arg 15-->Trp) in the protein C (PROC) gene  
RT causing type 2 protein C deficiency and recurrent venous  
RT thrombosis.";  
RL Blood Coagul. Fibrinolysis 4:345-347(1993).  
RN [23]  
RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.  
RX MEDLINE=94122329; PubMed=8292730;  
RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,  
RA Koepfer M.A., Coughlin J., Griffin J.H.;  
RT "Genetic mutations in ten unrelated American patients with  
RT symptomatic type 1 protein C deficiency.";  
RL Blood Coagul. Fibrinolysis 4:791-796(1993).  
RN [24]  
RP VARIANT SER-423.  
RX MEDLINE=94001606; PubMed=8398832;  
RA Marchetti G., Patrascchini P., Gemmati D., Castagna G., Rodighiero F.,  
RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;  
RT "Symptomatic type II protein C deficiency caused by a missense  
RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";  
RL Br. J. Haematol. 84:285-289(1993).  
RN [25]  
RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YOUNGO).

Query Match 45.0%; Score 86; DB 1; Length 461;  
Best Local Similarity 43.9%; Pred. No. 2e-07;  
Matches 18; Conservative 5; Mismatches 18; Indels 0;  
Gaps 0;

OY 1 ANAFLXLLNGSLKRXCKXXQCSFFXAEXEIFDPAKTKLFW 41  
          |      |      |      |      |      |      |  
Db 43 ANSFLLEELHSHLSLERCEIEICDFEBAKKIFPNVDDTLAFW 83  
          |      |      |      |      |      |      |

Search completed: March 19, 2003, 14:52:48  
Job time : 6.625 secs

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(without alignments)  
196.288 Million cell updates/sec

Title: 10ASN28G1U  
Perfect score: 191  
Sequence: 1 ANAPFLXLLNGSLXRCCKX.....XXAEXIFKQAXRTKLFMISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 1          | 158   | 82.7        | 701       | 4  | Q96PQ8      |
| 2          | 113   | 59.2        | 446       | 11 | Q61109      |
| 3          | 101   | 52.9        | 460       | 11 | Q91WN8      |
| 4          | 95    | 49.7        | 460       | 11 | Q99PC6      |
| 5          | 92    | 48.2        | 482       | 11 | Q63207      |
| 6          | 91    | 47.6        | 456       | 6  | Q9TTR0      |
| 7          | 90    | 47.1        | 469       | 6  | Q9GMD9      |
| 8          | 90    | 47.1        | 481       | 11 | Q54740      |
| 9          | 90    | 47.1        | 481       | 11 | Q99L32      |
| 10         | 90    | 47.1        | 481       | 11 | Q88947      |
| 11         | 84    | 44.0        | 100       | 4  | Q15253      |
| 12         | 81    | 42.4        | 49        | 6  | Q95ME8      |
| 13         | 78    | 40.8        | 456       | 4  | Q14316      |
| 14         | 78    | 40.8        | 461       | 6  | Q95ND7      |
| 15         | 78    | 40.8        | 461       | 6  | Q95ND6      |
| 16         | 75    | 39.3        | 179       | 4  | Q8TAS3      |

|    |      |      |     |    |        |                     |
|----|------|------|-----|----|--------|---------------------|
| 17 | 75   | 39.3 | 198 | 11 | Q8R182 | Q8R182 mus musculus |
| 18 | 74   | 38.7 | 138 | 6  | Q28994 | Q28994 sus scrofa   |
| 19 | 71   | 37.2 | 433 | 13 | Q90YK1 | Q90YK1 brachydanio  |
| 20 | 65   | 34.0 | 648 | 6  | Q29094 | Q29094 sus scrofa   |
| 21 | 64   | 33.5 | 98  | 13 | P82807 | P82807 notechis sc  |
| 22 | 62   | 32.5 | 399 | 11 | Q9CQW3 | Q9CQW3 mus musculus |
| 23 | 62   | 32.5 | 608 | 13 | Q9PTW7 | Q9PTW7 struthio ca  |
| 24 | 60   | 31.4 | 650 | 4  | Q9NSD0 | Q9NSD0 homo sapien  |
| 25 | 60   | 31.4 | 650 | 4  | Q16519 | Q16519 homo sapien  |
| 26 | 59   | 30.9 | 607 | 13 | Q91001 | Q91001 gallus gall  |
| 27 | 58.5 | 30.6 | 492 | 10 | Q9SMJ7 | Q9SMJ7 cicer ariet  |
| 28 | 57.5 | 30.1 | 196 | 10 | Q04284 | Q04284 belaginelia  |
| 29 | 57.5 | 30.1 | 431 | 10 | Q94EY5 | Q94EY5 arabidopsis  |
| 30 | 57.5 | 30.1 | 543 | 10 | Q9MB23 | Q9MB23 arabidopsis  |
| 31 | 57.5 | 30.1 | 576 | 10 | Q9C9U4 | Q9C9U4 arabidopsis  |
| 32 | 57.5 | 30.1 | 589 | 10 | Q9LMS2 | Q9LMS2 arabidopsis  |
| 33 | 55.5 | 29.1 | 459 | 10 | Q9SE22 | Q9SE22 oryza sativ  |
| 34 | 55.5 | 29.1 | 542 | 5  | Q8T613 | Q8T613 halocynthia  |
| 35 | 54.5 | 28.5 | 506 | 10 | Q9SE23 | Q9SE23 oryza sativ  |
| 36 | 54.5 | 28.5 | 506 | 10 | Q9SE23 | Q9SE23 oryza sativ  |
| 37 | 54.5 | 28.5 | 567 | 10 | Q8W4J2 | Q8W4J2 arabidopsis  |
| 38 | 54   | 28.3 | 25  | 11 | Q9QVH6 | Q9QVH6 rattus sp.   |
| 39 | 53.5 | 28.0 | 510 | 10 | Q9MB22 | Q9MB22 arabidopsis  |
| 40 | 53.5 | 28.0 | 619 | 10 | Q9LV37 | Q9LV37 arabidopsis  |
| 41 | 52.5 | 27.5 | 603 | 10 | Q9LP67 | Q9LP67 arabidopsis  |
| 42 | 52.5 | 27.5 | 606 | 10 | Q9SJG9 | Q9SJG9 arabidopsis  |
| 43 | 52.5 | 27.5 | 651 | 10 | Q8S218 | Q8S218 oryza sativ  |
| 44 | 51.5 | 27.0 | 575 | 10 | Q94E17 | Q94E17 oryza sativ  |
| 45 | 51.5 | 27.0 | 588 | 10 | Q91M33 | Q91M33 arabidopsis  |

## ALIGNMENTS

### RESULT 1

| ID | Q96PQ8   | PRELIMINARY;                            | PRT; | 701 AA. |
|----|--|---|------|---------|
| AC | Q96PQ8   |   |      |         |
| DT | 01-DEC-2001  | (T-EMBLrel. 19, Created)                |      |         |
| DT | 01-DEC-2001  | (T-EMBLrel. 19, Last sequence update)   |      |         |
| DT | 01-MAR-2002  | (T-EMBLrel. 20, Last annotation update) |      |         |
| DE | Factor VII active site mutant immunocognate.                           |   |      |         |
| OS | Homo sapiens (Human).  |   |      |         |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                |   |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.              |   |      |         |
| ON | NCBI_TaxID=9606;   |   |      |         |
| RX | SEQUENCE FROM N.A.   |   |      |         |
| RX | MEDLINE=21477448; PubMed=11593034;                                     |   |      |         |
| RA | Hu Z., Garen A.;   |   |      |         |
| RT | "Targeting tissue factor on tumor vascular endothelial cells and tumor |   |      |         |
| RT | cells for immunotherapy in mouse models of prostatic cancer."          |   |      |         |
| RL | Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).                    |   |      |         |
| DR | EMBL; AF272774; AAKS8686.1; -  |   |      |         |
| DR | InterPro; IPR000152; Asx hydroxyl.                                     |   |      |         |
| DR | InterPro; IPR000561; EGF-like.   |   |      |         |
| DR | InterPro; IPR000742; EGF_2.  |   |      |         |
| DR | InterPro; IPR001881; EGF_Ca.   |   |      |         |
| DR | InterPro; IPR003006; IG_MHC.   |   |      |         |
| DR | InterPro; IPR001254; Ser protease Try.                                 |   |      |         |
| DR | InterPro; IPR000294; VitK_dep_GLA.                                     |   |      |         |
| DR | Pfam; PF00008; EGF_2.  |   |      |         |
| DR | Pfam; PF00594; GLA; 1.   |   |      |         |
| DR | Pfam; PF00047; IG; 2.  |   |      |         |
| DR | Pfam; PF00089; trypsin; 1.   |   |      |         |
| DR | SMART; SM00181; EGF_2.   |   |      |         |
| DR | PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.                             |   |      |         |
| DR | PROSITE; PS00023; EGF_1; UNKNOWN_1.                                    |   |      |         |
| DR | PROSITE; PS01186; EGF_2; UNKNOWN_1.                                    |   |      |         |
| DR | PROSITE; PS01187; EGF_CA; UNKNOWN_1.                                   |   |      |         |
| DR | PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.                        |   |      |         |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN_1.                                   |   |      |         |
| DR | PROSITE; PSS0240; TRYPSIN_DOM; 1.                                      |   |      |         |

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CBA42CC992F CRC64;

Query Match 82.7%; Score 158; DB 4; Length 701;  
Best Local Similarity 72.7%; Pred. No. 1,1e-20;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
DB 61 ANAFLEELRPSGLERCKECCSFEEAREIFDAERTKLFWISY 104

## RESULT 2

ID 061109 PRELIMINARY; PRT; 446 AA.  
AC 061109;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Coagulation factor VII.  
GN F7 OR FVII.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96276538; PubMed=8701412;  
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
RA Castellino F.J.;  
RT "Characterization of a cDNA encoding murine coagulation factor VII";  
RL Thomb. Haemost. 75:481-487(1996).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPsin FAMILY.  
DR EMBL; U4795; AAC52570.1; -.  
DR HSSP; P08709; 1PAK.  
DR MEROPS; S01.215; -.  
DR MGD; MGI:109325; F7.  
DR InterPro; IPR002086; Aldehyde dehydr.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Set\_protease\_Try.  
DR InterPro; IPR00294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; Gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00070; ALDEHYDE DEHYDR. CYS; UNKNOWN\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
KW Serine protease.  
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 59.2%; Score 113; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 1.8e-12;  
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;  
QY 1 ANAFLLXLRNGSLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
DB 42 ANSLLEELMPGSLERCKECCSFEEAREIFKSPERTQFWIVY 85

## RESULT 3

ID 091WN8 PRELIMINARY; PRT; 460 AA.  
AC 091WN8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Similar to protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013896; AAHL3896.1; -.  
DR MGD; MGI:97771; PROC.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF\_like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Set\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; Gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 460 AA; 51818 MW; 0117P26E68FCC274 CRC64;

Query Match 52.9%; Score 101; DB 11; Length 460;  
Best Local Similarity 45.5%; Pred. No. 3.3e-10;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;  
QY 1 ANAFLLXLRNGSLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
DB 42 ANSLLEELMPGSLERCKECCSFEEAREIFQNVDTLAFWIKY 85

RESULT 4  
ID 099PC6 PRELIMINARY; PRT; 460 AA.  
AC 099PC6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Anticoagulant protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL;  
Korf I.;

"Complete sequence of UC72A01."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
 DR EMBL: AF318182; AK07918.1; -.  
 DR HSSP: P04070; 1PCU.  
 DR MEROPS: S01.218; -.  
 DR MGD: MGI:97771; Proc.  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00594; gla; 1.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00001; EGF\_like; 2.  
 DR SMART: SM00001; EGF\_like; 2.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TYP\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KM Hydroxylation; Repeat; Serine protease.  
 SQ SEQUENCE 460 AA; 51784 MW; 0293BC35ED9D3ED16 CRC64;

Query Match 49.7%; Score 95; DB 11; Length 460;  
 Best local Similarity 43.2%; Pred. No. 4.3e-09;  
 Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXCKKXQCSFXAXEIPKDXRTKLFWISY 44  
 DB 42 ANSFLEMRPGSLERECMEICDLEBAQEIFQVNEVDTLAFWIKY 85

RESULT 5  
 Q63207 PRELIMINARY; PRT; 482 AA.  
 AC O63207;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
 DE Factor X.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 OC NCBI\_TaxID=10116;  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=96093366; PubMed=8578539;  
 RA Stanton C., Ross R.P., Hutson S., Wallin R.;  
 RT Evidence for competition between vitamin K-dependent clotting factors  
 RT for intracellular processing by the vitamin K-dependent gamma-  
 RT carboxylase.";  
 RL Thromb. Res. 80:63-73(1995).  
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
 CC EMBL: X79807; CA56202.1; -.  
 DR HSSP: P00742; 1XKA.  
 DR MEROPS: S01.216; -.  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00594; gla; 1.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_like; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TYP\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KM Hydroxylation; Repeat; Serine protease.  
 SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 48.2%; Score 92; DB 11; Length 482;  
 Best local Similarity 38.6%; Pred. No. 1.7e-08;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFELXLRNGSLRXCKKXQCSFXAXEIPKDXRTKLFWISY 44  
 DB 41 ANSFEEIKGNLRECEVERICSFEBARVEFDNEKTEPMNKY 84

RESULT 6  
 Q9TTR0 PRELIMINARY; PRT; 456 AA.  
 AC Q9TTR0;  
 DT 01-MAY-2000 (TEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
 DE Protein C precursor.  
 GN PROC.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,  
 RA Bregig B.;  
 RT "Molecular characterization and chromosomal assignment of the canine  
 RT protein C gene.";  
 RL Mamm. Genome 10:135-139(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99371952; PubMed=10443005;  
 RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Bregig B.;  
 RT Analysis of canine protein C gene polymorphisms.";  
 RL Anim. Genet. 30:237-238(1999)  
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
 CC EMBL: AF001979; CA05126.1; -.  
 DR HSSP: P04070; 1PCU.  
 DR MEROPS: S01.218; -.  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KM Hydroxylation; Repeat; Serine protease; Signal.  
 FT SIGNAL 1 42 POTENTIAL.  
 FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.  
 FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.  
 FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.  
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 47.6%; Score 91; DB 6; Length 456;  
 Best Local Similarity 40.9%; Pred. No. 2.4e-08;  
 Matches 18; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFXXLRNGSLXRXCKXQCSFXAXEIPFDAXRTKLFWISY 44  
 Db 43 ANSLFEELKAGSLERECNEETCSYEAREVEFDTKNEFWNIY 86

## RESULT 7

Q9GMD9 PRELIMINARY; PRT; 469 AA.  
 AC Q9GMD9; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Coagulation factor X.  
 OS Ornithorhynchus anatinus (Duckbill platypus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.  
 OX NCBI\_TaxId=9258;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21015017; PubMed=1132153;  
 RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;  
 RT "Identification and structural analysis of four serine proteases in a  
 monokaryote, the platypus, Ornithorhynchus anatinus";  
 RL Immunogenetics 52:19-28(2000).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL; AF275654; AAG00453.1; -.  
 DR HSSP; P00742; 1XKB.  
 DR MEROPS; S01.216; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF-2.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00179; EGF\_CA; 1.

DR SMART; SM00001; EGF\_like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolase; Serine protease.  
 SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 47.1%; Score 90; DB 6; Length 469;  
 Best Local Similarity 36.4%; Pred. No. 3.8e-08;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFXXLRNGSLXRXCKXQCSFXAXEIPFDAXRTKLFWISY 44  
 Db 41 ANSLFEELKAGSLERECNEETCSYEAREVEFDTKNEFWNIY 84

## RESULT 8

Q54740 PRELIMINARY; PRT; 481 AA.  
 AC Q54740; 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6).  
 GN F10 OR F410.  
 OS Mus musculus (Mouse).  
 OC Plasmid pluescript.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=98454993; PubMed=9783672;  
 RA Heidemann H.H., Kontermann R.E.;  
 RT "Cloning and recombinant expression of mouse coagulation factor X";  
 RL Thromb. Res. 92:33-41(1998).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL; AJ222677; CAA10933.1; -.  
 DR HSSP; P00742; 1XKA.  
 DR MEROPS; S01.216; -.  
 DR MGD; MGI:103107; F10.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF-2.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;  
 KW Repeat; Serine protease; Signal.  
 FT SIGNAL 1 40  
 FT CHAIN 41 481  
 FT SEQUENCE 481 AA; 53986 MW; CF702DE5EPD97AE CRC64;

Query Match 47.1%; Score 90; DB 11; Length 481;  
 Best Local Similarity 36.4%; Pred. No. 3.9e-08;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRXCKXKXQCSFXAXEJFKDAXRTKLFMISY 44  
 Db 41 ANSFFEFKKGNLRECEMEICSYEEVREIFEDDEKTKYWTXY 84

RESULT 9  
 ID 099L32 PRELIMINARY; PRT; 481 AA.  
 AC 099L32;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Coagulation factor X.  
 GN F10.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 CC EMBL; BC003877; AA03877.1; -.  
 CC HSSP; P00742; 1XKA.  
 DR MEROPS; S01.216; -.  
 DR MGD; MGI:103107; F10.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; gla\_1.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00101; EGFBL00D.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00181; EGF\_2.  
 DR SMART; SM00001; EGF-like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
 KW Serine protease; Signal.  
 FT SIGNAL 1 40  
 FT CHAIN 41 481  
 FT SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 47.1%; Score 90; DB 11; Length 481;  
 Best Local Similarity 36.4%; Pred. No. 3.9e-08;

Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 ANAFLLXLRNGSLRXCKXKXQCSFXAXEJFKDAXRTKLFMISY 44  
 Db 41 ANSFFEFKKGNLRECEMEICSYEEVREIFEDDEKTKYWTXY 84

RESULT 10  
 ID 088947 PRELIMINARY; PRT; 481 AA.  
 AC 088947;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Coagulation factor X precursor.  
 GN F10.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;  
 RX MEDLINE=98347933; PubMed=9684791;  
 RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,  
 RA Castellino F.J., Rosen E.D.;  
 RT "Cloning and characterization of a cDNA encoding murine coagulation  
 RT factor X.";  
 RL Thromb. Haemost. 80:87-91(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvJ;  
 RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;  
 RT "Cloning and characterization of the murine Factor X Gene.";  
 RL Thromb. Haemost. 0:0-0(2000).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 CC EMBL; AF087644; AAC36345.1; -.  
 CC EMBL; AF211347; AAF22980.1; -.  
 DR HSSP; P00742; 1XKA.  
 DR MEROPS; S01.216; -.  
 DR MGD; MGI:103107; F10.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; gla\_1.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_Ca; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
 KW Serine protease; Signal.  
 FT SIGNAL 1 40  
 FT CHAIN 41 481  
 FT SEQUENCE 481 AA; 54018 MW; 8AC09DE5EPD271E CRC64;

Query Match 47.1%; Score 90; DB 11; Length 481;  
 Best Local Similarity 36.4%; Pred. No. 3.9e-08;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLKRXCKXQCSFXXAEIFKDXARTLFWISY 44  
 DB 41 ANSFPEEFKGNLRECKMEICISYEAREFEDDEKTEIWTKY 84

## RESULT 11

Q15253 PRELIMINARY; PRT; 100 AA.

AC Q15253;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Thrombin precursor (Fragment).  
 GN F2.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=87182874; PubMed=3471151;  
 RA McGilivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;  
 RT "Recombinant genetic approaches to functional mapping of thrombin.";  
 RL Ann. N.Y. Acad. Sci. 485:73-79(1986).  
 DR EMBL; M33031; AAA60220.1; -.

DR HSSP; P00735; 2PFI.  
 DR InterPro; IPR02383; GLA\_blood.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00594; Gla; 1.  
 DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00069; GLA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.

KW Signal.  
 FT SIGNAL 1 43 POTENTIAL.  
 FT CHAIN 44 >100 POTENTIAL.  
 FT NON TER 100 100

SQ SEQUENCE 100 AA; 11302 MW; PD0E5D0174B1F6FE CRC64;

Query Match 44.0%; Score 84; DB 4; Length 100;  
 Best Local Similarity 36.4%; Pred. No. 1e-07;  
 Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLKRXCKXQCSFXXAEIFKDXARTLFWISY 44  
 DB 44 ANTFLEVRKGNLRECKVEETCSYEAEFALBSSTATDVFWAKY 87

## RESULT 12

Q95ME8 PRELIMINARY; PRT; 49 AA.

AC Q95ME8;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Coagulation factor IX (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.

NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mizlata M.N., Amarel E.J.;  
 RT "Partial sequence of bovine F9 coding gene.";  
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF34598; AAK7556.1; -.

DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00594; Gla; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.

FT NON TER 1 1  
 SQ NON\_TER 49 49  
 SEQUENCE 49 AA; 6023 MW; DISC6DE9CCBA4A14 CRC64;

Query Match 42.4%; Score 81; DB 6; Length 49;  
 Best Local Similarity 41.2%; Pred. No. 1.7e-07;  
 Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLRXCKXQCSFXXAEIFKDXARTLFWISY 44  
 DB 15 GNLERCKEKKCSFEAREVENTETTEFWKQY 48

## RESULT 13

Q14316 PRELIMINARY; PRT; 456 AA.

AC Q14316;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-AUG-1999 (IPR00111, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas disease, HAEMOPHILIA B)) (Factor IX).  
 GN F9 OR FACTOR IX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Bird C.;  
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 3-19 FROM N.A.  
 RX MEDLINE=88327116; PubMed=3416069;  
 RA Reltima P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,  
 RA Briet E.;

RT "The putative factor IX gene promoter in hemophilia B Leyden.";  
 RL Blood 72:1074-1076(1988).  
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
 CC EMBL; AL033403; CAA21954.1; -.

DR EMBL; X55008; CAB3845.2; -.  
 DR HSSP; P00740; ICFH.  
 DR MEROPS; S01.214; -.

DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; clypein; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGFBLD.  
 DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF 2; 2.

DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Repeat;  
 KW Serine protease.  
 SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 40.8%; Score 78; DB 4; Length 456;  
Best Local Similarity 41.2%; Pred. No. 6.4e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXAXEYFKDAXRTKLFWISY 44  
Db 53 GNLERCEMEKCSFEAREVENTERTTEFWKQY 86

RESULT 14  
Q95ND7 PRELIMINARY; PRT; 461 AA.

AC Q95ND7; 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
DE Coagulation factor XI.  
GN F9.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OC NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=504;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and  
RT chimpanzees.";  
RL Genes Genet. Syst. 0:0-0(2001).  
DR EMBL; AB062470; BAB58885.1; JOINED.  
DR EMBL; AB062458; BAB58885.1; JOINED.  
DR EMBL; AB062460; BAB58885.1; JOINED.  
DR EMBL; AB062462; BAB58885.1; JOINED.  
DR EMBL; AB062464; BAB58885.1; JOINED.  
DR EMBL; AB062466; BAB58885.1; JOINED.  
DR EMBL; AB062468; BAB58885.1; JOINED.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PR00008; EGF\_2.  
DR Pfam; PR00594; gla\_1.  
DR Pfam; PR00089; trypsin\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS00240; TRYPsin\_DOM; 1.  
DR PROSITE; PS00134; TRYPsin\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPsin\_SER; UNKNOWN\_1.  
KW Hydrolyase; Serine protease.  
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 40.8%; Score 78; DB 6; Length 461;  
Best Local Similarity 41.2%; Pred. No. 6.5e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXAXEYFKDAXRTKLFWISY 44  
Db 58 GNLERCEMEKCSFEAREVENTERTTEFWKQY 91

RESULT 15  
Q95ND6 PRELIMINARY; PRT; 461 AA.

AC Q95ND6; 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)

DE Coagulation factor XI.  
GN F9.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OC NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=505;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and  
RT chimpanzees.";  
RL Genes Genet. Syst. 0:0-0(2001).  
DR EMBL; AB062471; BAB58886.1; JOINED.  
DR EMBL; AB062459; BAB58886.1; JOINED.  
DR EMBL; AB062461; BAB58886.1; JOINED.  
DR EMBL; AB062463; BAB58886.1; JOINED.  
DR EMBL; AB062465; BAB58886.1; JOINED.  
DR EMBL; AB062467; BAB58886.1; JOINED.  
DR EMBL; AB062469; BAB58886.1; JOINED.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PR00008; EGF\_2.  
DR Pfam; PR00594; gla\_1.  
DR Pfam; PR00089; trypsin\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS00240; TRYPsin\_DOM; 1.  
DR PROSITE; PS00134; TRYPsin\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPsin\_SER; UNKNOWN\_1.  
KW Hydrolyase; Serine protease.  
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 40.8%; Score 78; DB 6; Length 461;  
Best Local Similarity 41.2%; Pred. No. 6.5e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXAXEYFKDAXRTKLFWISY 44  
Db 58 GNLERCEMEKCSFEAREVENTERTTEFWKQY 91

Search completed: March 19, 2003, 15:13:30  
Job time : 47.3125 sec

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds  
(without alignments)  
280.876 Million cell updates/sec

Title: 10ASN28GLU  
Perfect score: 191  
Sequence: 1 ANAFLLXLRNGSLRXKCKXX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US05\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 158   | 82.7        | 406    | 9     | US-10-109-498-1    |
| 2          | 97    | 50.8        | 419    | 9     | US-10-182-263-3    |
| 3          | 97    | 50.8        | 419    | 9     | US-10-182-263-4    |
| 4          | 97    | 50.8        | 419    | 9     | US-10-182-263-5    |
| 5          | 96    | 50.3        | 419    | 9     | US-10-182-263-6    |
| 6          | 86    | 45.0        | 419    | 9     | US-10-182-263-1    |
| 7          | 86    | 45.0        | 419    | 9     | US-09-978-917A-4   |
| 8          | 86    | 45.0        | 461    | 9     | US-10-182-263-2    |
| 9          | 86    | 45.0        | 461    | 9     | US-09-978-917A-2   |
| 10         | 78    | 40.8        | 415    | 10    | US-09-118-748-2    |
| 11         | 78    | 40.8        | 461    | 9     | US-10-132-829-5    |
| 12         | 78    | 40.8        | 461    | 10    | US-09-884-901-3    |
| 13         | 69    | 36.1        | 96     | 9     | US-09-759-1308-313 |
| 14         | 69    | 36.1        | 209    | 9     | US-09-759-1308-312 |
| 15         | 69    | 36.1        | 226    | 9     | US-09-759-1308-310 |
| 16         | 54    | 28.3        | 95     | 9     | US-09-759-1308-356 |
| 17         | 54    | 28.3        | 208    | 9     | US-09-759-1308-355 |
| 18         | 54    | 28.3        | 225    | 9     | US-09-759-1308-353 |
| 19         | 44    | 23.0        | 273    | 9     | US-09-764-868-968  |

|    |      |      |      |    |                     |                    |
|----|------|------|------|----|---------------------|--------------------|
| 20 | 43   | 22.5 | 1266 | 9  | US-09-931-969A-2    | Sequence 2, Appli  |
| 21 | 43   | 22.5 | 1266 | 9  | US-10-079-699-2     | Sequence 2, Appli  |
| 22 | 43   | 22.5 | 1266 | 10 | US-09-757-781-63    | Sequence 63, Appli |
| 23 | 43   | 22.5 | 1356 | 10 | US-09-757-781-2     | Sequence 2, Appli  |
| 24 | 42   | 22.0 | 88   | 10 | US-09-811-284-194   | Sequence 194, App  |
| 25 | 42   | 22.0 | 608  | 10 | US-09-908-664-5     | Sequence 5, Appli  |
| 26 | 42   | 22.0 | 1258 | 10 | US-09-922-543-1     | Sequence 1, Appli  |
| 27 | 42   | 22.0 | 1274 | 10 | US-09-746-491-12    | Sequence 12, Appli |
| 28 | 41.5 | 21.7 | 440  | 9  | US-09-910-186A-8    | Sequence 8, Appli  |
| 29 | 41   | 21.5 | 729  | 9  | US-10-145-396-11    | Sequence 11, Appli |
| 30 | 40.5 | 21.2 | 1149 | 10 | US-09-969-528-5     | Sequence 5, Appli  |
| 31 | 40   | 20.9 | 292  | 10 | US-09-764-864-1261  | Sequence 1261, Ap  |
| 32 | 40   | 20.9 | 744  | 10 | US-09-862-179A-1    | Sequence 1, Appli  |
| 33 | 40   | 20.9 | 1337 | 10 | US-09-757-781-62    | Sequence 62, Appli |
| 34 | 39.5 | 20.7 | 49   | 10 | US-09-764-864-1054  | Sequence 1054, Ap  |
| 35 | 39.5 | 20.7 | 420  | 10 | US-09-853-386-129   | Sequence 129, App  |
| 36 | 39   | 20.4 | 447  | 10 | US-09-815-242-13490 | Sequence 13490, A  |
| 37 | 39   | 20.4 | 447  | 10 | US-09-815-242-13612 | Sequence 13612, A  |
| 38 | 39   | 20.4 | 447  | 10 | US-09-735-564-2     | Sequence 2, Appli  |
| 39 | 39   | 20.4 | 873  | 9  | US-10-200-154-2     | Sequence 2, Appli  |
| 40 | 39   | 20.4 | 873  | 10 | US-09-954-043-2     | Sequence 2, Appli  |
| 41 | 38.5 | 20.2 | 348  | 10 | US-09-982-610-18    | Sequence 18, Appli |
| 42 | 38.5 | 20.2 | 1298 | 10 | US-09-982-610-33    | Sequence 33, Appli |
| 43 | 38.5 | 20.2 | 1363 | 9  | US-09-375-248-2     | Sequence 2, Appli  |
| 44 | 38.5 | 20.2 | 1363 | 9  | US-09-375-248-19    | Sequence 19, Appli |
| 45 | 38   | 19.9 | 47   | 10 | US-09-739-254-109   | Sequence 109, App  |

#### ALIGNMENTS

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RESULT 1
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      82.7%; Score 158; DB 9; Length 406;
Best Local Similarity 95.5%; Pred. No. 1.9e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXKCKXXQGSFFXXAEXIFKDXRTKLFWISY 44
Db 1 ANAFLLXLRNGSLRXKCKXXQGSFFXXAEXIFKDXRTKLFWISY 44

RESULT 2
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
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1  APPLICANT: Grinnell, Brian W
2  TITLE OF INVENTION: PROTEIN C DERIVATIVES
3  FILE REFERENCE: X-13611
4  CURRENT APPLICATION NUMBER: US/10/182.263
5  CURRENT FILING DATE: 2002-07-22
6  PRIOR APPLICATION NUMBER: 60/181948
7  PRIOR FILING DATE: 2002-02-11
8  PRIOR APPLICATION NUMBER: 60/189199
9  PRIOR FILING DATE: 2000-03-14
10 NUMBER OF SEQ ID NOS: 12
11 SOFTWARE: PatentIn version 3.1
12
13 SEQ ID NO 3
14     LENGTH: 419
15     TYPE: prt
16 ORGANISM: Homo sapiens
17
18 US-10-182-263-3

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|                       |       |              |         |            |
|-----------------------|-------|--------------|---------|------------|
| Query Match           | 97    | Score 97     | DB 9    | Length 419 |
| Best Local Similarity | 48.8% | Pred. No.    | 1.9e-09 |            |
| Matches               | 20    | Mismatches   | 17      | Indels 0   |
|                       |       | Conservative |         | Gaps 0     |

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Qy      1 ANAFLLXLRNGSLRXRCCKXQCSXXAEIIFKQAXRTLLFW 411
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Db      1 ANSFLEELRHGSLERECIEIICPFEAKIIFEDVDTLAFW 411

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RESULT 3
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

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|    |  |       |                   |      |                                     |
|----|--|-------|-------------------|------|-------------------------------------|
|    | Query Match                                    | 50.8% | Score 97          | DB 9 | Length 419                          |
|    | Best Local Similarity                          | 48.8% | Pred. No. 1.9e-09 |      |                                     |
|    | Matches  | 20    | Conservative      | 4    | Mismatches 17<br>Indels 0<br>Gaps 0 |
| OY | 1 ANAFLLXNLNGSLTXRCKXXKCSFFXAEXIFPKAXTKLFW     | 41    |                   |      |                                     |
|    | .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: . |       |                   |      |                                     |
| D6 | 1 ANSFLEELRHSGLSERECIEIICDFEBAKLFPEVDVDTLFW    | 41    |                   |      |                                     |

RESULT 4  
US-10-182-263-5  
Sequence 5, Application US/10182263  
Publication No. US20030022354A1  
GENERAL INFORMATION:  
APPLICANT: Gerlitz, Bruce E  
APPLICANT: Jones, Bryan E  
APPLICANT: Grinnell, Brian W  
TITLE OF INVENTION: PROTEIN C DERIVATIVES  
FILE REFERENCE: X-13611  
CURRENT APPLICATION NUMBER: US/10/182,263  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: 60/181948  
PRIOR FILING DATE: 2002-02-11

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? PRIOR APPLICATION NUMBER: 60/183195
? PRIOR FILING DATE: 2000-03-14
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 5
? LENGTH: 419
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-182-263-5

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|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 50.8%          | Score 97          | DB 9     | Length 419 |
| Best Local Similarity | 48.8%          | Pred. No. 1.9e-09 |          |            |
| Matches 20            | Conservative 4 | Mismatches 17     | Indels 0 | Gaps 0     |

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QY      1 ANAFLLXLPNGSLXRXCKXQCSFXXAEIFKQAXRTLFW 411
        ||:|||||:|||||:|||||
DB      1 ANSPLEELRHGSLERECEIEICPFEAKEIFEVDVDTLAFW 411

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```

US-10-182-263-6
RESULT 5
: Sequence 6, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-11611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2002-02-11
: PRIOR APPLICATION NUMBER: 60/189199
: PRIOR FILING DATE: 2000-03-10
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6
: LENGTH: 419
: TYPE: prt
: ORGANISM: Homo sapiens
US-10-182-263-6

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|                       |       |  |      |                         |
|-----------------------|-------|--|------|-------------------------|
| Query Match           | 50.3% | Score 96                                 | DB 9 | Length 419              |
| Best Local Similarity | 48.8% | Pred. No. 2.9e-09                        |      |                         |
| Matches               | 20    | Conservative                             | 3    | Mismatches 18; Indels 0 |
| QY                    | 1     | ANAFLXLLNNGSLRXKXKXQCSFXXAEITFDKARTKFLW  | 41   |                         |
| DB                    | 1     | ANSFLEELRQGSLEERCIEICDFFEDAKITFEDVDITLFW | 41   |                         |

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RESULT 6
US-10-182-263-1
: Sequence 1, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan B
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182, 263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2002-02-11
: PRIOR APPLICATION NUMBER: 60/189199
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 419
: TYPE: PRT
:

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ORGANISM: Homo sapiens  
US-10-182-263-1

Query Match 45.0%; Score 86; DB 9; Length 419;  
Best Local Similarity 43.9%; Pred. No. 1.8e-07;  
Matches 18; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41  
DB 1 ANSFLELRHSSLERECIEICDFEAKKEIFQNVDTLAFW 41

RESULT 7

US-09-978-917A-4  
Sequence 4, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:

APPLICANT: Maxygen Aps; Maxygen Holdings

TITLE OF INVENTION: Protein C or activated protein C-like molecules

FILE REFERENCE: 0219us310 - protein C

CURRENT APPLICATION NUMBER: US/09/978, 917A

CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US-09-978-917A-4

Query Match 45.0%; Score 86; DB 9; Length 419;  
Best Local Similarity 43.9%; Pred. No. 1.8e-07;  
Matches 18; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41  
DB 1 ANSFLELRHSSLERECIEICDFEAKKEIFQNVDTLAFW 41

RESULT 8

US-10-182-263-2

Sequence 2, Application US/10182263

Publication No. US20030022354A1

GENERAL INFORMATION:

APPLICANT: Geflicz, Bruce E

APPLICANT: Jones, Bryan E

APPLICANT: Grinnell, Brian W

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-13611

CURRENT APPLICATION NUMBER: US/10/182, 263

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: 60/189199

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 461

TYPE: PRT

ORGANISM: Homo sapiens

US-10-182-263-2

Query Match 45.0%; Score 86; DB 9; Length 461;  
Best Local Similarity 43.9%; Pred. No. 2e-07;  
Matches 18; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41  
DB 43 ANSFLELRHSSLERECIEICDFEAKKEIFQNVDTLAFW 83

RESULT 9

US-09-978-917A-2  
Sequence 2, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:

APPLICANT: Maxygen Aps; Maxygen Holdings

TITLE OF INVENTION: Protein C or activated protein C-like molecules

FILE REFERENCE: 0219us310 - protein C

CURRENT APPLICATION NUMBER: US/09/978, 917A

CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 461

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(42)

FEATURE:

NAME/KEY: CHAIN

LOCATION: (43)...(461)

US-09-978-917A-2

Query Match 45.0%; Score 86; DB 9; Length 461;  
Best Local Similarity 43.9%; Pred. No. 2e-07;  
Matches 18; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRXCKXQCSFXXAEXIFKDXARTKLFW 41  
DB 43 ANSFLELRHSSLERECIEICDFEAKKEIFQNVDTLAFW 83

RESULT 10

US-09-118-748-2

Sequence 2, Application US/09118748A

Patent No. US20020031799A1

GENERAL INFORMATION:

APPLICANT: Stafford, Darrel W.

APPLICANT: Chang, Jinli

TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting

FILE REFERENCE: 5470-183

CURRENT APPLICATION NUMBER: US/09/118, 748A

CURRENT FILING DATE: 1998-07-17

EARLIER APPLICATION NUMBER: 60/053, 571

EARLIER FILING DATE: 1997-07-21

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 415

TYPE: PRT

ORGANISM: Homo sapiens

US-09-118-748-2

Query Match 40.8%; Score 78; DB 10; Length 415;  
Best Local Similarity 41.2%; Pred. No. 5e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLRXCKXQCSFXXAEXIFKDXARTKLFWISY 44  
DB 12 GNLRECEMEKCSFEARBEVENTERTTTFWKQY 45

RESULT 11

US-10-132-829-5

Sequence 5, Application US/10132829

Publication No. US20030044982A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R

APPLICANT: Hoshijima, Masahiko

TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII:

FILE REFERENCE: 6627-Pal170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5
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Query Match          40.8%; Score 78; DB 9; Length 461;
Best Local Similarity 41.2%; Pred. No. 5.6e-06;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
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Qy 11 GSLRXCKXKXOCSPFXAXEIFKDAKRTKLFWISY 44
Db 58 GNLERECMEBKCSFEAREVFEKTERITTEFWKQY 91
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## RESULT 12

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US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: HomoSapien
US-09-884-901-3
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Query Match          40.8%; Score 78; DB 10; Length 461;
Best Local Similarity 41.2%; Pred. No. 5.6e-06;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
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```
Qy 11 GSLRXCKXKXOCSPFXAXEIFKDAKRTKLFWISY 44
Db 58 GNLERECMEBKCSFEAREVFEKTERITTEFWKQY 91
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## RESULT 13

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US-09-759-1308-313
; Sequence 313, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-1308-313
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Query Match          36.1%; Score 69; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 4.4e-05;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
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Qy 11 GSLRXCKXKXOCSPFXAXEIFKDAKRTKLFWISY 44
Db 46 GNLERECNEELCNVEAREIFVDEKTIATFWQY 79
```

## RESULT 14

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US-09-759-1308-312
; Sequence 312, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
```

; PRIOR APPLICATION NUMBER: US 09/508,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 312  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-130B-312

Query Match 36.1%; Score 69; DB 9; Length 209;  
Best Local Similarity 38.2%; Pred. No. 0.0001;  
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 11 GSLRXKCKXXQCSPXXAEXIFKDXRKLFWISY 44  
DB 46 GNLERECNEELCNVEARLIFVDEKTIAPWQEX 79

## RESULT 15

US-09-759-130B-310  
; Sequence 310, Application US/09759130B  
; Publication No. US20030022279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Frazer, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirtel, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; TITLE OF INVENTION: USBS.  
; FILE REFERENCE: MP100-535OMNIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: US 09/608,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 310  
; LENGTH: 226  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-759-130B-310

Query Match 36.1%; Score 69; DB 9; Length 226;  
Best Local Similarity 38.2%; Pred. No. 0.00011;  
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 11 GSLRXKCKXXQCSPXXAEXIFKDXRKLFWISY 44  
DB 63 GNLERECNEELCNVEARLIFVDEKTIAPWQEX 96

Search completed: March 20, 2003, 13:30:10  
Job time : 8.375 secs

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2003, 13:28:03 ; Search time 19.8125 Seconds  
(without alignments)  
290.824 Million cell updates/sec

Title: 10ASN28GLU  
Perfect score: 191  
Sequence: 1 ANAFLXLRNGSLXRXCKXX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 607744 seqs, 130953579 residues

Total number of hits satisfying chosen parameters: 607744

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/prodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/paa/US08\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/prodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                  | Description        |
|------------|-------|-------------|--------|------------------------|--------------------|
| 1          | 158   | 82.7        | 44     | 6 US-10-298-330-3      | Sequence 3, Appl1  |
| 2          | 158   | 82.7        | 406    | 6 US-10-281-727-1      | Sequence 1, Appl1  |
| 3          | 158   | 82.7        | 444    | 1 PCT-US02-33263-8     | Sequence 8, Appl1  |
| 4          | 158   | 82.7        | 444    | 6 US-10-287-994-8      | Sequence 8, Appl1  |
| 5          | 158   | 82.7        | 466    | 1 PCT-US02-31696-2     | Sequence 2, Appl1  |
| 6          | 134   | 70.2        | 40     | 6 US-10-298-330-23     | Sequence 23, Appl1 |
| 7          | 132   | 69.1        | 40     | 6 US-10-298-330-22     | Sequence 22, Appl1 |
| 8          | 128   | 67.5        | 40     | 6 US-10-298-330-25     | Sequence 25, Appl1 |
| 9          | 127   | 66.0        | 40     | 6 US-10-298-330-26     | Sequence 26, Appl1 |
| 10         | 126   | 66.0        | 40     | 6 US-10-298-330-24     | Sequence 24, Appl1 |
| 11         | 122   | 63.9        | 44     | 6 US-10-298-330-4      | Sequence 4, Appl1  |
| 12         | 104.5 | 54.7        | 41     | 6 US-10-298-330-27     | Sequence 27, Appl1 |
| 13         | 98    | 51.3        | 153    | 5 US-09-724-676-60067  | Sequence 60067, A  |
| 14         | 98    | 51.3        | 153    | 5 US-09-724-676A-60067 | Sequence 60067, A  |
| 15         | 98    | 51.3        | 377    | 1 PCT-US03-02500-29    | Sequence 29, Appl1 |
| 16         | 98    | 51.3        | 442    | 1 PCT-US03-02500-30    | Sequence 30, Appl1 |
| 17         | 98    | 51.3        | 444    | 1 PCT-US03-02500-28    | Sequence 28, Appl1 |
| 18         | 97    | 50.8        | 44     | 6 US-10-298-330-18     | Sequence 18, Appl1 |
| 19         | 97    | 50.8        | 419    | 6 US-10-168-407-3      | Sequence 3, Appl1  |
| 20         | 97    | 50.8        | 419    | 6 US-10-168-407-4      | Sequence 4, Appl1  |
| 21         | 96    | 50.3        | 419    | 6 US-10-168-407-5      | Sequence 5, Appl1  |
| 22         | 96    | 50.3        | 419    | 6 US-10-168-407-6      | Sequence 6, Appl1  |
| 23         | 95    | 49.7        | 218    | 5 US-09-724-676-82391  | Sequence 82391, A  |
| 24         | 95    | 49.7        | 218    | 5 US-09-724-676A-82391 | Sequence 82391, A  |
| 25         | 94    | 49.2        | 426    | 5 US-09-951-121A-1     | Sequence 1, Appl1  |
| 26         | 94    | 49.2        | 426    | 6 US-10-295-682-1      | Sequence 1, Appl1  |

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|----|----|------|-----|------------------------|--------------------|
| 27 | 90 | 47.1 | 44  | 6 US-10-298-330-2      | Sequence 2, Appl1  |
| 28 | 86 | 45.0 | 44  | 6 US-10-298-330-1      | Sequence 1, Appl1  |
| 29 | 86 | 45.0 | 415 | 5 US-09-763-153-2      | Sequence 2, Appl1  |
| 30 | 86 | 45.0 | 419 | 1 PCT-US03-05046-3     | Sequence 3, Appl1  |
| 31 | 86 | 45.0 | 419 | 6 US-10-168-407-1      | Sequence 1, Appl1  |
| 32 | 86 | 45.0 | 461 | 6 US-10-168-407-1      | Sequence 2, Appl1  |
| 33 | 84 | 44.0 | 453 | 7 US-60-443-566-2652   | Sequence 2652, Ap  |
| 34 | 84 | 44.0 | 465 | 5 US-09-724-676-63736  | Sequence 63736, A  |
| 35 | 84 | 44.0 | 465 | 5 US-09-724-676A-63736 | Sequence 63736, A  |
| 36 | 84 | 44.0 | 494 | 7 US-60-443-566-2653   | Sequence 2653, Ap  |
| 37 | 84 | 44.0 | 622 | 1 PCT-US02-19017-29    | Sequence 29, Appl1 |
| 38 | 84 | 44.0 | 622 | 6 US-10-017-631-2      | Sequence 2, Appl1  |
| 39 | 84 | 44.0 | 622 | 6 US-10-214-932-116    | Sequence 116, Ap   |
| 40 | 84 | 44.0 | 622 | 7 US-60-443-566-2651   | Sequence 2651, Ap  |
| 41 | 78 | 40.8 | 45  | 6 US-10-298-330-5      | Sequence 5, Appl1  |
| 42 | 78 | 40.8 | 456 | 6 US-10-038-854-95     | Sequence 95, Appl1 |
| 43 | 78 | 40.8 | 456 | 6 US-10-038-854-96     | Sequence 96, Appl1 |
| 44 | 78 | 40.8 | 461 | 6 US-10-234-406-6      | Sequence 6, Appl1  |
| 45 | 78 | 40.8 | 461 | 6 US-10-234-406-8      | Sequence 8, Appl1  |

## ALIGNMENTS

```

RESULT 1
US-10-298-330-3
; Sequence 3, Application US/10298330
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-3

Query Match      82.7%  Score 158, DB 6, Length 44;
Best Local Similarity 95.5%  Pred. No. 2, 8e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLXLRNGSLXRXCKXXOCSPFXAEXIFKDXRTKLFWISY 44
Db 1 ANAFLXLRNGSLXRXCKXXOCSPFXAEXIFKDXRTKLFWISY 44

RESULT 2
US-10-281-727-1
; Sequence 1, Application US/10281727
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Human Coagulation Factor VII
; FILE REFERENCE: 6410,200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627

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; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1
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Query Match      82.7%; Score 158; DB 6; Length 406;
Best Local Similarity 95.5%; Pred. No. 2.6e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 1 ANAFLXLRNGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 44
Db 1 ANAFLXLRPGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 44
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RESULT 3
PCT-US02-32263-8
; Sequence 8, Application PC/TUS0232263
; GENERAL INFORMATION:
; APPLICANT: Necose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bove, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5050MC
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-32263-8
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Query Match      82.7%; Score 158; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 2.8e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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OY 1 ANAFLXLRNGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 44
Db 39 ANAFLXLRPGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 82
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RESULT 4
US-10-287-994-8
; Sequence 8, Application US/10287994
; GENERAL INFORMATION:
; APPLICANT: Necose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bove, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-994-8
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Query Match      82.7%; Score 158; DB 6; Length 444;
Best Local Similarity 72.7%; Pred. No. 2.8e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY 1 ANAFLXLRNGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 44
Db 39 ANAFLXLRPGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 82
```

```
RESULT 5
PCT-US02-31696-2
; Sequence 2, Application PC/TUS0231696
; GENERAL INFORMATION:
; APPLICANT: Vitiivety, Inc., et al.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: NMT-007PC
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US02/31696
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/327,487
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 10/017,122
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-31696-2
```

```
Query Match      82.7%; Score 158; DB 1; Length 466;
Best Local Similarity 72.7%; Pred. No. 2.9e-20;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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```
OY 1 ANAFLXLRNGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 44
Db 39 ANAFLXLRPGSLKRXCKXQCSFYXAXEIFKDAKRTKLFWISY 82
```



Db 61 ANAFLEELRPGSLRCKEBCQCSFEAREIFKDAERTKLFWSY 104

RESULT 6  
US-10-298-330-23

/ Sequence 23, Application US/10298330  
/ GENERAL INFORMATION:  
/ APPLICANT: Nelisestuen, Gary L.  
/ TITLE OF INVENTION: Modified Vitamin K-Dependent  
/ FILE REFERENCE: 09531-127001  
/ CURRENT APPLICATION NUMBER: US/10/298,330  
/ PRIOR FILING DATE: 2002-11-18  
/ PRIOR APPLICATION NUMBER: 09/497,591  
/ PRIOR FILING DATE: 2000-02-03  
/ PRIOR APPLICATION NUMBER: 09/302,239  
/ PRIOR FILING DATE: 1999-04-29  
/ PRIOR APPLICATION NUMBER: 08/955,636  
/ PRIOR FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 27  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 23  
/ LENGTH: 40  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35  
/ OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-23

Query Match 70.2%; Score 134; DB 6; Length 40;  
Best Local Similarity 95.0%; Pred. No. 5.7e-17;  
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40  
Db 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40

RESULT 7  
US-10-298-330-22

/ Sequence 22, Application US/10298330  
/ GENERAL INFORMATION:  
/ APPLICANT: Nelisestuen, Gary L.  
/ TITLE OF INVENTION: Modified Vitamin K-Dependent  
/ FILE REFERENCE: 09531-127001  
/ CURRENT APPLICATION NUMBER: US/10/298,330  
/ PRIOR FILING DATE: 2002-11-18  
/ PRIOR APPLICATION NUMBER: 09/497,591  
/ PRIOR FILING DATE: 2000-02-03  
/ PRIOR APPLICATION NUMBER: 09/302,239  
/ PRIOR FILING DATE: 1999-04-29  
/ PRIOR APPLICATION NUMBER: 08/955,636  
/ PRIOR FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 27  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 22  
/ LENGTH: 40  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35  
/ OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-22

Query Match 69.1%; Score 132; DB 6; Length 40;  
Best Local Similarity 95.0%; Pred. No. 1.3e-16;  
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40

Db 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40

RESULT 8  
US-10-298-330-25

/ Sequence 25, Application US/10298330  
/ GENERAL INFORMATION:  
/ APPLICANT: Nelisestuen, Gary L.  
/ TITLE OF INVENTION: Modified Vitamin K-Dependent  
/ FILE REFERENCE: 09531-127001  
/ CURRENT APPLICATION NUMBER: US/10/298,330  
/ PRIOR FILING DATE: 2002-11-18  
/ PRIOR APPLICATION NUMBER: 09/497,591  
/ PRIOR FILING DATE: 2000-02-03  
/ PRIOR APPLICATION NUMBER: 09/302,239  
/ PRIOR FILING DATE: 1999-04-29  
/ PRIOR APPLICATION NUMBER: 08/955,636  
/ PRIOR FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 27  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 25  
/ LENGTH: 40  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35  
/ OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-25

Query Match 67.0%; Score 128; DB 6; Length 40;  
Best Local Similarity 92.5%; Pred. No. 7e-16;  
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40  
Db 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40

RESULT 9  
US-10-298-330-26

/ Sequence 26, Application US/10298330  
/ GENERAL INFORMATION:  
/ APPLICANT: Nelisestuen, Gary L.  
/ TITLE OF INVENTION: Modified Vitamin K-Dependent  
/ FILE REFERENCE: 09531-127001  
/ CURRENT APPLICATION NUMBER: US/10/298,330  
/ PRIOR FILING DATE: 2002-11-18  
/ PRIOR APPLICATION NUMBER: 09/497,591  
/ PRIOR FILING DATE: 2000-02-03  
/ PRIOR APPLICATION NUMBER: 09/302,239  
/ PRIOR FILING DATE: 1999-04-29  
/ PRIOR APPLICATION NUMBER: 08/955,636  
/ PRIOR FILING DATE: 1997-10-23  
/ NUMBER OF SEQ ID NOS: 27  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 26  
/ LENGTH: 40  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 33, 35  
/ OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-26

Query Match 66.5%; Score 127; DB 6; Length 40;  
Best Local Similarity 92.5%; Pred. No. 1.1e-15;  
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLRCKCKXQCSEFXAXEYIFKDXARTKLF 40

OY 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 40  
|||  
Db 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 40

RESULT 10  
US-10-298-330-24

; Sequence 24, Application US/10298330  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; PRIOR FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35  
; OTHER INFORMATION: xaa = gamma carboxyglutamic acid  
US-10-298-330-24

Query Match 66.0%; Score 126; DB 6; Length 40;  
Best Local Similarity 92.5%; Pred. No. 1.6e-15;  
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 40  
|||  
Db 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 40

RESULT 11  
US-10-298-330-4

; Sequence 4, Application US/10298330  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; PRIOR FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35  
; OTHER INFORMATION: xaa = gamma carboxyglutamic acid or glutamic acid  
US-10-298-330-4

Query Match 63.9%; Score 122; DB 6; Length 44;  
Best Local Similarity 75.0%; Pred. No. 9.5e-15;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 44  
|||  
Db 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 44

RESULT 12  
US-10-298-330-27

; Sequence 27, Application US/10298330  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; PRIOR FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: 7, 8, 15, 17, 20, 21, 26, 27, 30, 33, 35, 36  
; OTHER INFORMATION: xaa = gamma carboxyglutamic acid  
US-10-298-330-27

Query Match 54.7%; Score 104.5; DB 6; Length 41;  
Best Local Similarity 85.4%; Pred. No. 1.3e-11;  
Matches 35; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 40  
|||  
Db 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 41

RESULT 13  
US-09-724-676-60067

; Sequence 60067, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 60067  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-724-676-60067

Query Match 51.3%; Score 98; DB 5; Length 153;  
Best Local Similarity 38.6%; Pred. No. 7.3e-10;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 44  
|||  
Db 41 ANAFLXLRNGSLKRXCKXQCSPFXAXEIPKDAKRTKLF 84

RESULT 14  
US-09-724-676A-60067  
; Sequence 60067, Application US/09724676A  
; GENERAL INFORMATION:

Db 41 ANSFLEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKY 84  
Search completed: March 20, 2003, 13:35:35  
Job time : 20.8125 secs

APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 60067  
LENGTH: 153  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-60067

Query Match 51.3%; Score 98; DB 5; Length 153;  
Best Local Similarity 38.6%; Pred. No. 7.3e-10;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44  
DB 41 ANSFLEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKY 84

RESULT 15

PCT-US03-02500-29  
Sequence 29, Application PC/TUS0302500  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; HAFALIA, April J.A.;  
APPLICANT: LI, Joana X.; GORVAD, Ann E.;  
APPLICANT: CHAWLA, Nandinder K.; SPRAGUE, William W.;  
APPLICANT: LEE, Soo Yeun; CHANG, Hsin-Ru;  
APPLICANT: ELIOTT, Vicki S.; RAMKUMAR, Jayalaxmi;  
APPLICANT: KHARE, Reena; EMERLING, Brooke M.;  
APPLICANT: KABLE, Amy E.; TANG, Y. Tom;  
APPLICANT: YUE, Henry; GIETZEN, Kimberly J.;  
APPLICANT: LEE, Sally; SWARNAKAR, Anita;  
APPLICANT: BAUGHN, Mariah R.; WILSON, Amy D.;  
APPLICANT: JIN, Pei; CHEN, David;  
APPLICANT: HAWKINS, Phillip R.; JIANG, Xin;  
APPLICANT: JACKSON, Alan A.; BHATIA, Umesh;  
APPLICANT: BURRILL, John D.; BLAKE, Julie J.;  
APPLICANT: HO, Anne; ZHENG, Wenjin;  
APPLICANT: ISON, Craig H.; MARQUIS, Joseph P.;  
APPLICANT: TRAN, Uyen K.; LAL, Preeti G.;  
APPLICANT: WARREN, Bridget A.; XU, Yuming;  
APPLICANT: HONCHEL, Cynthia D.; BECHA, Shanya D.;  
APPLICANT: LEHR-WASON, Patricia M.  
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES  
FILE REFERENCE: PF-1362 PCT  
CURRENT APPLICATION NUMBER: PCT/US03/02500  
CURRENT FILING DATE: 2003-01-23  
PRIOR APPLICATION NUMBER: US 60/351,928  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: US 60/359,903  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: US 60/366,837  
PRIOR FILING DATE: 2002-03-21  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PERL Program  
SEQ ID NO 29  
LENGTH: 377  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: 7509140CD1  
PCT-US03-02500-29

Query Match 51.3%; Score 98; DB 1; Length 377;  
Best Local Similarity 38.6%; Pred. No. 1.8e-09;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXCKXQCSFXXAEXIFKDXRTKLFWISY 44  
DB 41 ANSFLEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKY 84

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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds  
(without alignments)  
186.869 Million cell updates/sec

Title: 10ASN28PHE

Perfect score: 192  
Sequence: 1 ANAFLLXLRNGLXRXCKXX.....XXAFYIFDXAKTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq.101002:\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 164   | 85.4        | 44     | 20    | AA18312     |
| 2          | 158   | 82.3        | 44     | 20    | AA18311     |
| 3          | 157   | 81.8        | 44     | 20    | AA18310     |
| 4          | 155   | 80.7        | 44     | 20    | AA18305     |
| 5          | 155   | 80.7        | 44     | 22    | AA18395     |
| 6          | 155   | 80.7        | 401    | 22    | AA184870    |
| 7          | 155   | 80.7        | 401    | 22    | AA184871    |
| 8          | 155   | 80.7        | 406    | 14    | AA185764    |
| 9          | 155   | 80.7        | 406    | 18    | AA14509     |
| 10         | 155   | 80.7        | 406    | 18    | AA14510     |

|    |     |      |     |    |          |                    |
|----|-----|------|-----|----|----------|--------------------|
| 11 | 155 | 80.7 | 406 | 22 | AAU77745 | Human factor VIIa  |
| 12 | 155 | 80.7 | 406 | 22 | AA152171 | Human FVII Seq ID  |
| 13 | 155 | 80.7 | 406 | 22 | AA152172 | Mammalian express  |
| 14 | 155 | 80.7 | 406 | 22 | AA152181 | Human FVII mutant  |
| 15 | 155 | 80.7 | 406 | 22 | AA152182 | Human FVII mutant  |
| 16 | 155 | 80.7 | 406 | 22 | AA152183 | Human FVII mutant  |
| 17 | 155 | 80.7 | 406 | 22 | AA152184 | Human FVII mutant  |
| 18 | 155 | 80.7 | 406 | 22 | AA152185 | Human FVII mutant  |
| 19 | 155 | 80.7 | 406 | 22 | AA152186 | Human FVII mutant  |
| 20 | 155 | 80.7 | 406 | 22 | AA152187 | Human FVII mutant  |
| 21 | 155 | 80.7 | 406 | 22 | AA152188 | Wild-type human b1 |
| 22 | 155 | 80.7 | 406 | 22 | AA152189 | Mutant blood coagu |
| 23 | 155 | 80.7 | 406 | 22 | AA152190 | Mutant blood coagu |
| 24 | 155 | 80.7 | 406 | 22 | AA152191 | Mutant blood coagu |
| 25 | 155 | 80.7 | 406 | 22 | AA152192 | Human coagulation  |
| 26 | 155 | 80.7 | 406 | 22 | AA152193 | Human coagulation  |
| 27 | 155 | 80.7 | 406 | 22 | AA152194 | Human coagulation  |
| 28 | 155 | 80.7 | 406 | 22 | AA152195 | Human coagulation  |
| 29 | 155 | 80.7 | 406 | 22 | AA152196 | Human coagulation  |
| 30 | 155 | 80.7 | 406 | 22 | AA152197 | Human coagulation  |
| 31 | 155 | 80.7 | 406 | 22 | AA152198 | Human coagulation  |
| 32 | 155 | 80.7 | 406 | 22 | AA152199 | Human coagulation  |
| 33 | 155 | 80.7 | 406 | 22 | AA152200 | Human coagulation  |
| 34 | 155 | 80.7 | 406 | 22 | AA152201 | Human coagulation  |
| 35 | 155 | 80.7 | 406 | 22 | AA152202 | Human coagulation  |
| 36 | 155 | 80.7 | 406 | 22 | AA152203 | Human coagulation  |
| 37 | 155 | 80.7 | 406 | 22 | AA152204 | Human coagulation  |
| 38 | 155 | 80.7 | 406 | 22 | AA152205 | Human coagulation  |
| 39 | 155 | 80.7 | 406 | 22 | AA152206 | Human coagulation  |
| 40 | 155 | 80.7 | 406 | 22 | AA152207 | Human coagulation  |
| 41 | 155 | 80.7 | 406 | 22 | AA152208 | Human coagulation  |
| 42 | 155 | 80.7 | 406 | 22 | AA152209 | Human coagulation  |
| 43 | 155 | 80.7 | 406 | 22 | AA152210 | Human coagulation  |
| 44 | 155 | 80.7 | 406 | 22 | AA152211 | Human coagulation  |
| 45 | 155 | 80.7 | 406 | 22 | AA152212 | Human coagulation  |

#### ALIGNMENTS

|          |  |  |
|----------|--|--|
| RESULT 1 | AA18312  | AA18312 standard; peptide; 44 AA.                          |
| ID       | AA18312  |  |
| AC       | AA18312  |  |
| DT       | 17-AUG-1999  | (first entry)  |
| DE       | Modified GLA domain of vitamin K-dependent protein.                |  |
| KW       | GLA domain; mutem; vitamin K-dependent protein; clotting disorder; |  |
| KW       | therapy.   |  |
| XX       | Homo sapiens.  |  |
| OS       | Synthetic.   |  |
| FT       | Key  | Location/Qualifiers  |
| FT       | Misc-difference 1..44  | /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid" |
| FT       | FT   |  |
| FT       | FT   |  |
| PN       | MO9920767-A1.  |  |
| PD       | 29-APR-1999.   |  |
| PF       | 20-OCT-1998;   | 98WO-US22152.  |
| PR       | 23-OCT-1997;   | 97US-0955636.  |
| PA       | (MINU ) UNIV MINNESOTA.  |  |
| PI       | Nelsetstuen GL;  |  |
| XX       |  |  |

DR WPI; 1999-288309/24.  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
Query Match 85.4%; Score 164; DB 20; Length 44;  
Best Local Similarity 97.7%; Pred. No. 2.3e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFIXLRLNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
DB 1 ANAFIXLRLNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
RESULT 2  
AA18311  
ID AA18311 standard; peptide; 44 AA.  
XX  
XX AA18311;  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KW therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
FT  
XX  
XX W09920767-A1.  
XX  
XX 29-APR-1999.  
XX  
XX 20-OCT-1998; 98WO-US22152.  
XX  
XX 23-OCT-1997; 97US-0955636.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX  
XX Neleestuen GL;  
PI WPI; 1999-288309/24.  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;

CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
XX  
SQ Sequence 44 AA;  
Query Match 82.3%; Score 158; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2.4e-19;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFIXLRLNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
DB 1 ANAFIXLRLNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
RESULT 3  
AA18310  
ID AA18310 standard; peptide; 44 AA.  
XX  
XX AA18310;  
AC  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KW therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
FT  
XX  
XX W09920767-A1.  
XX  
XX 29-APR-1999.  
XX  
XX 20-OCT-1998; 98WO-US22152.  
XX  
XX 23-OCT-1997; 97US-0955636.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX  
XX Neleestuen GL;  
PI WPI; 1999-288309/24.  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
Query Match 81.8%; Score 157; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 3.5e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 ANAFIXLRLNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
DB 1 ANAFIXLRLNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44

```

RESULT 4
AAV18305
ID AAV18305 standard; peptide; 44 AA.
XX
AC AAV18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder;
KM therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
PN WO920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98MO-US22152.
XX
PR 23-OCT-1997; 97US-0955636.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
DT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 80.7%; Score 155; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 7.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ANAFLLXLRGSLRXKCKXXQCSEFXAXIFKDXRRTKLFWISY 44
DB 1 ANAFLLXLRGSLRXKCKXXQCSEFXAXIFKDXRRTKLFWISY 44
XX
RESULT 5
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
AC AAB36395;
XX
DT 27-FEB-2001 (first entry)
XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KM factor X; prothrombin; enhanced membrane binding affinity;

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```

KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
KM liver disease.
XX
OS Homo sapiens.
XX
PN WO200066753-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US11416.
XX
PR 29-APR-1999; 99US-0302239.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 2001-007226/01.
XX
DT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity
XX
PS Disclosure; Page 12; 81pp; English.
XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;
XX
Query Match 80.7%; Score 155; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 7.7e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ANAFLLXLRGSLRXKCKXXQCSEFXAXIFKDXRRTKLFWISY 44
DB 1 ANAFLLXLRGSLRXKCKXXQCSEFXAXIFKDXRRTKLFWISY 44
XX
RESULT 6
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
AC AAB84870;
XX
DT 31-JUL-2001 (first entry)
XX
DE Mutant blood coagulant factor VII (FVII-31).
XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KM mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX

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PN JP2001061479-A.  
 XX  
 PD 13-MAR-2001.  
 XX  
 PF 24-AUG-1999; 99JP-0237610.  
 XX  
 PR 24-AUG-1999; 99JP-0237610.  
 XX  
 PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 XX  
 DR WPI: 2001-310677/33.  
 DR N-PSDB; AAH19463.  
 XX  
 PT Mutant of blood coagulant factor VII, used for substitution therapy in  
 XX the treatment of hemophilia -  
 PS Claim 14; Page 20-21; 29pp; Japanese.  
 XX  
 CC The present invention relates to mutants of blood coagulant factor VII  
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present  
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an  
 CC agent for the substitution therapy of haemophilia inhibitor patients.  
 XX  
 SQ Sequence 401 AA;  
 Query Match 80.7%; Score 155; DB 22; Length 401;  
 Best Local Similarity 72.7%; Pred. No. 7.6e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ANAFLEXLRNGSLRXCKXQCSEFXKXAFKPDARTLFWISY 44  
 Db 1 ANAFLELRPGSLERECKEQCSEFEAREIFPDARTLFWISY 44  
 RESULT 7  
 AAB84871 ID AAB84871 standard; Procein; 401 AA.  
 XX  
 AC AAB84871;  
 XX  
 DT 31-JUL-2001 (first entry)  
 XX  
 DE Mutant blood coagulant factor VII (FVII-39).  
 XX  
 KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;  
 KM mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 235..239  
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by  
 FT Asp-Arg-Lys-Thr-Leu"  
 FT Misc-difference 311..317  
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp  
 FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"  
 XX  
 PN JP2001061479-A.  
 XX  
 PD 13-MAR-2001.  
 XX  
 PF 24-AUG-1999; 99JP-0237610.  
 XX  
 PR 24-AUG-1999; 99JP-0237610.  
 XX  
 PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 XX  
 DR WPI: 2001-310677/33.  
 DR N-PSDB; AAH19464.  
 XX  
 PT Mutant of blood coagulant factor VII, used for substitution therapy in  
 PT the treatment of hemophilia -

XX  
 PS Claim 16; Page 23-24; 29pp; Japanese.  
 XX  
 CC The present invention relates to mutants of blood coagulant factor VII  
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present  
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an  
 CC agent for the substitution therapy of haemophilia inhibitor patients.  
 XX  
 SQ Sequence 401 AA;  
 Query Match 80.7%; Score 155; DB 22; Length 401;  
 Best Local Similarity 72.7%; Pred. No. 7.6e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ANAFLEXLRNGSLRXCKXQCSEFXKXAFKPDARTLFWISY 44  
 Db 1 ANAFLELRPGSLERECKEQCSEFEAREIFPDARTLFWISY 44  
 RESULT 8  
 AAR35764 ID AAR35764 standard; protein; 406 AA.  
 XX  
 AC AAR35764;  
 XX  
 DT 24-SEP-1993 (first entry)  
 XX  
 DE Factor VII (VII).  
 XX  
 KM PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;  
 KM Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;  
 KM exosite; catalytic activity.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..152  
 FT /note= "Factor VII light chain"  
 FT Region 153..406  
 FT /note= "Factor VII heavy chain"  
 FT Peptide 374..388  
 FT /note= "exosite 1"  
 FT Peptide 290..310  
 FT /note= "exosite 2"  
 FT Peptide 290..310  
 FT /note= "pref. PC polypeptide; claim 2, page 136"  
 FT Peptide 374..388  
 FT /note= "pref. PC polypeptide; claim 2, page 136"  
 FT Peptide 289..304  
 FT /note= "pref. PC polypeptide; claim 4, page 137"  
 FT Peptide 290..304  
 FT /note= "pref. PC polypeptide; claim 4, page 137"  
 FT Peptide 245..266  
 FT /note= "claim 9, page 138-139 describes an antibody  
 FT that reacts with Factor VII; fragments  
 FT 289-304, 290-304, 290-310, 374-388 and  
 FT 400-414 but not with fragment 245-266"  
 XX  
 PN WO9309804-A.  
 XX  
 PD 27-MAY-1993.  
 XX  
 PF 18-NOV-1992; 92WO-US10242.  
 XX  
 PR 18-NOV-1991; 91US-0793989.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Griffiin JH, Meesters RM;  
 XX  
 DR WPI: 1993-182244/22.  
 DR  
 XX  
 PT Serine protease derived-polypeptide(s) and anti-peptide



PT antibodies - for inhibiting coagulation and assaying for the  
 PT presence of serine protease in fluid samples  
 XX  
 PS Disclosure; Page 133-135; 149pp; English.  
 XX The PC polypeptides indicated in the Features Table inhibit  
 CC coagulation (they prevent binding of serine protease to natural  
 CC substrates), esp. when admin. to give an intravascular blood  
 CC concn. of 0.1-100 (pref. 0.5-10) microM.  
 CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described  
 CC in the specification but have not yet been added to the SEQUENCE  
 CC LISTING.  
 CC  
 XX  
 SQ Sequence 406 AA;  
 Query Match 80.7%; Score 155; DB 14; Length 406;  
 Best Local Similarity 72.7%; Pred. No. 7.7e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ANAPLXXLRNGSLRXCKXXQCSPFXAFIFKDXRTKLFWISY 44  
 1 ANAPLEELRPGLRBECKECCSFEEAREIFKDXRTKLFWISY 44  
 DB  
 RESULT 9  
 AAM14509  
 ID AAM14509 standard; protein; 406 AA.  
 XX  
 AC AAM14509;  
 XX  
 DT 14-MAY-1997 (first entry)  
 XX  
 DE Modified blood coagulation Factor VII (R290S).  
 XX  
 KW Blood coagulation; factor 7; mutein; mutation; modification;  
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 7 /label= OTHER  
 FT Modified-site 7 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 14 /label= OTHER  
 FT Modified-site 14 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 16 /label= OTHER  
 FT Modified-site 16 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 19 /label= OTHER  
 FT Modified-site 19 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 20 /label= OTHER  
 FT Modified-site 20 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 25 /label= OTHER  
 FT Disulfide-bond 25 /label= OTHER  
 FT Modified-site 25 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 26 /label= OTHER  
 FT Modified-site 26 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 29 /label= OTHER  
 FT Modified-site 29 /label= OTHER  
 FT /note= "gamma-carboxyglutamic acid"  
 FT 32..33 /label= OTHER  
 FT Cleavage-site 32..33 /note= "gamma-carboxyglutamic acid"  
 FT 35 /label= OTHER  
 FT Modified-site 35 /label= OTHER

FT /note= "gamma-carboxyglutamic acid"  
 FT 38..39 /label= OTHER  
 FT Cleavage-site 38..39 /note= "gamma-carboxyglutamic acid"  
 FT 42..43 /label= OTHER  
 FT Cleavage-site 42..43 /note= "gamma-carboxyglutamic acid"  
 FT 44..45 /label= OTHER  
 FT Cleavage-site 44..45 /note= "gamma-carboxyglutamic acid"  
 FT 50..61 /label= OTHER  
 FT Disulfide-bond 50..61 /note= "gamma-carboxyglutamic acid"  
 FT 55..70 /label= OTHER  
 FT Disulfide-bond 55..70 /note= "gamma-carboxyglutamic acid"  
 FT 63 /label= OTHER  
 FT Modified-site 63 /label= OTHER  
 FT /note= "beta-hydroxy-aspartic acid"  
 FT 72..81 /label= OTHER  
 FT Disulfide-bond 72..81 /note= "beta-hydroxy-aspartic acid"  
 FT 91..102 /label= OTHER  
 FT Disulfide-bond 91..102 /note= "beta-hydroxy-aspartic acid"  
 FT 98..112 /label= OTHER  
 FT Disulfide-bond 98..112 /note= "beta-hydroxy-aspartic acid"  
 FT 114..127 /label= OTHER  
 FT Disulfide-bond 114..127 /note= "beta-hydroxy-aspartic acid"  
 FT 135..162 /label= OTHER  
 FT Disulfide-bond 135..162 /note= "beta-hydroxy-aspartic acid"  
 FT 143..144 /label= OTHER  
 FT Cleavage-site 143..144 /note= "beta-hydroxy-aspartic acid"  
 FT 145 /label= OTHER  
 FT Modified-site 145 /label= OTHER  
 FT /note= "glycosylation site"  
 FT 159..164 /label= OTHER  
 FT Disulfide-bond 159..164 /note= "glycosylation site"  
 FT 178..194 /label= OTHER  
 FT Disulfide-bond 178..194 /note= "glycosylation site"  
 FT 193 /label= OTHER  
 FT Active-site 193 /note= "glycosylation site"  
 FT 242 /label= OTHER  
 FT Active-site 242 /note= "glycosylation site"  
 FT 344 /label= OTHER  
 FT Active-site 344 /note= "glycosylation site"  
 FT 290..291 /label= OTHER  
 FT Cleavage-site 290..291 /note= "glycosylation site"  
 FT 290 /label= OTHER  
 FT Misc-difference 290 /note= "glycosylation site"  
 FT /note= "native Arg290 has been substituted by Ser to  
 FT provide a proteolytically more stable peptide  
 FT bond"  
 FT 310..329 /label= OTHER  
 FT Disulfide-bond 310..329 /note= "glycosylation site"  
 FT 315..316 /label= OTHER  
 FT Cleavage-site 315..316 /note= "glycosylation site"  
 FT 322 /label= OTHER  
 FT Modified-site 322 /note= "glycosylation site"  
 FT 340..368 /label= OTHER  
 FT Disulfide-bond 340..368 /note= "glycosylation site"  
 FT 341..342 /label= OTHER  
 FT Cleavage-site 341..342 /note= "glycosylation site"  
 FT 392..393 /label= OTHER  
 FT Cleavage-site 392..393 /note= "glycosylation site"  
 FT 396..397 /label= OTHER  
 FT Cleavage-site 396..397 /note= "glycosylation site"  
 FT 402..403 /label= OTHER  
 FT Cleavage-site 402..403 /note= "glycosylation site"  
 FT /note= "proteolytic site"  
 XX  
 XX USS580560-A.  
 XX  
 XX  
 XX 03-DEC-1996.  
 PD  
 XX  
 XX 13-NOV-1989; 89US-0434149.  
 PF  
 XX  
 XX 09-AUG-1993; 93US-0104509.  
 PR  
 XX 13-NOV-1989; 89US-0434149.  
 PR  
 XX 12-JUN-1992; 92US-0898248.  
 PR  
 XX 22-AUG-1994; 94US-0293778.  
 PR  
 XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 XX  
 PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;  
 XX  
 XX WPI; 1997-033523/03.  
 DR  
 XX  
 XX Mutated human factor VII or VIIa proteins - with amino acid  
 PT substitutions to improve proteolytic stability  
 PT  
 PS Example 3; Page -, 28pp; English.  
 XX  
 XX Modified human factor VII or VIIa proteins are stabilised against  
 CC proteolytic cleavage by substitution of one of the residues Lys32,  
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and  
 CC Lys341 by an amino acid that provides a proteolytically more stable

CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,  
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating  
CC bleeding disorders such as thrombocytopenia and von Willebrand's  
CC disease. They are also suitable for addition to plasma substitutes.  
CC The present sequence is a specific example of a modified factor VII  
CC protein.

XX  
SQ Sequence 406 AA;

Query Match 80.7%; Score 155; DB 18; Length 406;  
Best Local Similarity 72.7%; Pred. No. 7.7e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFIXLRNGSLRXCKXQCSFXAXFIFDAXRTKLFWISY 44  
Db 1 ANAFLELRPGSLERECKECCSFEEAREIFDASRTKLFWISY 44

RESULT 10  
AAW14510  
ID AAW14510 standard; protein; 406 AA.  
XX  
AC AAW14510;  
XX  
DT 14-MAY-1997 (first entry)  
XX  
DE Modified blood coagulation Factor VII (R31SS).  
XX  
KM Blood coagulation; factor 7; mutein; mutation; modification;  
KM thrombocytopenia; von Willebrand's disease; plasma substitute.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 6 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Modified-site 7 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Modified-site 14 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Modified-site 16 /note= "gamma-carboxylutamic acid"  
FT Modified-site 19 /note= "gamma-carboxylutamic acid"  
FT Modified-site 20 /note= "gamma-carboxylutamic acid"  
FT Modified-site 20 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Disulfide-bond 25.17..22 /label= OTHER  
FT Modified-site 25 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Modified-site 26 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Modified-site 29 /note= "gamma-carboxylutamic acid"  
FT Modified-site 29 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Cleavage-site 32..33 /note= "proteolytic site"  
FT Modified-site 35 /label= OTHER  
FT /note= "gamma-carboxylutamic acid"  
FT Cleavage-site 38..39 /note= "gamma-carboxylutamic acid"  
FT Cleavage-site 42..43 /note= "proteolytic site"  
FT Cleavage-site 44..45 /note= "proteolytic site"

FT /note= "proteolytic site"  
FT Disulfide-bond 50..61  
FT Disulfide-bond 55..70  
FT Modified-site 63 /label= OTHER  
FT /note= "beta-hydroxy-aspartic acid"  
FT Disulfide-bond 72..81  
FT Disulfide-bond 91..102  
FT Disulfide-bond 98..112  
FT Disulfide-bond 114..127  
FT Disulfide-bond 135..162  
FT Cleavage-site 143..144 /note= "proteolytic site"  
FT /note= "proteolytic site"  
FT Modified-site 145 /note= "glycosylation site"  
FT Disulfide-bond 159..164  
FT Disulfide-bond 178..194  
FT Active-site 193  
FT Active-site 242  
FT Active-site 344  
FT Cleavage-site 290..291 /note= "proteolytic site"  
FT Disulfide-bond 310..329 /note= "proteolytic site"  
FT Cleavage-site 315..316 /note= "proteolytic site in unmodified factor VII"  
FT Misc-difference 315 /note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"  
FT Modified-site 322 /note= "glycosylation site"  
FT Disulfide-bond 340..368  
FT Cleavage-site 341..342 /note= "proteolytic site"  
FT Cleavage-site 392..393 /note= "proteolytic site"  
FT Cleavage-site 396..397 /note= "proteolytic site"  
FT Cleavage-site 402..403 /note= "proteolytic site"  
XX  
XX US5580560-A.  
XX  
XX PD 03-DEC-1996.  
XX  
XX PF 13-NOV-1989; 89US-0434149.  
XX  
XX PR 09-AUG-1993; 93US-0104509.  
XX PR 13-NOV-1989; 89US-0434149.  
XX PR 12-JUN-1992; 92US-0898248.  
XX PR 22-AUG-1994; 94US-0293778.  
XX  
XX PA (NOVO ) NOVO-NORDISK AS.  
XX  
XX PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;  
XX WPI; 1997-033523/03.  
XX  
XX PT Mutated human factor VII or VIIa proteins - with amino acid  
XX substitutions to improve proteolytic stability  
XX  
XX Example 4; Page -; 28pp; English.  
XX  
XX Modified human factor VII or VIIa proteins are stabilised against  
XX proteolytic cleavage by substitution of one of the residues Lys32,  
XX Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and  
XX Lys341 by an amino acid that provides a proteolytically more stable  
XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,  
XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating  
XX bleeding disorders such as thrombocytopenia and von Willebrand's  
XX disease. They are also suitable for addition to plasma substitutes.  
XX The present sequence is a specific example of a modified factor VII  
XX protein.



```
XX 16-AUG-2001.
PD
XX
XX 12-FEB-2001; 2001WO-DK00094.
PF
XX 11-FEB-2000; 2000DK-0000218.
PR
XX 18-OCT-2000; 2000DK-0001558.
PR
XX (MAXY-) MAXYGEN APS.
PA
XX
XX Andersen KV, Pedersen AH, Bornaes C;
PI
XX WPI; 2001-581807/65.
DR
XX N-PSDB; AAI99982.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Claim 1; Page 81-83; 89pp; English.
PS
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
XX Sequence 406 AA;
SQ
XX
XX Query Match 80.7%; Score 155; DB 22; Length 406;
XX Best Local Similarity 95.5%; Pred. No. 7.7e-18;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY
XX 1 ANAFLXLRNGSLXRXCKXQCSFYXAFXIFKDAKRTKLFWISY 44
XX |||||
DB 1 ANAFLXLRPGSLXRXCKXQCSFYXARXIFKDAKRTKLFWISY 44
XX |||||
RESULT 13
AAM52172
ID AAM52172 standard; Protein; 406 AA.
XX
XX AAM52172;
AC
XX
XX 07-FEB-2002 (first entry)
DT
XX
XX Mammalian expressed human FVII SEQ ID NO 3.
DE
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 52
FT /note= "O-glycosylated"
FT 60
FT Modified-site /note= "O-glycosylated"
FT 145
FT Modified-site /note= "N-glycosylated"
FT 152..153
FT Cleavage-site
```

```
FT /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT Modified-site 322
FT /note= "N-glycosylated"
FT
XX WO200158935-A2.
XX
XX 16-AUG-2001.
PD
XX
XX 12-FEB-2001; 2001WO-DK00094.
PF
XX 11-FEB-2000; 2000DK-0000218.
PR
XX 18-OCT-2000; 2000DK-0001558.
PR
XX (MAXY-) MAXYGEN APS.
PA
XX
XX Andersen KV, Pedersen AH, Bornaes C;
PI
XX WPI; 2001-581807/65.
DR
XX N-PSDB; AAI99983.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
PT disorders such as haemophilia, liver disease, myocardial infarction and
PT deep-vein thrombosis, comprises non-polypeptide group covalently
PT attached to polypeptide group -
XX
XX Disclosure; Page 85-86; 89pp; English.
PS
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC polypeptide conjugates, comprising at least one non-polypeptide group
CC covalently attached to a polypeptide, where the amino acid sequence of
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections.
XX
XX Sequence 406 AA;
SQ
XX
XX Query Match 80.7%; Score 155; DB 22; Length 406;
XX Best Local Similarity 72.7%; Pred. No. 7.7e-18;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY
XX 1 ANAFLXLRNGSLXRXCKXQCSFYXAFXIFKDAKRTKLFWISY 44
XX |||||
DB 1 ANAFLBELRPGSLBRECKEQCSFEAREIFKDAKRTKLFWISY 44
XX |||||
RESULT 14
AAM52181
ID AAM52181 standard; Protein; 406 AA.
XX
XX AAM52181;
AC
XX
XX 07-FEB-2002 (first entry)
DT
XX
XX Human FVII mutant T106N.
DE
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX muten.
XX
XX Homo sapiens.
OS
XX Synthetic.
```

```

XX Key Location/Qualifiers
FH Misc-difference 6 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 35 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Modified-site 52 /note="O-glycosylated"
FT Modified-site 60 /note="O-glycosylated"
FT Misc-difference 106 /note="O-glycosylated"
FT Modified-site 145 /note="Wild-type Thr substituted by Asn"
FT Cleavage-site 152..153 /note="N-glycosylated"
FT /note="proteolytic cleavage site converting FVII zymogen
to an activated form, comprising two chains
linked by a single disulphide bridge"
FT Modified-site 322 /note="N-glycosylated"
FT WO200158935-A2.
XX 16-AUG-2001.
XX 12-FEB-2001; 2001WO-DK00094.
XX 11-FEB-2000; 2000DK-0000218.
XX 18-OCT-2000; 2000DK-0001558.
XX (MAXY-) MAXYGEN APS.
XX Andersen KV, Pedersen AH, Bornaes C;
XX WPI; 2001-581807/65.
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3; Page -, 89pp; English.
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at

```

```

CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
CC cerebroprotective activity and are useful for treating FVIIa/FI-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX
XX Sequence 406 AA;
SQ
Query Match 80.7%; Score 155; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 7,7e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ANAFLLXRLRNGSLRXKCKXXQCSFXXAFIIFKDAKRTKFWISY 44
1 ANAFLLXRLRNGSLRXKCKXXQCSFXXAFIIFKDAKRTKFWISY 44
Db 1 ANAFLLXRLRNGSLRXKCKXXQCSFXXAFIIFKDAKRTKFWISY 44
RESULT 15
AAM52182
ID AAM52182 standard; Protein; 406 AA.
XX
XX AAM52182;
AC
XX 07-FEB-2002 (first entry)
DT
XX Human FVII mutant K143N/N145T.
DE
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 7 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 14 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 16 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 19 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 20 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 25 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 26 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT Misc-difference 29 /label= Glu, OTHER
FT /note="OTHER = gamma carboxyglutamic acid"
FT /label= Glu, OTHER

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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 seconds  
(without alignments) 145.545 Million cell updates/sec

Title: 10ASN28PHE  
Perfect score: 192  
Sequence: 1 ANAFLLXRLRNGSLRXCKXX.....XXAFKIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 155   | 80.7        | 466    | 1 KFHU7  | coagulation factor  |
| 2          | 121   | 63.0        | 443    | 2 I46932 | coagulation factor  |
| 3          | 113   | 58.9        | 407    | 1 KFB07  | coagulation factor  |
| 4          | 96    | 50.0        | 461    | 1 JX0210 | protein C (activat  |
| 5          | 95    | 49.5        | 461    | 1 S18394 | protein C (activat  |
| 6          | 95    | 49.5        | 488    | 1 EXHU   | coagulation factor  |
| 7          | 94    | 49.0        | 492    | 1 EXBO   | coagulation factor  |
| 8          | 93    | 48.4        | 622    | 1 TBHU   | thrombin (EC 3.4.2  |
| 9          | 89    | 46.4        | 482    | 1 EXRT   | coagulation factor  |
| 10         | 89    | 46.4        | 617    | 2 S10511 | thrombin (EC 3.4.2  |
| 11         | 89    | 46.4        | 618    | 2 A35827 | thrombin (EC 3.4.2  |
| 12         | 87    | 45.3        | 466    | 1 KXBO   | protein C (activat  |
| 13         | 84    | 43.8        | 475    | 1 EXCH   | coagulation factor  |
| 14         | 82    | 42.7        | 461    | 1 KXHU   | protein C (activat  |
| 15         | 78    | 40.6        | 416    | 1 KFB0   | coagulation factor  |
| 16         | 75    | 39.1        | 461    | 1 KFHU   | coagulation factor  |
| 17         | 73    | 38.0        | 625    | 1 TBBO   | thrombin (EC 3.4.2  |
| 18         | 70    | 36.5        | 452    | 1 A30351 | coagulation factor  |
| 19         | 70    | 36.5        | 459    | 2 J00419 | coagulation factor  |
| 20         | 62    | 32.3        | 642    | 2 S53433 | plasma protein S p  |
| 21         | 59    | 30.7        | 675    | 1 KXBO   | plasma protein S p  |
| 22         | 57    | 29.7        | 642    | 2 S53434 | plasma protein S p  |
| 23         | 57    | 29.7        | 646    | 2 S38819 | plasma protein S p  |
| 24         | 57    | 29.7        | 676    | 1 KXHU   | plasma protein S p  |
| 25         | 56    | 29.2        | 396    | 1 KXBO   | plasma protein Z p  |
| 26         | 56    | 29.2        | 675    | 1 KXRT   | plasma protein Z p  |
| 27         | 54.5  | 28.4        | 576    | 2 G96763 | probable MAP kinase |
| 28         | 51    | 26.6        | 422    | 1 KXHU   | plasma protein Z p  |
| 29         | 49.5  | 25.8        | 594    | 2 D84859 | probable MAP kinase |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 49.5 | 25.8 | 603  | 2 C96575 | probable MAP kinase |
| 31 | 49   | 25.5 | 675  | 1 KXMS   | plasma protein S p  |
| 32 | 48   | 25.0 | 673  | 1 A48089 | growth arrest-spec  |
| 33 | 46.5 | 24.2 | 83   | 2 T17839 | hypothetical prote  |
| 34 | 46.5 | 24.2 | 336  | 2 AH1133 | hypothetical prote  |
| 35 | 46   | 24.0 | 674  | 2 I55476 | growth potentialin  |
| 36 | 46   | 24.0 | 678  | 2 B48089 | growth arrest-spec  |
| 37 | 45.5 | 23.7 | 389  | 2 D82223 | ribonucleoside-dip  |
| 38 | 45   | 23.4 | 271  | 2 S66691 | hypothetical membra |
| 39 | 45   | 23.4 | 879  | 2 S55864 | hypothetical prote  |
| 40 | 45   | 23.4 | 907  | 2 T15792 | hypothetical prote  |
| 41 | 44.5 | 23.2 | 1217 | 2 T21403 | hypothetical prote  |
| 42 | 44   | 22.9 | 172  | 2 F89103 | protein C18B10.3 (  |
| 43 | 44   | 22.9 | 306  | 2 I49068 | protein kinase STY  |
| 44 | 43   | 22.4 | 394  | 1 S30286 | tetracycline resis  |
| 45 | 43   | 22.4 | 440  | 2 C70198 | conserved hypothe   |

## ALIGNMENTS

## RESULT 1

KFHU7  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text\_change 08-Dec-2000  
C:Accession: A28322; A23819; A31186; B31186; S63524  
R,O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Inley, M.Y.; Hagen, F.S.; Murri  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende  
A:Reference number: A28322; PMID:87260948; PMID:3037537  
A:Accession: A28322  
A:Molecule type: DNA  
A:Residues: 1-466 <OH>  
A:Cross-references: GB:002933; NID:g180333; PIDN:AAA51983.1; PID:g180334  
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A:Title: Characterization of a cDNA coding for human factor VII.  
A:Reference number: A23819; PMID:86205965; PMID:3486420  
A:Accession: A23819  
A:Molecule type: mRNA  
A:Residues: 1-466 <HAG>  
A:Cross-references: GB:M1332; NID:g182799; PIDN:AAA8040.1; PID:g182801  
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.  
Biochemistry 27, 7785-7793, 1988  
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a fr  
A:Reference number: A90539; PMID:89088153; PMID:3264725  
A:Accession: A31186  
A:Molecule type: Protein  
A:Residues: 61-212 <THI>  
A:Accession: B31186  
A:Molecule type: Protein  
A:Residues: 213-466 <TH>  
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen, A.  
J. Biol. Chem. 266, 11051-11057, 1991  
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at  
A:Reference number: A40529; PMID:91250411; PMID:1804059  
R:Parson, E.; Petersen, L.C.  
Eur. J. Biochem. 234, 293-300, 1995  
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy  
A:Reference number: S63524; PMID:96096752; PMID:8529655  
A:Accession: S63524  
A:Molecule type: Protein  
A:Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>  
C:Genetics:  
A:Gene: GDB:F7  
A:Cross-references: GDB:119897; OMIM:227500  
A:Map position: 13q34-13q34  
A:Functions: 22/1, 44/1, 97/3, 106/1, 144/1, 191/1, 227/3, 269/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen  
coagulation factor IX in the presence of calcium and tissue factor

A;Pathway: blood coagulation extrinsic pathway  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-60/Domain: propeptide #status predicted <PRO>  
F;45-106/Domain: Gla domain homology <Gla>  
F;61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F;110-141/Domain: EGF homology <EG1>  
F;151-187/Domain: EGF homology <EG2>  
F;213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F;213-447/Domain: trypsin homology <TRY>  
F;66-67,74,76,79,80,85,86,88,95/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F;77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,  
F;112,120/Binding site: carboxylate (Ser) (covalent) #status experimental  
F;123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
F;205,382/Binding site: carboxylate (Asn) (covalent) #status experimental  
F;212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental  
F;253,302,404/Active site: His, Asp, Ser #status predicted  
F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 80.7%; Score 155; DB 1; Length 466;  
Best Local Similarity 72.7%; Pred. No. 1e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRNGLXKXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 61 ANAFLEELRPSLRECKEELCSFEAREIFXDARTKLFWISY 104

RESULT 2  
146932  
coagulation factor VII - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
C;Accession: I46932  
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.  
Thromb. Res. 69, 231-238, 1993  
A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
A;Reference number: I46932; MUID:93190306; PMID:8383365  
A;Accession: I46932  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-443 <BRO>  
A;Cross-references: GB:S56300; NID:G266294; PID:G266295  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
F;24-83/Domain: Gla domain homology <Gla>  
F;89-120/Domain: EGF homology <EG1>  
F;130-166/Domain: EGF homology <EG2>  
F;192-425/Domain: trypsin homology <TRY>

Query Match 63.0%; Score 121; DB 2; Length 443;  
Best Local Similarity 54.5%; Pred. No. 7.3e-13;  
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRNGLXKXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 40 ANSFLEELRPSLRECKEELCSFEAREVFPSTERTKQFWISY 83

RESULT 3  
KFB07  
coagulation factor VIIa (EC 3.4.21.21) - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
C;Accession: A31979; C20274  
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
J. Biol. Chem. 263, 14868-14877, 1988  
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.  
A;Reference number: A31979; MUID:89008362; PMID:3049594  
A;Accession: A31979  
A;Molecule type: protein  
A;Residues: 1-407 <TAK>  
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VIIa  
A;Reference number: A20274; MUID:83308813; PMID:6688526  
A;Accession: C20274  
A;Molecule type: protein  
A;Residues: 58-62, 'X', 64-68 <MCM>  
A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid  
R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.  
J. Biochem. 104, 867-868, 1988  
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor VIIa  
A;Reference number: A44556; MUID:99231999; PMID:3149637  
A;Contents: annotation  
A;Note: structure and location of covalently bound carbohydrate  
C;Function:  
A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor  
A;Pathway: blood coagulation extrinsic pathway  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F;1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F;1-44/Domain: Gla domain homology (fragment) <Gla>  
F;50-81/Domain: EGF homology <EG1>  
F;91-127/Domain: EGF homology <EG2>  
F;153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F;153-387/Domain: trypsin homology <TRY>  
F;6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F;17-22,50-61,55-70,72-81,91-102,98-112,114-127,133-262,159-164,178-194,310-329,340-368/1  
F;52/Binding site: carboxylate (Ser) (covalent) #status experimental  
F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental  
F;145,203/Binding site: carboxylate (Asn) (covalent) #status experimental  
F;152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental  
F;193,242,344/Active site: His, Asp, Ser #status predicted  
F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 58.9%; Score 113; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 1.6e-11;  
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy 1 ANAFPLXLRNGLXKXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 1 ANGFLEELRPSLRECKEELCSFEAREIFRNERTRQFWISY 44

RESULT 4  
JX0210  
protein C (activated) (EC 3.4.21.69) precursor - mouse  
N;Alternate names: vitamin K-dependent serine proteinase  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C;Accession: JX0210  
R;Tada, N.; Sato, M.; TeuJimura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
J. Biochem. 111, 491-495, 1992  
A;Title: Isolation and characterization of a mouse protein C cDNA.  
A;Reference number: JX0210; MUID:92316897; PMID:1618739  
A;Accession: JX0210  
A;Molecule type: mRNA  
A;Residues: 1-461 <TAD>  
A;Cross-references: GB:D10445; NID:G220385; PID:BA01235.1; PID:G220386  
A;Experimental source: liver  
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that regulates blood coagulation  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;27-85/Domain: Gla domain homology <Gla>  
F;34-41/Domain: propeptide #status predicted <PRO>  
F;42-196,199-461/Product: protein C #status predicted <PRC>  
F;42-196/Domain: light chain #status predicted <PLC>  
F;91-130/Domain: EGF homology <EG1>  
F;139-174/Domain: EGF homology <EG2>  
F;199-461/Domain: heavy chain #status predicted <PCH>  
F;199-211/Domain: activation peptide #status predicted <ACT>  
F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VTP>





J. Mol. Biol. 232, 947-966, 1993  
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A9458; MUID:93360277; PMID:8355279  
 A:Contents: annotation: X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 C:Genetics:  
 A:Gene: GDB:F10  
 A:Cross-references: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A>Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-234/Domain: activation peptide #status experimental <APT>  
 F:235-462/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:235-462/Domain: trypsin homology <TRY>  
 F:46-47.54.56.59.60.65.66.69.72.79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
 F:57-62/Disulfide bonds: #status predicted  
 F:90-101.95-110.112-121.129-140.136-149.151-164.172-342.241-246.261-277.390-404.415-443/  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:199.211/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:221.231/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:276.322.419/Active site: His, Asp, Ser #status experimental

Query Match 49.5%; Score 95; DB 1; Length 488;  
 Best Local Similarity 38.6%; Pred. No. 2.4e-08;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAPLXLRNGSLRXCKKXCSFXKAFIPDKARKTKLFWISY 44  
 Db 41 ANSFLSEMKGHLRECEETSCSYEARVEFSDSDTKTFNMKY 84

RESULT 7  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N/Alternate names: Stuart factor  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R/Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; MUID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FNU>  
 A:Cross-references: GB:X00673; NID:G192; PID:CAA2586.1; PID:G193  
 R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Tiliat, K.  
 Biochemistry 19, 659-667, 1980  
 A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, 'N', 104-180 <ENF>  
 R/McMillen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308613; PMID:6688526  
 A:Contents: annotation: revision to residue 103  
 R/Tiliat, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-232,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKRG', 446-492 <T  
 A>Note: carboxylate binding sites and disulfide bonds were determined  
 R/Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Gehlin, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; MUID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A>Note: beta-hydroxyaspartic acid site  
 R/Rinow, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196;199-209;216-233 <INO>  
 A>Note: carboxylate binding sites  
 R/Tiliat, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; Dr  
 Biochemistry 11, 4899-4903, 1972  
 A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
 A:Reference number: A12453; MUID:73053314; PMID:4264286  
 A:Contents: annotation: active site  
 R/Fujikawa, K.; Tiliat, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to f  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation: activation  
 R/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic  
 A:Reference number: A38024; MUID:84185716; PMID:6546930  
 A:Contents: annotation: calcium binding  
 R/Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:66140210; PMID:33949800  
 A:Contents: annotation: sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of two  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), or  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stron  
 C:Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin  
 C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <APT>  
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:234-492/Domain: trypsin homology <TRY>  
 F:46-47.54.56.59.60.65.66.69.72.75.79/Modified site: gamma-carboxylglutamic acid (Glu) #st  
 F:57-62.90-101.95-110.112-121.129-140.136-149.151-164.172-341/Disulfide bonds: #status p  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:200/Binding site: sulfite (Thr) (covalent) #status experimental  
 F:208.485/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat



A/Reference number: I46196; MUID:94222160; PMID:8168596  
 A/Accession: I62745  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 285-383, 'G', 385-455 <MUR>  
 A/Cross-references: GB:D21215; NID:g415309; PIDN:BA04756.1; PID:g455396  
 C/Function:  
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium ions  
 A/Pathway: blood coagulation  
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid  
 F,1-23/Domain: signal sequence #status predicted <SIG>  
 F,24-40/Domain: propeptide #status predicted <PRO>  
 F,25-84/Domain: Gla domain homology <Gla>  
 F,41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F,90-121/Domain: EGF homology <EGF>  
 F,129-164/Domain: EGF homology <EG2>  
 F,183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F,183-231/Domain: activation peptide #status predicted <AP2>  
 F,232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F,232-460/Domain: trypsin homology <TRY>  
 F,46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #status predicted <MOD>  
 F,57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,411-413/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted <MOD>  
 F,187/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F,208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F,218/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F,231-232/Cleavage site: His-116 (coagulation factor IXa, coagulation factor VIIa) #status predicted  
 F,274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 46.4%; Score 89; DB 1; Length 482;  
 Best Local Similarity 38.6%; Pred. No. 2.6e-07;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXRLNGSLXRXCKXQCSFYXAFIFPDAXRTKLFWISY 44  
 Db 41 ANSFPEELKGNLRECVCEQCSYEAFALSPQDTDFWAKY 84

## RESULT 10

thrombin (EC 3.4.21.5) precursor - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 07-May-1993 #sequence revision 07-May-1993 #text\_change 03-May-2002  
 C/Accession: S10511; A60576; B42696  
 R/Dhanich, M.; Monard, D.  
 Nucleic Acids Res. 18, 4251, 1990  
 A/Title: cDNA sequence of rat prothrombin.  
 A/Reference number: S10511; MUID:90332426; PMID:2377469  
 A/Accession: S10511  
 A/Molecule type: mRNA  
 A/Residues: 1-617 <DIH>  
 A/Cross-references: EMBL:X52835; NID:g56969; PIDN:CAA37017.1; PID:g56970  
 R/Henriksson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.  
 Endocrinology 126, 167-175, 1990  
 A/Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.  
 A/Reference number: A60576; MUID:90091942; PMID:2293980  
 A/Accession: A60576  
 A/Molecule type: protein  
 A/Residues: 44-58 <HEN>  
 A/Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uterus  
 R/Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A/Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing  
 A/Reference number: A42696; MUID:92212913; PMID:1557383  
 A/Accession: B42696  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 383-617, 'E', <BAN>  
 A/Cross-references: GB:M81397  
 C/Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology  
 C/Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydrolytic  
 F,1-24/Domain: signal sequence #status predicted <SIG>

F,25-43/Domain: propeptide #status predicted <PRO>  
 F,28-88/Domain: Gla domain homology <Gla>  
 F,44-617/Product: prothrombin #status experimental <PMAT>  
 F,109-187/Domain: kringe homology <KR1>  
 F,215-292/Domain: kringe homology <KR2>  
 F,360-609/Domain: trypsin homology <TRY>  
 F,50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #status predicted <MOD>  
 F,61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,561-564/Active site: His, Asp, Ser #status predicted

Query Match 46.4%; Score 89; DB 2; Length 617;  
 Best Local Similarity 39.5%; Pred. No. 3.3e-07;  
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NAFLXRLNGSLXRXCKXQCSFYXAFIFPDAXRTKLFWISY 44  
 Db 46 SGFLEELKGNLRECVCEQCSYEAFALSPQDTDFWAKY 88

## RESULT 11

thrombin (EC 3.4.21.5) precursor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text\_change 03-May-2002  
 C/Accession: A35827; A42696; S12081  
 R/Degen, S.U.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.; DNA Cell Biol. 9, 487-498, 1990  
 A/Title: Characterization of the cDNA coding for mouse prothrombin and localization of the gene  
 A/Reference number: A35827; MUID:91025551; PMID:2222810  
 A/Accession: A35827  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-618 <DEG>  
 A/Cross-references: GB:X52308; NID:g53813; PIDN:CAA36548.1; PID:g53814  
 A/Note: the data were obtained from females resulting from the cross of M. domesticus and M. musculus  
 R/Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A/Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing  
 A/Reference number: A42696; MUID:92212913; PMID:1557383  
 A/Accession: A42696  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 384-618, 'E', <BAN>  
 A/Cross-references: GB:M81394  
 C/Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology  
 C/Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydrolytic  
 F,1-24/Domain: signal sequence #status predicted <PRO>  
 F,25-43/Domain: propeptide #status predicted <PRO>  
 F,28-88/Domain: Gla domain homology <Gla>  
 F,44-618/Product: prothrombin B #status predicted <MAT>  
 F,109-187/Domain: kringe homology <KR1>  
 F,215-293/Domain: kringe homology <KR2>  
 F,361-610/Domain: trypsin homology <TRY>  
 F,50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #status predicted <MOD>  
 F,61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,561-565/Active site: His, Asp, Ser #status predicted

Query Match 46.4%; Score 89; DB 2; Length 618;  
 Best Local Similarity 39.5%; Pred. No. 3.3e-07;  
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NAFLXRLNGSLXRXCKXQCSFYXAFIFPDAXRTKLFWISY 44  
 Db 46 SGFLEELKGNLRECVCEQCSYEAFALSPQDTDFWAKY 88

## RESULT 12

prothrombin C (activated) (EC 3.4.21.69) precursor - bovine (fragment)  
 N/Alternate names: autoproteolytic prothrombin IIA; plasma protein C  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999



A:Reference number: A25426; MUID:86120978; PMID:3511471  
 A:Accession: A25426  
 A:Molecule type: DNA  
 A:Residues: 1-445,'L',446-461 <PLU>  
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
 R:Poster, D.; Davie, E.W.  
 A:Title: Characterization of a cDNA coding for human protein C.  
 A:Reference number: A21781; MUID:84272714; PMID:6589623  
 A:Accession: A21781  
 A:Molecule type: mRNA  
 A:Residues: 'C',107-461 <FOS2>  
 A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323  
 R:Beckmann, R.J.; Schmidt, R.J.; Sautter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
 A:Title: The structure and evolution of a 461 amino acid human protein C precursor and 1  
 A:Reference number: A23789; MUID:85269639; PMID:2991859  
 A:Accession: A23789  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <BEC>  
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120  
 R:Millerich, J.P.; Broze Jr., G.J.  
 J. Biol. Chem. 265, 11397-11404, 1990  
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m  
 A:Reference number: A44605; MUID:90293094; PMID:1694179  
 A:Contents: annotation; carbohydrate binding sites; activation peptide  
 A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
 R:Harrie, R.J.; Ling, V.T.; Spellman, M.W.  
 J. Biol. Chem. 267, 5102-5107, 1992  
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of facto  
 A:Reference number: A44606; MUID:92184750; PMID:1544894  
 A:Contents: annotation; beta-hydroxyaspartic acid  
 A:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
 A:Comment: Protein C is strongly enhanced by complexing with protein S. Protein C also h  
 A:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
 C:Genetics:  
 A:Gene: GDB:PROC  
 A:Cross-references: GDB:120317; OMIM:176860  
 A:Map position: 2q13-q21  
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:27-86/Domain: Gla domain homology <Gla>  
 F:33-42/Domain: propeptide #status predicted <PRO>  
 F:43-197/Product: protein C light chain #status predicted <LCH>  
 F:92-131/Domain: EGF homology <EG1>  
 F:140-175/Domain: EGF homology <EG2>  
 F:200-461/Product: protein C heavy chain #status predicted <HCH>  
 F:200-211/Domain: activation peptide #status experimental <APT>  
 F:212-445/Domain: trypsin homology <TRY>  
 F:48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
 F:59-64,92-105,101-120,132-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D  
 F:106-111/Disulfide bonds: #status predicted  
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent  
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:139,230,355/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
 F:253,299,402/Active site: His, Asp, Ser #status predicted  
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 42.7%; Score 82; DB 1; Length 461;  
 Best Local Similarity 43.9%; Pred. No. 4e-06;  
 Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRCXKXQCSFXXAFIFKDXARTKLFW 41  
 Db 43 ANSFLLELRHSLRECEICDFEAKKEIFQVDDTLAFW 83

RESULT 15  
 KRBO

coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
 N:Alternate names: Christmas factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text change 16-Jul-1999  
 C:Accession: A14757; B20274; I5891; A00923  
 R:Kakayama, K.; Ericsson, L.H.; Enfield, D.L.; Waleh, K.A.; Neurath, H.; Davie, E.W.; Til  
 A:Title: Christmas factor IXa (EC 3.4.21.22) precursor - bovine  
 A:Reference number: A14757; MUID:80036619; PMID:291916  
 A:Accession: A14757  
 A:Molecule type: protein  
 A:Residues: 1-63,'T',65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Accession: B20274  
 A:Molecule type: protein  
 A:Residues: 59-63,'X',65-69 <MCM>  
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
 Nature 299, 178-180, 1982  
 A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.  
 A:Reference number: A45891; MUID:82272386; PMID:6287289  
 A:Accession: A45891  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 52-139 <CHO>  
 A:Cross-references: GB:U00007; NID:g163053; PIDN:AAA30520.1; PID:g163054  
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S  
 J. Biochem. 190, 867-868, 1988  
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag  
 A:Reference number: A44556; MUID:89213999; PMID:3194637  
 A:Contents: annotation  
 A>Note: structure and location of a carbohydrate covalently bound to Ser  
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide p  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen  
 A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamu  
 F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:1-45/Domain: Gla domain homology (fragment) <Gla>  
 F:51-82/Domain: EGF homology <EG1>  
 F:88-124/Domain: EGF homology <EG2>  
 F:147-181/Domain: activation peptide #status experimental <APT>  
 F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:182-409/Domain: trypsin homology <TRY>  
 F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide  
 F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 40.6%; Score 78; DB 1; Length 416;  
 Best Local Similarity 41.2%; Pred. No. 1.8e-05;  
 Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 11 GSLXRCXKXQCSFXXAFIFKDXARTKLFWISY 44  
 Db 12 GNLERCKEERKCSFEAREVEFTEKTEFWKQY 45

Search completed: March 19, 2003, 15:00:53  
 Job time : 30.125 secs

GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)

328.082 Million cell updates/sec

Title: 10ASN28PNE  
Perfect score: 192  
Sequence: 1 ANAFLXLLRNGSLXRCCKX.....XXAFKIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 155   | 80.7        | 466    | 1     | FA7_HUMAN   |
| 2          | 121   | 63.0        | 444    | 1     | FA7_RABIT   |
| 3          | 113   | 58.9        | 407    | 1     | FA7_BOVIN   |
| 4          | 110   | 57.3        | 446    | 1     | FA7_MOUSE   |
| 5          | 101   | 52.6        | 430    | 1     | FA10_RABIT  |
| 6          | 97    | 50.5        | 459    | 1     | PRTC_PIG    |
| 7          | 96    | 50.0        | 461    | 1     | PRTC_MOUSE  |
| 8          | 95    | 49.5        | 461    | 1     | PRTC_RAT    |
| 9          | 95    | 49.5        | 488    | 1     | FA10_HUMAN  |
| 10         | 94    | 49.0        | 482    | 1     | FA10_BOVIN  |
| 11         | 93    | 48.4        | 622    | 1     | THRB_HUMAN  |
| 12         | 92    | 47.9        | 218    | 1     | TMG1_HUMAN  |
| 13         | 89    | 46.4        | 617    | 1     | THRB_RAT    |
| 14         | 89    | 46.4        | 618    | 1     | THRB_MOUSE  |
| 15         | 87    | 45.3        | 466    | 1     | PRTC_BOVIN  |
| 16         | 84    | 43.8        | 231    | 1     | TMG3_HUMAN  |
| 17         | 84    | 43.8        | 475    | 1     | FA10_CHICK  |
| 18         | 82    | 42.7        | 461    | 1     | PRTC_HUMAN  |
| 19         | 80    | 41.7        | 458    | 1     | PRTC_RABIT  |
| 20         | 78    | 40.6        | 416    | 1     | FA9_BOVIN   |
| 21         | 75    | 39.1        | 376    | 1     | FA10_TROCA  |
| 22         | 75    | 39.1        | 461    | 1     | FA9_HUMAN   |
| 23         | 73    | 38.0        | 625    | 1     | THRB_BOVIN  |
| 24         | 72    | 37.5        | 202    | 1     | TMG2_HUMAN  |
| 25         | 70    | 36.5        | 452    | 1     | FA9_CANPA   |
| 26         | 70    | 36.5        | 459    | 1     | FA9_MOUSE   |
| 27         | 66    | 34.4        | 236    | 1     | TMG4_HUMAN  |
| 28         | 59    | 30.7        | 675    | 1     | PRTC_BOVIN  |
| 29         | 57    | 29.7        | 646    | 1     | PRTC_RABIT  |
| 30         | 57    | 29.7        | 649    | 1     | PRTC_MACMU  |
| 31         | 57    | 29.7        | 676    | 1     | PRTC_HUMAN  |
| 32         | 56    | 29.2        | 396    | 1     | PRTC_BOVIN  |
| 33         | 56    | 29.2        | 675    | 1     | PRTC_RAT    |

|    |      |      |     |   |            |
|----|------|------|-----|---|------------|
| 34 | 51   | 26.6 | 400 | 1 | PRT2_HUMAN |
| 35 | 49   | 25.5 | 675 | 1 | PRTS_MOUSE |
| 36 | 45   | 23.4 | 271 | 1 | MD12_YEAST |
| 37 | 45   | 23.4 | 879 | 1 | Y865_YEAST |
| 38 | 43   | 22.4 | 394 | 1 | TCR4_GALOR |
| 39 | 43   | 22.4 | 440 | 1 | Y788_BORBU |
| 40 | 42   | 21.9 | 818 | 1 | CDB1_HUMAN |
| 41 | 41   | 21.4 | 263 | 1 | PFLA_STRMU |
| 42 | 41   | 21.4 | 353 | 1 | MLIA_CHICK |
| 43 | 41   | 21.4 | 393 | 1 | DPSS_PINSY |
| 44 | 41   | 21.4 | 616 | 1 | JEN1_YEAST |
| 45 | 40.5 | 21.1 | 147 | 1 | YK6_YEAST  |

## ALIGNMENTS

| RESULT 1 | FA7_HUMAN  | STANDARD; | PRT; | 466 AA. |
|----------|--|-----------|------|---------|
| ID       | FA7_HUMAN  |           |      |         |
| AC       | P08709; O14339;  |           |      |         |
| DT       | 01-JAN-1988 (Rel. 06, Created)   |           |      |         |
| DT       | 01-JAN-1988 (Rel. 06, Last sequence update)  |           |      |         |
| DT       | 15-JUN-2002 (Rel. 41, Last annotation update)  |           |      |         |
| DE       | Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa). |           |      |         |
| GN       | P7.  |           |      |         |
| OS       | Homo sapiens (Human).  |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |           |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  |           |      |         |
| OX       | NCBI_TaxID=9606;   |           |      |         |
| RN       | [1]  |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |      |         |
| RC       | TISSUE=Liver;  |           |      |         |
| RX       | MEDLINE=86205965; PubMed=3486420;  |           |      |         |
| RA       | Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  |           |      |         |
| RA       | Woodbury R.G., Hart C.E., Insley M.Y., Kistel W., Kurachi K.,  |           |      |         |
| RA       | Davie E.W.;  |           |      |         |
| RT       | "Characterization of a cDNA coding for human factor VII.;"   |           |      |         |
| RL       | Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  |           |      |         |
| RN       | [2]  |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |      |         |
| RX       | MEDLINE=87260948; PubMed=3037537;  |           |      |         |
| RA       | O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  |           |      |         |
| RA       | Hagen F.S., Murray M.J.;   |           |      |         |
| RT       | "Nucleotide sequence of the gene coding for human factor VII, a  |           |      |         |
| RT       | vitamin K-dependent protein participating in blood coagulation.;"  |           |      |         |
| RL       | Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  |           |      |         |
| RN       | [3]  |           |      |         |
| RP       | SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.   |           |      |         |
| RA       | Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  |           |      |         |
| RA       | Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;   |           |      |         |
| RL       | Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  |           |      |         |
| RN       | [4]  |           |      |         |
| RP       | SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  |           |      |         |
| RX       | MEDLINE=89088153; PubMed=3264725;  |           |      |         |
| RA       | Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  |           |      |         |
| RA       | Pedersen A.H., Hedner U.;  |           |      |         |
| RT       | "Amino acid sequence and posttranslational modifications of human  |           |      |         |
| RT       | factor VIIa from plasma and transfected baby hamster kidney cells.;"                                       |           |      |         |
| RL       | Biochemistry 27:7785-7793(1988).   |           |      |         |
| RN       | [5]  |           |      |         |
| RP       | CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  |           |      |         |
| RX       | MEDLINE=91250411; PubMed=1904059;  |           |      |         |
| RA       | Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,  |           |      |         |
| RA       | Komiyama Y., Pedersen A.H., Kistel W.;   |           |      |         |
| RT       | "Human plasma and recombinant factor VII. Characterization of O-   |           |      |         |
| RT       | glycosylations at serine residues 52 and 60 and effects of site-   |           |      |         |
| RT       | directed mutagenesis of serine 52 to alanine.;"  |           |      |         |
| RL       | J. Biol. Chem. 266:11051-11057(1991).  |           |      |         |
| RN       | [6]  |           |      |         |
| RP       | STRUCTURE OF CARBOHYDRATE ON SER-112.  |           |      |         |
| RX       | MEDLINE=9062160; PubMed=2511201;   |           |      |         |



RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimomura Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [7]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=858903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RL Nature 380:41-46(1996).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99125538; PubMed=9925787;  
 RA Zhang B., St. Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a Bp1 mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gipeert G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Rodorigo G., Caonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=9337811; PubMed=8364544;  
 RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 RT (115His and 333Ser) in the human coagulation factor VII gene";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamaya O., Kembell-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lunley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RX MEDLINE=94264305; PubMed=8204879;  
 RA Chaing S., Clarke B., Stridman S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor";  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";  
 RL Thromb. Haemost. 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS W-283, K-325, V-358, Q-364, E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferrarese P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,  
 RA Zatzov R., Seligsohn U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN [21]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerif C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:5189-S191(1998).  
 CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWYGOEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -I- TISSUE SPECIFICITY: PLASMA.  
 CC -I- PTM: THE VITAMIN K-DEPENDENT. ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -I- PHARMACEUTICAL: Available under the names Nistabae or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in



Query Match 80.7%; Score 155; DB 1; Length 466;  
Best Local Similarity 72.7%; Pred. No. 2, 1e-19;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLKRCCKXXQCSFAXAIFKQAXRTKLFMISY 44  
DB 61 ANAFLEELRPGSLERECCKECSFEARERIFKQARTKLFMISY 104

RESULT 2  
FA7\_RABIT STANDARD; PRT; 444 AA.  
AC P98139; P79224;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-JUN-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93190306; PubMed=8383365;  
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII";  
RT Thromb. Res. Suppl. 69:231-238(1993).  
RN [2]  
RP REVISION TO 395.  
RC TISSUE=Liver;  
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA. FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.1sb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; U77477; AAB37326.1; -.  
CC DR HSSP; P08709; 1FAK.  
CC DR MEROPS; S01.215; -.  
CC DR InterPro; IPR000152; Asx\_hydroxyl-  
CC DR InterPro; IPR001314; Chymotrypsin.  
CC DR InterPro; IPR000561; EGF-like.  
CC DR InterPro; IPR000742; EGF\_2.  
CC DR InterPro; IPR001881; EGF\_CA.  
CC DR InterPro; IPR002383; GLA\_blood.  
CC DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00089; trypsin\_1.  
DR Pfam; PF00594; gla\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRY\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR HydroLase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
KW EGF-like domain; Repeat; Signal; Hydroxylation.  
FT SIGNAL 1 21  
FT PROPEP 22 39  
FT CHAIN 40 191  
FT CHAIN 192 444  
FT DOMAIN 45 74  
FT DOMAIN 85 121  
FT DOMAIN 126 167  
FT DOMAIN 192 444  
FT SITE 191 192  
FT ACT\_SITE 232 232  
FT ACT\_SITE 281 281  
FT ACT\_SITE 383 383  
FT BINDING 377 377  
FT DISULFID 56 61  
FT DISULFID 89 100  
FT DISULFID 94 109  
FT DISULFID 111 120  
FT DISULFID 130 141  
FT DISULFID 137 151  
FT DISULFID 153 166  
FT DISULFID 174 303  
FT DISULFID 198 201  
FT DISULFID 217 233  
FT DISULFID 349 368  
FT DISULFID 379 407  
FT MOD\_RES 45 45  
FT MOD\_RES 46 46  
FT MOD\_RES 53 53  
FT MOD\_RES 55 55  
FT MOD\_RES 58 58  
FT MOD\_RES 59 59  
FT MOD\_RES 64 64  
FT MOD\_RES 65 65  
FT MOD\_RES 68 68  
FT MOD\_RES 74 74  
FT MOD\_RES 102 102  
FT CARBOHYD 211 211  
FT CARBOHYD 242 242  
FT CARBOHYD 306 306  
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 63.0%; Score 121; DB 1; Length 444;  
Best Local Similarity 54.5%; Pred. No. 1, 8e-13;  
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLKRCCKXXQCSFAXAIFKQAXRTKLFMISY 44  
DB 40 ANAFLEELRPGSLERECCKECSFEARERVFQSTERTKQWITY 83

RESULT 3

FA7 BOVIN  
ID -FA7\_BOVIN STANDARD; PRT; 407 AA.  
AC P22457;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=89008362; PubMed=3049594;  
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;  
RT "Bovine factor VII. Its purification and complete amino acid sequence.";  
RT J. Biol. Chem. 263:14868-14877(1988).  
RN [2]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=89213999; PubMed=3149637;  
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX.";  
RT J. Biochem. 104:867-868(1988).  
RN [3]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";  
RT Adv. Exp. Med. Biol. 281:121-131(1990).  
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC PIR: A31979; A31979.  
DR HSSP; P08709; 1BF9.  
DR MEROPS; S01.215; -.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF-2.  
DR InterPro: IPR001811; EGF-Ca.  
DR InterPro: IPR001438; EGF-II.  
DR InterPro: IPR002383; GLA blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR Pfam; PF00594; Gla; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00010; EGFblood.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.

DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRY\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.  
KW EGF-like domain; Repeat.  
FT CHAIN 1 152  
FT CHAIN 153 407  
FT DOMAIN 6 35  
FT DOMAIN 46 82  
FT DOMAIN 87 128  
FT DOMAIN 153 407  
FT SITE 152 153  
FT ACT SITE 193 193  
FT ACT SITE 242 242  
FT ACT SITE 344 344  
FT BINDING 338 338  
FT DISULFID 17 22  
FT DISULFID 50 61  
FT DISULFID 72 81  
FT DISULFID 91 102  
FT DISULFID 98 112  
FT DISULFID 114 127  
FT DISULFID 135 262  
FT DISULFID 159 164  
FT DISULFID 178 194  
FT DISULFID 310 329  
FT DISULFID 340 368  
FT MOD RES 6 7  
FT MOD RES 7 7  
FT MOD RES 14 14  
FT MOD RES 16 16  
FT MOD RES 19 19  
FT MOD RES 20 20  
FT MOD RES 25 25  
FT MOD RES 26 26  
FT MOD RES 29 29  
FT MOD RES 35 35  
FT MOD RES 52 52  
FT CARBOHYD 145 145  
FT CARBOHYD 203 203  
FT SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;  
Query Match 58.9%; Score 113; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 4, 1e-12;  
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;  
QY 1 ANAFLXLRLNGSLRXKXQCSFYXAFXIFKDAKRTLFWISY 44  
DB 1 ANGFLLELLPGLSLERECREBELCSFEAEHIFRNERTNQFWVS 44  
RESULT 4  
FA7 MOUSE  
ID -FA7\_MOUSE STANDARD; PRT; 446 AA.  
AC P70375;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
DE F7 OR CF7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



CC CALCIUM (BY SIMILARITY).  
 CC -1- PTH: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PTH: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)  
 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL; AF003200; AAB62542.1; -.  
 DR HSSP; P00742; IHCG.  
 DR MEROPS; S01.216; -.  
 DR InterPro; IPR000152; Aex\_Hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VltK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR SMART; SM00059; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolyase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
 FT PROPEP 21 40  
 FT CHAIN 41 180  
 FT CHAIN 184 490  
 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT DOMAIN 86 122  
 FT DOMAIN 125 165  
 FT DOMAIN 233 490  
 FT MOD\_RES 46 46  
 FT MOD\_RES 47 47  
 FT MOD\_RES 54 54  
 FT MOD\_RES 56 56  
 FT MOD\_RES 59 59  
 FT MOD\_RES 60 60  
 FT MOD\_RES 65 65  
 FT MOD\_RES 66 66

FT MOD\_RES 69 69  
 FT MOD\_RES 72 72  
 FT MOD\_RES 75 75  
 FT MOD\_RES 79 79  
 FT MOD\_RES 103 103  
 FT ACT\_SITE 274 274  
 FT ACT\_SITE 320 320  
 FT ACT\_SITE 417 417  
 FT DISULFID 90 101  
 FT DISULFID 95 110  
 FT DISULFID 112 121  
 FT DISULFID 129 140  
 FT DISULFID 136 149  
 FT DISULFID 151 164  
 FT DISULFID 172 340  
 FT DISULFID 239 244  
 FT DISULFID 259 275  
 FT DISULFID 388 402  
 FT DISULFID 413 441  
 FT CARBOHYD 61 61  
 FT CARBOHYD 187 187  
 FT CARBOHYD 205 205  
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;  
 Query Match 52.6%; Score 101; DB 1; Length 490;  
 Best Local Similarity 40.9%; Pred. No. 6,1e-10;  
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;  
 Qy 1 ANAFPLXLRNGSLKRXCKXOCSEFFXAFKIPKAXRTLFWISY 44  
 Db 41 ANSFLEELKKNLEKRECMENCSEYEALEVEDREKTNFNNKY 84  
 RESULT 6  
 PRTC\_PIG STANDARD; PRT; 459 AA.  
 AC 09GLP2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin II) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=2112490; PubMed=11229814;  
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,  
 RA Kim H.K.W.;  
 RA "Porcine factor V: cDNA cloning, gene mapping, three-dimensional  
 RA protein modeling of membrane binding sites and comparative anatomy of  
 RA domain";  
 RL Cell. Mol. Life Sci. 58:148-159(2001).  
 CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that  
 CC regulates blood coagulation by inactivating factors Va and VIIIa  
 CC in the presence of calcium ions and phospholipids.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIa.  
 CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved  
 CC into a light chain and a heavy chain held together by a disulfide  
 CC bond. The enzyme is then activated by thrombin, which cleaves a  
 CC tetradecapeptide from the amino end of the heavy chain; this  
 CC reaction, which occurs at the surface of endothelial cells, is



RT "A comparative study of partial primary structures of the catalytic region of mammalian protein C." ;  
 RL Br. J. Haematol. 86:590-600(1994).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PPM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: D10445; BAA01235.1; -.  
 DR EMBL: AF034569; AAC33795.1; -.  
 DR PIR: JX0210; JX0210.  
 DR HSPSP: P04070; JPCU.  
 DR MEROPS: S01.218; -.  
 DR MGD: MGI:97771; Proc.  
 DR InterPro: IPR000152; Aax\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin\_1.  
 DR Pfam: PF00594; gla\_1.  
 DR PRINTS: PRO0722; CHYMOTRYPSIN.  
 DR PRINTS: PRO0001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_Like; 1.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; TYP\_Spec; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Blood coagulation: Glycoprotein; Serine protease;  
 KM Blood coagulation: Glycoprotein; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 33  
 FT PROPEP 34 41 BY SIMILARITY.  
 FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).  
 FT CHAIN 199 496 PROTEIN C HEAVY CHAIN (BY SIMILARITY).  
 FT PEPTIDE 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).  
 FT SITE 212 213 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).  
 FT DOMAIN 96 131 EGF-LIKE 1.

FT DOMAIN 135 175 EGF-LIKE 2.  
 FT DOMAIN 213 461 SERINE PROTEASE.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).  
 FT MOD\_RES 112 112 HYDROXYLATION (BY SIMILARITY).  
 FT ACT\_SITE 253 253 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 299 299 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 402 402 CHARGE RELAY SYSTEM.  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 110 BY SIMILARITY.  
 FT DISULFID 100 105 BY SIMILARITY.  
 FT DISULFID 104 119 BY SIMILARITY.  
 FT DISULFID 121 130 BY SIMILARITY.  
 FT DISULFID 139 150 BY SIMILARITY.  
 FT DISULFID 146 159 BY SIMILARITY.  
 FT DISULFID 161 174 BY SIMILARITY.  
 FT DISULFID 182 319 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 238 254 BY SIMILARITY.  
 FT DISULFID 373 387 BY SIMILARITY.  
 FT DISULFID 398 426 BY SIMILARITY.  
 FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 328 328 MISSING (IN REF. 2).  
 FT CONFLICT 393 393 N -> D (IN REF. 2).  
 SQ SEQUENCE 461 AA; 51945 MW; 53FAA0D85B194D8E CRC64;  
 Query Match 50.0%; Score 96; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 4.3e-09;  
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;  
 Oy 1 ANAPLXLRNGSLKRXCKXOCSPXAXIFKDXRTLFWISY 44  
 Db 42 ANSFLEMRPGSLERECEMEICDFEAGEIFQWVEDTLAFWIKY 85  
 RESULT 8  
 BRTC\_RAT STANDARD; PRT; 461 AA.  
 AC P31394;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (Ec 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistat; TISSUE=Liver;  
 RX MEDLINE=92329550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C." ;

RL Biochim. Biophys. Acta 1131:329-332 (1992).

CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT

CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA

CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va

CC and VIIIA.

CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED

CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE

CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A

CC PEPTIDASE PEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS

CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS

CC STRONGLY PROMOTED BY THROMBOMODULIN.

CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME

CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO

CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING

CC SITE IS NECESSARY FOR THE RECOGNITION OF THE

CC THROMBIN-THROMBOMODULIN COMPLEX.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC -----

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CC -----

DR EMBL; X64336; CAA45617.1; -.

DR PIR; S18994; S18994.

DR PIR; S24312; S24312.

DR HSSP; P04070; 1PCU.

DR MEROPS; S01.218; -.

DR InterPro; IPR000152; Aex\_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR002383; GLA\_blood.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PF00584; gla; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM000179; EGF\_CA; 1.

DR SMART; SM00001; EGF\_Like; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp\_Spc; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; 1.

DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01187; EGF\_CA; 1.

DR PROSITE; PS00011; GLU CARBOXYLATION; 1.

DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; 1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KM Blood coagulation; Glycoprotein; Serine protease;

KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.

FT SIGNAL 1 32

FT PROPEP 33 41

FT CHAIN 42 196

FT CHAIN 199 461

FT PEPTIDE 199 212

FT SITE 212 213

FT DOMAIN 96 131

FT DOMAIN 135 175

FT DOMAIN 213 461

FT MOD\_RES 47 47

(BY SIMILARITY).

FT MOD\_RES 48 48

FT MOD\_RES 55 55

FT MOD\_RES 57 57

FT MOD\_RES 60 60

FT MOD\_RES 61 61

FT MOD\_RES 66 66

FT MOD\_RES 67 67

FT MOD\_RES 70 70

FT MOD\_RES 112 112

FT ACT\_SITE 254 254

FT ACT\_SITE 300 300

FT ACT\_SITE 402 402

FT DISULFID 58 63

FT DISULFID 91 110

FT DISULFID 100 105

FT DISULFID 104 119

FT DISULFID 121 130

FT DISULFID 139 150

FT DISULFID 146 159

FT DISULFID 161 174

FT DISULFID 182 320

FT DISULFID 239 255

FT DISULFID 373 387

FT DISULFID 398 426

FT CARBOHYD 215 291

FT CARBOHYD 291 355

FT CARBOHYD 355 355

SEQ 461 AA; 51912 MW; 8A4CF9364EDACD5 CRC64;

Query Match 49.5%; Score 95; DB 1; Length 461;

Best Local Similarity 45.5%; Pred. No. 6; 4e-09;

Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXKCKXQCSFXXAFIFKDXAKRTLFWSY 44

Db 42 ANSFLEEVFRAGSLERECMEICDFEBAQEIFQNVEDTLARIMY 85

RESULT 9

ID FA10 HUMAN STANDARD; PRT; 488 AA.

AC P00742; O14340;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Coagulation.factor X precursor (EC 3.4.21.6) (Stuart factor).

GN F10.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91216473; PubMed=1902434;

RA Messier T.L., Pitman D.D., Long G.L., Kaufman R.J., Church W.R.;

RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding

RL human coagulation factor X.";

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=87026600; PubMed=3768336;

RA Luytus S.P., Foster D.C., Kurachi K., Davie E.W.;

RT "Gene for human factor X: a blood coagulation factor whose gene

RT organization is essentially identical with that of factor IX and

protein C.";

RL Biochemistry 25:5098-5102(1986).  
 RN [3]  
 RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RN [4]  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA.";  
 RL Gene 41:311-314(1986).  
 RN [5]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884(1983).  
 RN [6]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [7]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [8]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamaabhusanan K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K.P., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PM: THE VITAMIN K-DEPENDENT ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.

CC -1- PM: N- AND O-GLYCOSYLATED.  
 CC -1- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXa (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIa (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL, K03194; AAA52490.1; -;  
 CC EMBL, M57285; AAA52421.1; -;  
 CC EMBL, L29433; AAA52764.1; -;  
 CC EMBL, L00390; AAA52764.1; JOINED.  
 CC EMBL, L00391; AAA52764.1; JOINED.  
 CC EMBL, L00392; AAA52764.1; JOINED.  
 CC EMBL, L00393; AAA52764.1; JOINED.  
 CC EMBL, L00394; AAA52764.1; JOINED.  
 CC EMBL, L00395; AAA52764.1; JOINED.  
 CC EMBL, L00396; AAA52764.1; JOINED.  
 CC EMBL, M22613; AAA51984.1; -;  
 CC EMBL, K01886; AAA52486.1; -;  
 CC EMBL, M33297; AAA52636.1; -;  
 CC PIR, A00924; EXHU.  
 CC PIR, A25853; A25853.  
 CC PIR, A24478; A24478.  
 CC PDB, 1HCG; 08-MAY-95.  
 CC PDB, 1FXV; 17-JUN-96.  
 CC PDB, 1XKA; 23-MAR-99.  
 CC PDB, 1XKB; 23-MAR-99.  
 CC MEROPS; S01.216; -;  
 CC GlycoSuiteDB; P00742; -;  
 CC Genew; HGNC:3528; F10.  
 CC MIM; 134530; -;  
 CC MIM; 227600; -;  
 CC InterPro; IPR000152; Aex\_hydroxyl.  
 CC InterPro; IPR001314; Chymotrypsin.  
 CC InterPro; IPR000561; EGF-like.  
 CC InterPro; IPR007442; EGF\_2.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR002383; Gln\_Blood.  
 CC InterPro; IPR001254; Ser\_protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00008; EGF\_2.  
 CC Pfam; PF00089; trypsin\_1.  
 CC Pfam; PF00594; gla; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00001; GLABLOOD.  
 CC SMART; SM00179; EGF\_CA; 1.  
 CC SMART; SM00001; EGF\_Like; 1.  
 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; TRYD\_Spc; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 2.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GUO\_CARBOXYLATION; 1.  
 CC PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 CC Signal; Zymogen; EGF-Like domain; Repeat; 3d-structure.  
 CC SIGNAL 1 31 POTENTIAL.  
 CC FT PROPEP 32 40  
 CC FT CHAIN 41 179 FACTOR X LIGHT CHAIN.  
 CC FT CHAIN 183 488 FACTOR X HEAVY CHAIN.  
 CC FT PROPEP 183 234 ACTIVATION PEPTIDE.



```
FT CHAIN 235 488 ACTIVATED FACTOR Xa, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 HYDROXYLATION.
FT CARBOHYD 199 199 O-LINKED (GALNAC. . .).
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .).
FT ACT_SITE 276 276 /FTID=CAR_000013.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110 CHARGE RELAY SYSTEM.
FT DISULFID 112 121 CHARGE RELAY SYSTEM.
FT DISULFID 129 140 CHARGE RELAY SYSTEM.

Query Match 49.5%; Score 95; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 6.8e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

1 ANAFPLXLRNGSLKRCCKXQCFXAFYIPKAXRTKLFNYSY 44
41 ANSFLERKKGHLRECEBETCSYEAREVEDSDKTNEFNNKY 84
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```
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjork I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8116(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Teleman O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Strømthagen M., Ullner M., Persson E., Teleman O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
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RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sunnehaugen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,  
 RA Trewthella J.;  
 RT "The relative orientation of Glu and EGF domains in coagulation  
 factor X is altered by Ca2+ binding to the first EGF domain. A  
 combined NMR-small angle X-ray scattering study.";  
 RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, X00673; CA25286.1; -.  
 DR PIR, A00925; EXBO.  
 DR PDB, 1AFC; 31-JAN-94.  
 DR PDB, 1CCF; 31-MAY-94.  
 DR PDB, 1WHE; 15-MAY-97.  
 DR PDB, 1WHF; 15-MAY-97.  
 DR MEROPS, S01.216; -.  
 DR GlycoSuiteDB, P00743; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000134; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VltK\_dep\_GLA.  
 DR Pfam, PF00008; EGF\_2.  
 DR Pfam, PF00089; trypsin, 1.  
 DR Pfam, PF00594; Glu, 1.  
 DR PRINTS, PR00722; CHYMOTRYPSIN.  
 DR PRINTS, PR00001; GLABLOOD.  
 DR SMART, SM00179; EGF\_CA; 1.  
 DR SMART, SM00001; EGF\_like; 1.  
 DR SMART, SM00069; GLA; 1.  
 DR SMART, SM00020; Tryp\_Spc; 1.  
 DR PROSITE, PS00010; ASX\_HYDROXYL, 1.  
 DR PROSITE, PS00022; EGF\_1, 1.  
 DR PROSITE, PS01186; EGF\_2, 2.  
 DR PROSITE, PS01187; EGF\_CA; 1.  
 DR PROSITE, PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE, PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE, PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE, PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolyase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfate; 3D-structure.

| FT | SIGNAL   | 1   | 23  | POTENTIAL.                               |
|----|----------|-----|-----|--|
| FT | PROPEP   | 24  | 40  | FACTOR X LIGHT CHAIN.                    |
| FT | CHAIN    | 41  | 180 | FACTOR X HEAVY CHAIN.                    |
| FT | CHAIN    | 183 | 492 | ACTIVATION PEPTIDE.                      |
| FT | PROPEP   | 183 | 233 | ACTIVATED FACTOR XA, HEAVY CHAIN.        |
| FT | CHAIN    | 234 | 492 | MAY BE REMOVED BUT IS NOT NECESSARY FOR  |
| FT | PROPEP   | 476 | 492 | ACTIVATION.                              |
| FT | DOMAIN   | 86  | 122 | EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN   | 125 | 165 | EGF-LIKE 2.                              |
| FT | DOMAIN   | 234 | 492 | SERINE PROTEASE.                         |
| FT | ACT_SITE | 275 | 275 | CHARGE RELAY SYSTEM.                     |
| FT | ACT_SITE | 321 | 321 | CHARGE RELAY SYSTEM.                     |
| FT | ACT_SITE | 418 | 418 | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 46  | 46  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 47  | 47  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 54  | 54  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 55  | 56  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 59  | 59  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 60  | 60  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 65  | 65  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 66  | 66  | GAMMA-CARBOXYGLUTAMIC ACID.              |

Query Match 49.0%; Score 94; DB 1; Length 492;

Best Local Similarity 40.9%; Pred. No. 1e-08; Mismatches 19; Gaps 0;

Matches 18; Conservative 7; Indels 0;

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 Db 41 ANSFLEEVKQGNLRECELEACSLSEAREVEFDAQGTDFMSKY 84

RESULT 11  
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 AC P00734;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).  
 GN F2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88077877; PubMed=2825773;  
 RA Degen S.J.F., Davie E.W.;  
 RT "Nucleotide sequence of the gene for human prothrombin.";  
 RL Biochemistry 26:6165-6177(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT MET-165.  
 RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Ozuna M., Poel C.L., Toch B.J., Yi Q., Nickerson D.A.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBS databases.  
 RN [3]  
 RP SEQUENCE OF 8-622 FROM N.A.  
 RX MEDLINE=83231469; PubMed=6305407;  
 RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;  
 RT "Characterization of the complementary deoxyribonucleic acid and gene  
 coding for human prothrombin.";  
 RL Biochemistry 22:2087-2097(1983).  
 RN [4]  
 RP SEQUENCE OF 44-314.  
 RX MEDLINE=77193964; PubMed=266717;  
 RA Walz D.A., Hewett-Emlmet D., Seegers W.H.;  
 RT "Amino acid sequence of human prothrombin fragments 1 and 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).  
 RN [5]  
 RP SEQUENCE OF 315-622.  
 RX MEDLINE=77207112; PubMed=873923;  
 RA Butkewski R.J., Ellison J., Downing M.R., Mann K.G.;

RT "Primary structure of human prothrombin 2 and alpha-thrombin.";   
 RL J. Biol. Chem. 252:4942-4957(1977).   
 RN [6]   
 RP PROCESSING.   
 RX MEDLINE=87008532; PubMed=3759958;   
 RA Rabiet M.J., Blaschill A., Furie B.C.;   
 RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin   
 activation in human plasma.";   
 RL J. Biol. Chem. 261:13210-13215(1986).   
 RN [7]   
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).   
 RX MEDLINE=90059942; PubMed=2583108;   
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;   
 RT "The refined 1.9 Å crystal structure of human alpha-thrombin:   
 interaction with D-Phe-Pro-Arg chloromethylketone and significance of   
 the Tyr-Pro-Pro-Tyr insertion segment.";   
 RL EMBO J. 8:3467-3475(1989).   
 RN [8]   
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).   
 RX MEDLINE=90327074; PubMed=2374926;   
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,   
 RT "The structure of a complex of recombinant hirudin and human alpha-   
 thrombin.";   
 RL Science 249:277-280(1990).   
 RN [9]   
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).   
 RX MEDLINE=94350942; PubMed=8071320;   
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,   
 RT "Crystallographic structure of human gamma-thrombin.";   
 RL J. Biol. Chem. 269:22000-22006(1994).   
 RN [10]   
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).   
 RX MEDLINE=97357286; PubMed=9214615;   
 RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,   
 RT "The thrombin E192Q-BPI complex reveals gross structural   
 rearrangements: implications for the interaction with antithrombin   
 and thrombomodulin.";   
 RL EMBO J. 16:2977-2984(1997).   
 RN [11]   
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.   
 RX MEDLINE=99162521; PubMed=10051558;   
 RA Quinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;   
 RT "Unexpected crucial role of residue 225 in serine proteases.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).   
 RN [12]   
 RP VARIANT BARCELONA.   
 RX MEDLINE=87033739; PubMed=3771562;   
 RA Rabiet M.-J., Furie B.C., Furie B.;   
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine   
 for arginine at residue 273.";   
 RL J. Biol. Chem. 261:15045-15048(1986).   
 RN [13]   
 RP VARIANT FRANKFURT.   
 RX MEDLINE=95313001; PubMed=7792730;   
 RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;   
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by   
 substitution of Glu-466 by Ala.";   
 RL Thromb. Haemost. 73:203-209(1995).   
 RN [14]   
 RP VARIANTS HIMI-1 AND HIMI-2.   
 RX MEDLINE=93043342; PubMed=1421398;   
 RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,   
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional   
 prothrombin molecules (Met-337->Thr and Arg-388->His).";   
 RL Blood 80:2275-2280(1992).   
 RN [15]   
 RP VARIANT PADUA-1.   
 RX MEDLINE=95169898; PubMed=7865694;   
 RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;

RT "Prothrombin Padua I: incomplete activation due to an amino acid   
 substitution at a factor Xa cleavage site.";   
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).   
 RN [16]   
 RP VARIANT QUICK-1.   
 RX MEDLINE=89207504; PubMed=3242619;   
 RA Henriksen R.A., Mann K.G.;   
 RT "Identification of the primary structural defect in the dyschrombin   
 thrombin Quick I: substitution of cysteine for arginine-382.";   
 RL Biochemistry 27:9160-9165(1988).   
 RN [17]   
 RP VARIANT QUICK-2.   
 RX MEDLINE=89247398; PubMed=2719946;   
 RA Henriksen R.A., Mann K.G.;   
 RT "Substitution of valine for glycine-558 in the congenital dyschrombin   
 thrombin Quick II alters primary substrate specificity.";   
 RL Biochemistry 28:2078-2082(1989).   
 RN [18]   
 RP VARIANT SALAKTA.   
 RX MEDLINE=92378975; PubMed=1354985;   
 RA Miyata T., Aruga R., Umeyama H., Bezeaud A., Guillin M.-C.,   
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine   
 reduces the fibrinogen clotting activity and the esterase activity.";   
 RL Biochemistry 31:7457-7462(1992).   
 RN [19]   
 RP VARIANT TOKUSHIMA.   
 RX MEDLINE=87185407; PubMed=3567158;   
 RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,   
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin   
 that impairs the fibrinogen clotting activity of derived thrombin   
 Tokushima.";   
 RL Biochemistry 26:1117-1122(1987).   
 RN [20]   
 RP VARIANT TOKUSHIMA.   
 RX MEDLINE=87101511; PubMed=3801671;   
 RA Inomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,   
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin   
 derived from a variant of human prothrombin.";   
 RL Blood 69:565-569(1987).   
 RN [21]   
 RP VARIANT TOKUSHIMA.   
 RX MEDLINE=92256895; PubMed=1349838;   
 RA Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,   
 RT "Detection of a single base substitution of the gene for prothrombin   
 Tokushima. The application of PCR-SSCP for the genetic and molecular   
 analysis of dysprothrombinemia.";   
 RL Int. J. Hematol. 55:93-100(1992).   
 RN [22]   
 RP VARIANT TYPE-3.   
 RX MEDLINE=83204687; PubMed=6405779;   
 RA Board P.G., Shaw D.C.;   
 RT "Determination of the amino acid substitution in human prothrombin   
 type 3 (157 Glu leads to Lys) and the localization of a third   
 thrombin cleavage site.";   
 RL Br. J. Haematol. 54:245-254(1983).   
 RN [23]   
 RP VARIANT THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS   
 FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,   
 AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.   
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Gly; activates   
 fibrinogen to fibrin and releases fibrinopeptide A and B.   
 CC -1- SUBCELLULAR LOCATION: Extracellular.   
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.   
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,   
 RESULT FROM THE CARBOXYGLUTAMYL OF GLUTAMYL RESIDUES BY A MICROSOML   
 ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES   
 ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY   
 CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION   
 OF PROTHROMBIN TO THROMBIN.   
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF

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CC DYSPROTHROMBINEMIA.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
CC NATURAL BLOOD CLOTTING.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
Query Match 48.4%; Score 93; DB 1; Length 622;
Best Local Similarity 38.6%; Pred. No. 1.9e-08;
Matches 17; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
QY 1 ANAFLLXLRNGLRCKXCKXQCSFYXAFXIFKDAKRTKLFWSY 44
Db 44 ANTFLEVRKGNLRECEVETCSYEAFALSSSTATDVFWMKY 87

RESULT 12
TMG1_HUMAN STANDARD; PRT; 218 AA.
AC 014668;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-
DE rich Gla protein 1) (Proline-rich gamma-carboxylglutamic acid protein
DE 1).
GN PRG1 OR TMG1 OR PRGP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxylglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; ICFH.
DR GenSeq; HGNC:9469; PRRG1.
DR MIM; 604428; -.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxylglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 21 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID

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FT FT DOMAIN 21 83 PROTEIN 1.
FT FT TRANSSEM 84 106 EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 107 218 POTENTIAL.
FT FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 24 61 GLA-RICH.
FT FT DOMAIN 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AE98 CRC64;

Query Match 47.9%; Score 92; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 1e-08;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY 1 ANAFLLXLRNGLRCKXCKXQCSFYXAFXIFKDAKRTKLFWSY 44
Db 21 ANGFPEIRQGNIRECKEFCFEAREAREFENNEKTEKFWSTY 64

RESULT 13
THRB_RAT STANDARD; PRT; 617 AA.
AC P18292;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prothrombin precursor (BC 3.4.21.5).
GN P2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxId=10116;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOAL
CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
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|    |          |     |     |                             |
|----|----------|-----|-----|-----------------------------|
| FT | DISULEID | 264 | 287 | BY SIMILARITY.              |
| FT | DISULEID | 332 | 478 | INTERCHAIN (BY SIMILARITY). |
| FT | DISULEID | 387 | 403 | BY SIMILARITY.              |
| FT | DISULEID | 532 | 546 | BY SIMILARITY.              |
|    |          |     |     | BY SIMILARITY.              |

| FT | DISUFID  | 264     | 287       | BY SIMILARITY.               |
|----|----------|---------|-----------|------------------------------|
| FT | DISUFID  | 332     | 478       | INTERCHAIN. (BY SIMILARITY). |
| FT | DISUFID  | 387     | 403       | BY SIMILARITY.               |
| FT | DISUFID  | 532     | 546       | BY SIMILARITY.               |
| FT | DISUFID  | 560     | 590       | BY SIMILARITY.               |
| SO | SEQUENCE | 617 AA; | 70411 MW; | AD27D1B71A45DBD CRC64;       |

  

| Query Match | Best Local Similarity | 46.4%;  | Score 89;      | DB 16; | Length 617; |
|-------------|-----------------------|---|----------------|--------|-------------|
| Matches 17; | Conservative          | 5;  | Mismatches 21; | Indels | Gaps 0;     |
| Qy          | 2                     | NAPLXLRLNGSLRXKCKKXQCSFXAXFIFDAXRTKLFWSY 44   |                |        |             |
| Db          | 46                    | SGFLEELRKGNLRECVBEQCYSBEAFBALESPODITVFMAYK 88 |                |        |             |

  

| RESULT 14 |  |           |              |
|-----------|--|-----------|--------------|
| ID        | THRB_MOUSE   | STANDARD; | PRT; 618 AA. |
| AC        | P19221;  |           |              |
| DT        | 01-NOV-1990 (Rel. 16, Created)   |           |              |
| DT        | 01-NOV-1990 (Rel. 16, Last sequence update)                                |           |              |
| DT        | 15-JUN-2002 (Rel. 41, Last annotation update)                              |           |              |
| DE        | Prothrombin precursor (EC 3.4.21.5).                                       |           |              |
| GN        | F2 OR CP2.   |           |              |
| OS        | Mus musculus (Mouse).  |           |              |
| OC        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;          |           |              |
| OC        | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.         |           |              |
| OX        | NCBI_Taxid=10090;  |           |              |
|           | [1]  |           |              |
| RP        | SEQUENCE FROM N.A.   |           |              |
| RC        | STRAIN=C57BL/6; TISSUE=Liver;  |           |              |
| RA        | MEDLINE=92212913; PubMed=1557383;  |           |              |
| RA        | Barfield D.K., Macgillivray R.T.;  |           |              |
| RT        | "Partial characterization of vertebrate prothrombin cDNAs:                 |           |              |
| RT        | amplification and sequence analysis of the B chain of thrombin from        |           |              |
| RT        | nine different species."   |           |              |
| RL        | Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).                          |           |              |
| RL        | Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).                          |           |              |
| RP        | SEQUENCE OF 384-618 FROM N.A.  |           |              |
| RP        | TISSUE=Liver;  |           |              |
| RC        | MEDLINE=92212913; PubMed=1557383;  |           |              |
| RA        | Barfield D.K., Macgillivray R.T.;  |           |              |
| RT        | "Partial characterization of vertebrate prothrombin cDNAs:                 |           |              |
| RT        | amplification and sequence analysis of the B chain of thrombin from        |           |              |
| RT        | nine different species."   |           |              |
| RL        | Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).                          |           |              |
| RL        | Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).                          |           |              |
| CC        | -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS      |           |              |
| CC        | FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VIII, VIII, XIII,            |           |              |
| CC        | AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C,                            |           |              |
| CC        | -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Gly; activates        |           |              |
| CC        | fibrinogen to fibrin and releases fibrinopeptide A and B.                  |           |              |
| CC        | -1- PFM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,      |           |              |
| CC        | RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL         |           |              |
| CC        | ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES         |           |              |
| CC        | ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY           |           |              |
| CC        | CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION        |           |              |
| CC        | OF PROTHROMBIN TO THROMBIN.  |           |              |
| CC        | -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A            |           |              |
| CC        | PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &            |           |              |
| CC        | FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES            |           |              |
| CC        | THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &           |           |              |
| CC        | HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR          |           |              |
| CC        | V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF              |           |              |
| CC        | THROMBIN.  |           |              |
| CC        | -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL           |           |              |
| CC        | FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION          |           |              |
| CC        | BY FACTOR XA.  |           |              |
| CC        | -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.                            |           |              |
| CC        | -1- SIMILARITY: CONTAINS 2 KIRINGE DOMAINS.                                |           |              |
| CC        | -----  |           |              |
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL; X52308; CA36548.1; -.  
 CC EMBL; M81394; AAA40435.1; -.  
 CC PIR; A35827; A35827.  
 CC HSP; P00734; 1B7X.  
 CC MEROPS; S01.217; -.  
 CC MGD; MGI:88380; F2.  
 CC InterPro; IPR003383; Chymotrypsin.  
 CC InterPro; IPR002383; GLA\_blood.  
 CC InterPro; IPR000001; Kringle.  
 CC InterPro; IPR003966; Prothrombin.  
 CC InterPro; IPR001254; Ser protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00051; Kringle; 2.  
 CC Pfam; PF00089; Trypsin; 1.  
 CC Pfam; PF00594; Gla; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00001; GLABLOOD.  
 CC PRINTS; PR00018; KRINGLE.  
 CC PRINTS; PR01505; PROTHROMBIN.  
 CC ProDom; PD000395; Kringle; 2.  
 CC SMART; SM00069; Gla; 1.  
 CC SMART; SM00130; KR; 2.  
 CC SMART; SM00020; Tryp\_Spc; 1.  
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 CC PROSITE; PS00021; KRINGLE\_1; 2.  
 CC PROSITE; PS50070; KRINGLE\_2; 2.  
 CC PROSITE; PS50240; TRYPsin\_DOM; 1.  
 CC PROSITE; PS00134; TRYPsin\_HIS; 1.  
 CC PROSITE; PS00135; TRYPsin\_SER; 1.  
 CC Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;  
 CC Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;  
 CC Hydroxylase; Serine protease; Kringle; Signal.  
 CC SIGNAL 1 24  
 CC PROPEP 25 43  
 CC CHAIN 44 618 PROTHROMBIN.  
 CC PEPTIDE 44 200 ACTIVATION PEPTIDE (FRAGMENT 1).  
 CC CHAIN 325 360 ACTIVATION PEPTIDE (FRAGMENT 2).  
 CC CHAIN 361 360 THROMBIN LIGHT CHAIN (A).  
 CC DOMAIN 109 187 THROMBIN HEAVY CHAIN (B).  
 CC DOMAIN 215 292 KRINGLE 1.  
 CC DOMAIN 361 618 KRINGLE 2.  
 CC SITE 200 201 SERINE PROTEASE.  
 CC SITE 324 325 CLEAVAGE (BY THROMBIN).  
 CC SITE 360 361 CLEAVAGE (BY FACTOR XA).  
 CC ACT\_SITE 403 403 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC ACT\_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC ACT\_SITE 565 565 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CC MOD\_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 CC MOD\_RES 77 77 BY SIMILARITY.  
 CC DISULFID 61 66 BY SIMILARITY.  
 CC DISULFID 91 104 BY SIMILARITY.  
 CC DISULFID 109 187 BY SIMILARITY.  
 CC DISULFID 130 170 BY SIMILARITY.  
 CC DISULFID 158 182 BY SIMILARITY.  
 CC DISULFID 215 293 BY SIMILARITY.  
 CC DISULFID 236 276 BY SIMILARITY.  
 CC DISULFID 264 288 BY SIMILARITY.  
 CC DISULFID 333 479 INTERCHAIN (BY SIMILARITY).

FT DISULFID 388 404 BY SIMILARITY.  
 FT DISULFID 533 547 BY SIMILARITY.  
 FT DISULFID 561 591 BY SIMILARITY.  
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 618 AA; 70268 MW; B89F719NAF0601E0 CRC64;

Query Match 46.4%; Score 89; DB 1; Length 618;  
 Best Local Similarity 39.5%; Pred. No. 9.5e-08;  
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Oy 2 NAFLLKPLNGSLKXCKXKQCFXAFIFKDAKRTKLFWLSY 44  
 Db 46 SGFLEELKGNLRECVBECQSYEAFAELSPDIDFWMKY 88

RESULT 15  
 PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid=9913;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.,  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 [2]  
 RP SEQUENCE OF 40-194.  
 RX MEDLINE=83007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.,  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 [3]  
 RP REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.,  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 [4]  
 RP SEQUENCE OF 197-456.  
 RX MEDLINE=83007326; PubMed=6896877;  
 RA Stenflo J., Fernlund P.,  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RL J. Biol. Chem. 257:12180-12190(1982).  
 [5]  
 RP PROCESSING, AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213513; PubMed=6304092;  
 RA Eamon N.L., Debault L.E., Eamon C.T.,  
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
 RT domainless protein C";  
 RL J. Biol. Chem. 258:5548-5553(1983).  
 [6]  
 RP PROCESSING, AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213514; PubMed=6406503;  
 RA Johnson A.E., Eamon N.L., Laue T.M., Eamon C.T.,  
 RT "Structural changes required for activation of protein C are induced  
 RT by Ca2+ binding to a high affinity site that does not contain gamma-  
 RT carboxyglutamic acid";  
 RL J. Biol. Chem. 258:5554-5560(1983).



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GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(without alignments)  
196.288 Million cell updates/sec

Title: 10ASN28PHE  
Perfect score: 192  
Sequence: 1 ANAFIXLRNGSLRXRCXX.....XXAFKIFDAXRKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: SPTRMBL\_21:\*
  - 2: sp\_archaea:\*
  - 3: sp\_bacteria:\*
  - 4: sp\_fungi:\*
  - 5: sp\_human:\*
  - 6: sp\_invertebrate:\*
  - 7: sp\_mammal:\*
  - 8: sp\_mhc:\*
  - 9: sp\_organelle:\*
  - 10: sp\_phage:\*
  - 11: sp\_plant:\*
  - 12: sp\_rodent:\*
  - 13: sp\_virus:\*
  - 14: sp Vertebrate:\*
  - 15: sp\_unclassified:\*
  - 16: sp\_rvirus:\*
  - 17: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 155   | 80.7        | 701    | 4     | Q96PQ8      |
| 2          | 110   | 57.3        | 446    | 11    | Q61109      |
| 3          | 96    | 50.0        | 460    | 11    | Q91WN8      |
| 4          | 93    | 48.4        | 100    | 4     | Q15253      |
| 5          | 90    | 46.9        | 460    | 11    | Q99PC6      |
| 6          | 89    | 46.4        | 482    | 11    | Q63207      |
| 7          | 87    | 45.3        | 456    | 6     | Q9TRR0      |
| 8          | 87    | 45.3        | 469    | 6     | Q9GMD9      |
| 9          | 87    | 45.3        | 481    | 11    | Q54740      |
| 10         | 87    | 45.3        | 481    | 11    | Q99132      |
| 11         | 87    | 45.3        | 481    | 11    | Q88947      |
| 12         | 87    | 45.3        | 481    | 11    | Q88947      |
| 13         | 78    | 40.6        | 49     | 6     | Q95ME8      |
| 14         | 75    | 39.1        | 456    | 4     | Q14316      |
| 15         | 75    | 39.1        | 461    | 6     | Q95ND7      |
| 16         | 72    | 37.5        | 461    | 6     | Q95ND6      |
|            |       |             | 179    | 4     | Q8TAS3      |

|    |      |      |     |    |        |                     |
|----|------|------|-----|----|--------|---------------------|
| 17 | 72   | 37.5 | 198 | 11 | Q8R182 | Q8R182 mus musculus |
| 18 | 71   | 37.0 | 138 | 6  | Q28994 | Q28994 sus scrofa   |
| 19 | 71   | 37.0 | 108 | 13 | Q9PTW7 | Q9PTW7 struthio ca  |
| 20 | 68   | 35.4 | 433 | 13 | Q90YK1 | Q90YK1 brachydanio  |
| 21 | 68   | 35.4 | 607 | 13 | Q91001 | Q91001 gallus gall  |
| 22 | 62   | 32.3 | 648 | 6  | Q29094 | Q29094 sus scrofa   |
| 23 | 61   | 31.8 | 98  | 11 | P82807 | P82807 notechis sc  |
| 24 | 59   | 30.7 | 139 | 11 | Q9COW3 | Q9COW3 mus musculus |
| 25 | 57   | 29.7 | 650 | 4  | Q9NSD0 | Q9NSD0 homo sapien  |
| 26 | 57   | 29.7 | 650 | 4  | Q16519 | Q16519 homo sapien  |
| 27 | 55.5 | 28.9 | 492 | 10 | Q9SMJ7 | Q9SMJ7 cicer ariet  |
| 28 | 54.5 | 28.4 | 196 | 10 | Q04284 | Q04284 setaiginella |
| 29 | 54.5 | 28.4 | 431 | 10 | Q94EY5 | Q94EY5 arabidopsis  |
| 30 | 54.5 | 28.4 | 543 | 10 | Q9MB23 | Q9MB23 arabidopsis  |
| 31 | 54.5 | 28.4 | 576 | 10 | Q9C9U4 | Q9C9U4 arabidopsis  |
| 32 | 54.5 | 28.4 | 589 | 10 | Q91MS2 | Q91MS2 arabidopsis  |
| 33 | 54   | 28.1 | 25  | 11 | Q9QVH6 | Q9QVH6 ratius sp.   |
| 34 | 52.5 | 27.3 | 459 | 10 | Q9SE22 | Q9SE22 oryza sativ  |
| 35 | 52.5 | 27.3 | 542 | 5  | Q8T613 | Q8T613 halocynthia  |
| 36 | 51.5 | 26.8 | 506 | 10 | Q9SPF0 | Q9SPF0 oryza sativ  |
| 37 | 51.5 | 26.8 | 506 | 10 | Q9SE23 | Q9SE23 arabidopsis  |
| 38 | 51.5 | 26.8 | 567 | 10 | Q8W4J2 | Q8W4J2 arabidopsis  |
| 39 | 50.5 | 26.3 | 510 | 10 | Q9MB22 | Q9MB22 arabidopsis  |
| 40 | 50.5 | 26.3 | 619 | 10 | Q9LV37 | Q9LV37 arabidopsis  |
| 41 | 49.5 | 25.8 | 603 | 10 | Q9LPG7 | Q9LPG7 arabidopsis  |
| 42 | 49.5 | 25.8 | 606 | 10 | Q9SJG9 | Q9SJG9 arabidopsis  |
| 43 | 49.5 | 25.8 | 651 | 10 | Q8S2I8 | Q8S2I8 oryza sativ  |
| 44 | 48.5 | 25.3 | 575 | 10 | Q94E17 | Q94E17 oryza sativ  |
| 45 | 48.5 | 25.3 | 588 | 10 | Q91MJ3 | Q91MJ3 arabidopsis  |

ALIGNMENTS

|          |  |              |      |         |
|----------|--|--------------|------|---------|
| RESULT 1 | Q96PQ8   | PRELIMINARY; | PRT; | 701 AA. |
| ID       | Q96PQ8   |              |      |         |
| AC       | Q96PQ8   |              |      |         |
| DT       | 01-DEC-2001 (TREMBLrel. 19, Created)                                   |              |      |         |
| DT       | 01-DEC-2001 (TREMBLrel. 19, Last sequence update)                      |              |      |         |
| DT       | 01-MAR-2002 (TREMBLrel. 20, Last annotation update)                    |              |      |         |
| DE       | Factor VII active site mutant immunconjugate.                          |              |      |         |
| OS       | Homo sapiens (Human).  |              |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |              |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.            |              |      |         |
| OX       | NCBI_TaxID=9606;   |              |      |         |
| RN       | [1]  |              |      |         |
| RP       | SEQUENCE FROM N.A.   |              |      |         |
| RX       | MEDLINE=21477448; PubMed=11593034;                                     |              |      |         |
| RA       | Hu Z., Garen A.;   |              |      |         |
| RT       | "Targeting tissue factor on tumor vascular endothelial cells and tumor |              |      |         |
| RT       | cells for immunotherapy in mouse models of prostatic cancer."          |              |      |         |
| RL       | Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).                    |              |      |         |
| DR       | EMBL; AF272774; AAK58686.1; -  |              |      |         |
| DR       | InterPro: IPR000152; Asx hydroxyl.                                     |              |      |         |
| DR       | InterPro: IPR000561; EGF-like.   |              |      |         |
| DR       | InterPro: IPR000742; EGF_2.  |              |      |         |
| DR       | InterPro: IPR001881; EGF_Ca.   |              |      |         |
| DR       | InterPro: IPR003006; IG_MHC.   |              |      |         |
| DR       | InterPro: IPR001254; Ser protease_Try.                                 |              |      |         |
| DR       | InterPro: IPR000294; VltK_dep_GLA.                                     |              |      |         |
| DR       | Pfam; PR00008; EGF_2.  |              |      |         |
| DR       | Pfam; PR00594; gla_1.  |              |      |         |
| DR       | Pfam; PR00047; Ig_2.   |              |      |         |
| DR       | Pfam; PR00089; trypsin_1.  |              |      |         |
| DR       | SMART; SMO0181; EGF_2.   |              |      |         |
| DR       | PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.                             |              |      |         |
| DR       | PROSITE; PS00022; EGF_1; UNKNOWN_1.                                    |              |      |         |
| DR       | PROSITE; PS01186; EGF_2; UNKNOWN_1.                                    |              |      |         |
| DR       | PROSITE; PS01187; EGF_CA; UNKNOWN_1.                                   |              |      |         |
| DR       | PROSITE; PS00011; GLU CARBOXYLATION; UNKNOWN_1.                        |              |      |         |
| DR       | PROSITE; PS00290; IG_MHC; UNKNOWN_1.                                   |              |      |         |
| DR       | PROSITE; PS50240; TRYPSIN_DOM; 1.                                      |              |      |         |

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
DR Hydrolase; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94ACGCEB42CC992F CRC64;

Query Match 80.7%; Score 155; DB 4; Length 701;  
Best Local Similarity 72.7%; Pred. No. 2.7e-20;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFILXLRNGSLKRXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 61 ANAFLEELRPGSLRECKEBCQSFEEAREIFKDAERTKLFWISY 104

## RESULT 2

ID Q61109 PRELIMINARY; PRT; 446 AA.  
AC Q61109;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Coagulation factor VII.  
GN F7 OR FVII.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER.  
RX MEDLINE=96276538; PubMed=8701412;  
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
RA Castellino F.J.;  
RT "Characterization of a cDNA encoding murine coagulation factor VII.";  
RL Thromb. Haemost. 75:481-487(1996).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; U44795; AAC52570.1; -.  
DR HSBP; P08709; IFAK.  
DR MEROPS; S01.215; -.  
DR MGD; MGI:109325; F7.  
DR InterPro; IPR002086; Aldehyde\_dehydr.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; Gla; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_spc; 1.  
DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS02440; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
KW Serine protease.  
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDD6870 CRC64;

Query Match 57.3%; Score 110; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 4.8e-12;  
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFILXLRNGSLKRXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 42 ANSLEELMPGSLRECKEBCQSFEEAREIFKSPERTQFWIV 85

## RESULT 3

ID Q91WN8 PRELIMINARY; PRT; 460 AA.  
AC Q91WN8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Similar to protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER.  
RA Strauberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013896; AAH13896.1; -.  
DR MGD; MGI:97771; Proc.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF\_like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; Gla; 1.  
DR PRINTS; PR00089; trypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS02440; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 460 AA; 51818 MW; 011726B68FCC274 CRC64;

Query Match 50.0%; Score 96; DB 11; Length 460;  
Best Local Similarity 45.5%; Pred. No. 2.1e-09;  
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFILXLRNGSLKRXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 42 ANSLEELMPGSLRECKEBCQSFEEAREIFQNVEDTLAFWIKY 85

RESULT 4

ID Q15253 PRELIMINARY; PRT; 100 AA.  
AC Q15253;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Thrombin precursor (Fragment).  
GN F2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87182874; PubMed=3471151;  
RA MacGillivray R.T., Irwin D.M., Guinlo E.R., Stone J.C.;

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"Recombinant genetic approaches to functional mapping of thrombin.";
RL   Ann. N. Y. Acad. Sci. 485:73-79 (1986).
DR   EMBL; M33031; AAA60220.1; -.
DR   HSSP; P00735; 2PPI.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR000294; Vltk_dep_GLA.
DR   Pfam; PF00594; gla; 1.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00069; GLA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
FT   SIGNAL.
FT   CHAIN   1         43      POTENTIAL.
FT   CHAIN   44      >100    POTENTIAL.
FT   NON_TER 100      100
SQ   SEQUENCE   100 AA; 11302 MW; FDOESD0174E1F6FE CRC64;

Query Match          48.4%; Score 93; DB 4; Length 100;
Best Local Similarity 38.6%; Pred. No. 1.6e-09;
Matches 17; Conservative 6; Mismatches 21; Indels 0; Gaps 0

QY      1 ANAFLLXLRLNGSLKRXCKXXQCSFYXAFIFPDARKTKLEWISY 44
        |||::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      44 ANTFLEEVKRGKGLRECEVETCSYEAEFALESSTATVDVFNKY 87

RESULT 5
Q99PC6 PRELIMINARY; PRT; 460 AA.
ID      Q99PC6
AC      Q99PC6;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Anticoagulant protein C.
GN      PROC.
OS      Mus musculus (Mouse) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL;
RT      Korf I.;
RA      "Complete sequence of UC72A01.";
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC      TRYPSIN FAMILY.
DR   EMBL; AF318182; AAK07918.1; -.
DR   HSSP; P04070; 1PCU.
DR   MEROPS; S01.218; -.
DR   MGD; MGI:97771; Proc.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   InterPro; IPR000294; Vltk_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PRO0722; CHYMOTRYPSIN.
DR   PRINTS; SM00181; EGF; 2.
DR   SMART; SM00001; EGF_like; 2.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00020; Tryp_spec; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00013; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS00240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

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| Query Match | Best Local Similarity  | 46.9%;         | Score 90; | DB 11;  | Length 460; |
|-------------|--|----------------|-----------|---------|-------------|
| Matches 19; | Conservative 4;  | Mismatches 21; | Indels 0; | Gaps 0; |             |
| 0y          | 1 ANAFLLXLRNGSLKRCCKXKXCSFKAAXIFKDAKRTLFWISY 44                        |                |           |         |             |
| Db          | 42 ANSFLEMRPGSLERECEMEICDLEEAQEIFQWEDTLAFWIKY 85                       |                |           |         |             |
| RESULT 6    |  |                |           |         |             |
| 063207      | PRELIMINARY;   | PRT;           | 482 AA.   |         |             |
| ID          | 063207   |                |           |         |             |
| AC          | 063207;  |                |           |         |             |
| DT          | 01-NOV-1996 (TREMblrel. 01, Created)                                   |                |           |         |             |
| DT          | 01-NOV-1996 (TREMblrel. 01, Last sequence update)                      |                |           |         |             |
| DT          | 01-MAR-2002 (TREMblrel. 20, Last annotation update)                    |                |           |         |             |
| DE          | Factor X.  |                |           |         |             |
| OS          | Rattus norvegicus (Rat).   |                |           |         |             |
| OC          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |                |           |         |             |
| OC          | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  |                |           |         |             |
| OX          | NCBI_TaxID=10116;  |                |           |         |             |
| RN          | [1]  |                |           |         |             |
| RP          | SEQUENCE FROM N.A.   |                |           |         |             |
| RC          | STRAIN=SPRAGUE-DAWLEY;   |                |           |         |             |
| RA          | MEDLINE=96093366; PubMed=8578539;                                      |                |           |         |             |
| RT          | Stanton C., Ross R.P., Hutson S., Wallin R.;                           |                |           |         |             |
| RT          | "Evidence for competition between vitamin K-dependent clotting factors |                |           |         |             |
| RT          | for intracellular processing by the vitamin K-dependent gamma-         |                |           |         |             |
| RT          | carboxylase.";   |                |           |         |             |
| RL          | Thromb. Res. 80:63-73(1995).   |                |           |         |             |
| CC          | -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE      |                |           |         |             |
| CC          | TRYPSIN FAMILY.  |                |           |         |             |
| CC          | EMBL; X79807; CAAS6202.1; -  |                |           |         |             |
| DR          | HSSP; P00742; 1KXA.  |                |           |         |             |
| DR          | MEROPS; S01.216; -   |                |           |         |             |
| DR          | InterPro; IPR000152; AaX_hydroxyl.                                     |                |           |         |             |
| DR          | InterPro; IPR001314; Chymotrypsin.                                     |                |           |         |             |
| DR          | InterPro; IPR000561; EGF_1like.  |                |           |         |             |
| DR          | InterPro; IPR000742; EGF 2.  |                |           |         |             |
| DR          | InterPro; IPR001881; EGF_Ca.   |                |           |         |             |
| DR          | InterPro; IPR002383; GLA_blood.  |                |           |         |             |
| DR          | InterPro; IPR001254; Ser_protease_Try.                                 |                |           |         |             |
| DR          | InterPro; IPR000294; VitK_dep_GLA.                                     |                |           |         |             |
| DR          | Pfam; PF00594; GLA; 2.   |                |           |         |             |
| DR          | Pfam; PF00089; trypsin. 1.   |                |           |         |             |
| DR          | PRINTS; PRO0722; CHYMOTRYPSIN.   |                |           |         |             |
| DR          | PRINTS; PRO0001; GLABLOOD.   |                |           |         |             |
| DR          | SMART; SM00179; EGF_CA; 1.   |                |           |         |             |
| DR          | SMART; SM00001; EGF_1like; 1.  |                |           |         |             |
| DR          | SMART; SM00069; GLA; 1.  |                |           |         |             |
| DR          | SMART; PS00020; Tryp_SPC; 1.   |                |           |         |             |
| DR          | PROSITE; PS00010; ASX_HYDROXYL; 1.                                     |                |           |         |             |
| DR          | PROSITE; PS00022; EGF_1; UNKNOWN_1.                                    |                |           |         |             |
| DR          | PROSITE; PS01186; EGF 2; 2.  |                |           |         |             |
| DR          | PROSITE; PS01187; EGF_CA; 1.   |                |           |         |             |
| DR          | PROSITE; PS00011; GLU_CARBOXYLATION; 1.                                |                |           |         |             |
| DR          | PROSITE; PS50240; TRYPSIN_DOM; 1.                                      |                |           |         |             |
| DR          | PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.                              |                |           |         |             |
| DR          | PROSITE; PS00135; TRYPSIN_SER; 1.                                      |                |           |         |             |
| KW          | Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;             |                |           |         |             |
| KW          | Hydroxylation; Repeat; Serine protease.                                |                |           |         |             |
| SO          | SEQUENCE 460 AA; 51784 MW; 0293RC25E9D3ED16 CRC64;                     |                |           |         |             |
| SO          | SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;                     |                |           |         |             |
| Query Match | Best Local Similarity  | 46.4%;         | Score 89; | DB 11;  | Length 482; |
| Matches 17; | Conservative 7;  | Mismatches 20; | Indels 0; | Gaps 0; |             |

OY 1 ANAFLLXLRNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
DB 41 ANSFEEIKKGNLRECEVEICSFEEAREVEFDNKTTEFWNKY 84

## RESULT 7

O9GTR0 ID O9GTR0 PRELIMINARY; PRT; 456 AA.  
AC O9GTR0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Protein C precursor.  
GN PROC.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxId=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,  
RA Breenig B.;  
RT "Molecular characterization and chromosomal assignment of the canine  
RT protein C gene.";  
RL Mamm. Genome 10:135-139(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9371952; PubMed=10443005;  
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breenig B.;  
RT "Analysis of canine protein C gene polymorphisms.";  
RL Anim. Genet. 30:237-238(1999).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL: AJ001979; CAA05126.1; -.  
DR HSSP: P04070; IPCU.  
DR MEROPS: S01.218; -.  
DR InterPro: IPR000152; Aex\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR00294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; Gla; 1.  
DR Pfam: PF00089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00659; GLA; 1.  
DR SMART: SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_Ca; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease; Signal.  
FT SIGNAL 1 42  
FT CHAIN 43 192 POTENTIAL.  
FT CHAIN 193 194 PROTEIN C LIGHT CHAIN.  
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.  
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34B59FF CRC64;

Query Match 45.3%; Score 87; DB 6; Length 456;  
Best Local Similarity 40.9%; Pred. No. 1e-07;  
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAFLLXLRNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
DB 41 ANSFEEIKKGNLRECEVEICSFEEAREVEFDNKTTEFWNKY 84

DB 43 ANSFEEIRAGSLRECEMEICDFEEAKEIRFQNVDDTLATVMSKY 86

## RESULT 8

O9GMD9 ID O9GMD9 PRELIMINARY; PRT; 469 AA.  
AC O9GMD9;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Coagulation factor X.  
OS Ornithorhynchus anatinus (Duckbill platypus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.  
OX NCBI\_TaxId=9258;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21015017; PubMed=11132153;  
RA Poorafshar M., Aveskog M., Munday B., Hellman L.;  
RT "Identification and structural analysis of four serine proteases in a  
RT monotreme, the platypus, Ornithorhynchus anatinus.";  
RL Immunogenetics 52:19-28(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL: AF275654; AAG00453.1; -.  
DR HSSP: P00742; IXKB.  
DR MEROPS: S01.216; -.  
DR InterPro: IPR000152; Aex\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR00294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; Gla; 1.  
DR Pfam: PF00089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00001; EGF\_Ca; 1.  
DR SMART: SM00179; EGF\_Ca; 1.  
DR SMART: SM00001; EGF\_2.  
DR SMART: SM00659; GLA; 1.  
DR SMART: SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_Ca; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 45.3%; Score 87; DB 6; Length 469;  
Best Local Similarity 36.4%; Pred. No. 1.1e-07;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAFLLXLRNGSLKRXCKXQCSFXAXFIKDAKRTKLFWISY 44  
DB 41 ANSFEEIKKGNLRECEMEICDFEEAKEIRFQNVDDTLATVMSKY 84

## RESULT 9

O54740 ID O54740 PRELIMINARY; PRT; 481 AA.  
AC O54740;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Coagulation factor X precursor (EC 3.4.21.6).

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GN F10 OR PA10.
OS Mus musculus (Mouse).
OG Plasmid pluscript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontemann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AJ222677; CAA10933.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYD_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DESEFPD97AE CRC64;

Query Match 45.3%; Score 87; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 1.1e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRCXXQCSPFXAFIFKDXARTKLFWISY 44
DB 41 ANSFEEFKGNLERECMERICSEVREIFEDDEKTKETWTKY 84

RESULT 10
099L32 PRELIMINARY; PRT; 481 AA.
AC 099L32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: BC003877; AAH03877.1; -.
DR HSSP: P00742; 1XKA.
DR MEROPS: S01.216; -.
DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYD_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 45.3%; Score 87; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 1.1e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLXRCXXQCSPFXAFIFKDXARTKLFWISY 44
DB 41 ANSFEEFKGNLERECMERICSEVREIFEDDEKTKETWTKY 84

RESULT 11
088947 PRELIMINARY; PRT; 481 AA.
AC 088947;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-NOV-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.V., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=129Sf;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RL Thromb. Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAF22980.1; -.
DR HSSP; P00742; ICKA.
DR MEROPS; S01.216; -.
DR MCD; MGI:103107; F10.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E9D271E CRC64;

Query Match 45.3%; Score 87; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 1.1e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRNGSLRXKXKXCSFXKAFIFPDARTKLFWISY 44
Db 41 ANSFPEERKGNLERECMEETCSYEVRREIFEDDEKTEKWTY 84

RESULT 12
Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RS SEQUENCE FROM N.A.
RA Mizlata M.N., Amaratil E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF345458; AAK75556.1; -.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

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FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6023 MW; D15C6DE9CCBA4A14 CRC64;

Query Match 40.6%; Score 78; DB 6; Length 49;
Best Local Similarity 41.2%; Pred. No. 4.9e-07;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLRXKXKXKXCSFXKAFIFKDAKRTKLFWISY 44
Db 15 GNLERECKEKSCSFEEAREVEVENTEKTEFWKQY 48

RESULT 13
Q14316 PRELIMINARY; PRT; 456 AA.
ID Q14316;
AC Q14316;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-AUG-1999 (TRENBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

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Query Match          39.1%; Score 75; DB 4; Length 456;
Best Local Similarity 41.2%; Pred. No. 1.9e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXAXFKDAXRTKLFWISY 44
Db 53 GNLERECMEKCSFEAREVFEVTEFTEFWKQY 86

RESULT 14
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satra Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees."
RL Genes GeneL. Syst. 0:0-0(2001).
DR EMBL; AB062470; BAB58885.1; -.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0P77F45 CRC64;

Query Match          39.1%; Score 75; DB 6; Length 461;
Best Local Similarity 41.2%; Pred. No. 1.9e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXAXFKDAXRTKLFWISY 44
Db 58 GNLERECMEKCSFEAREVFEVTEFTEFWKQY 91

RESULT 15
Q95ND6 PRELIMINARY; PRT; 461 AA.
AC Q95ND6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)

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DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Satra Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees."
RL Genes GeneL. Syst. 0:0-0(2001).
DR EMBL; AB062471; BAB58886.1; -.
DR EMBL; AB062459; BAB58886.1; JOINED.
DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
KW Hydroxylase; Serine protease.
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match          39.1%; Score 75; DB 6; Length 461;
Best Local Similarity 41.2%; Pred. No. 1.9e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXAXFKDAXRTKLFWISY 44
Db 58 GNLERECMEKCSFEAREVFEVTEFTEFWKQY 91

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Search completed: March 19, 2003, 15:13:34  
 Job time : 47.3125 secs

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## OM protein - protein search, using SW model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10ASN28PHE  
Perfect score: 192  
Sequence: 1 ANAFLXLRNGSLRXCKXX.....XXAFXIKDAXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/2/1aa/5A COMB.pep.\*  
3: /cgn2\_6/prodata/2/1aa/5A COMB.pep.\*  
4: /cgn2\_6/prodata/2/1aa/5A COMB.pep.\*  
5: /cgn2\_6/prodata/2/1aa/5A COMB.pep.\*  
6: /cgn2\_6/prodata/2/1aa/5A COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                        |
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| 1          | 164   | 85.4        | 44     | 3     | US-08-955-636-28 Sequence 28, Appl |
| 2          | 158   | 82.3        | 44     | 3     | US-08-955-636-27 Sequence 27, Appl |
| 3          | 157   | 81.8        | 44     | 3     | US-08-955-636-26 Sequence 26, Appl |
| 4          | 155   | 80.7        | 44     | 3     | US-08-955-636-3 Sequence 3, Appl   |
| 5          | 155   | 80.7        | 406    | 1     | US-08-293-778-24 Sequence 24, Appl |
| 6          | 155   | 80.7        | 406    | 1     | US-08-295-411-5 Sequence 5, Appl   |
| 7          | 155   | 80.7        | 406    | 2     | US-08-955-471-5 Sequence 5, Appl   |
| 8          | 155   | 80.7        | 406    | 5     | PCT-US92-10242-5 Sequence 5, Appl  |
| 9          | 155   | 80.7        | 444    | 1     | US-08-475-845-2 Sequence 2, Appl   |
| 10         | 155   | 80.7        | 444    | 2     | US-08-327-690-2 Sequence 2, Appl   |
| 11         | 155   | 80.7        | 444    | 2     | US-08-660-289-2 Sequence 2, Appl   |
| 12         | 155   | 80.7        | 444    | 2     | US-08-537-807-2 Sequence 2, Appl   |
| 13         | 155   | 80.7        | 444    | 2     | US-08-871-003-2 Sequence 2, Appl   |
| 14         | 155   | 80.7        | 444    | 3     | US-08-464-233-2 Sequence 2, Appl   |
| 15         | 155   | 80.7        | 444    | 4     | US-09-189-607-2 Sequence 2, Appl   |
| 16         | 155   | 80.7        | 444    | 4     | US-09-378-907-2 Sequence 2, Appl   |
| 17         | 155   | 80.7        | 444    | 5     | PCT-US94-05779-2 Sequence 2, Appl  |
| 18         | 155   | 80.7        | 466    | 1     | US-07-882-202A-4 Sequence 4, Appl  |
| 19         | 155   | 80.7        | 466    | 1     | US-08-021-615A-4 Sequence 4, Appl  |
| 20         | 155   | 80.7        | 466    | 1     | US-08-321-777-4 Sequence 4, Appl   |
| 21         | 155   | 80.7        | 466    | 4     | US-09-009-217-14 Sequence 14, Appl |
| 22         | 155   | 80.7        | 466    | 4     | US-09-009-656-14 Sequence 14, Appl |
| 23         | 155   | 80.7        | 466    | 5     | PCT-US93-04493-4 Sequence 4, Appl  |
| 24         | 153   | 79.7        | 44     | 3     | US-08-955-636-30 Sequence 30, Appl |
| 25         | 149   | 77.6        | 44     | 3     | US-08-955-636-29 Sequence 29, Appl |
| 26         | 140   | 72.9        | 41     | 1     | US-08-229-280-4 Sequence 4, Appl   |
| 27         | 121   | 63.0        | 44     | 3     | US-08-955-636-4 Sequence 4, Appl   |

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|----|-----|------|-----|---|------------------|-------------------|
| 28 | 104 | 54.2 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appl  |
| 29 | 104 | 54.2 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appl  |
| 30 | 104 | 54.2 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appl  |
| 31 | 104 | 54.2 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appl  |
| 32 | 104 | 54.2 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appl  |
| 33 | 104 | 54.2 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appl  |
| 34 | 104 | 54.2 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appl  |
| 35 | 96  | 50.0 | 44  | 3 | US-08-955-636-25 | Sequence 25, Appl |
| 36 | 95  | 49.5 | 448 | 1 | US-08-295-411-3  | Sequence 3, Appl  |
| 37 | 95  | 49.5 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appl  |
| 38 | 95  | 49.5 | 448 | 5 | PCT-US92-10068-1 | Sequence 1, Appl  |
| 39 | 95  | 49.5 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appl  |
| 40 | 94  | 49.0 | 44  | 3 | US-08-955-636-18 | Sequence 18, Appl |
| 41 | 94  | 49.0 | 487 | 1 | US-08-469-486-53 | Sequence 53, Appl |
| 42 | 94  | 49.0 | 487 | 2 | US-08-469-486-53 | Sequence 53, Appl |
| 43 | 94  | 49.0 | 492 | 1 | US-08-469-486-2  | Sequence 2, Appl  |
| 44 | 94  | 49.0 | 492 | 2 | US-08-469-658-2  | Sequence 2, Appl  |
| 45 | 93  | 48.4 | 579 | 1 | US-08-295-411-4  | Sequence 4, Appl  |

## ALIGNMENTS

RESULT 1  
US-08-955-636-28  
; Sequence 28, Application US/08955636A  
; Patent No. 6017882  
; GENERAL INFORMATION:  
; APPLICANT: Neisestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955, 636A  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (0)..(0)  
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-28

Query Match 85.4%; Score 164; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 6.5e-21;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLRXCKXXCFXAXFXIKDAXRTKLFWISY 44  
Db 1 ANAFLXLRNGSLRXCKXXCFXAXFXIKDAXRTKLFWISY 44

RESULT 2  
US-08-955-636-27  
; Sequence 27, Application US/08955636A  
; Patent No. 6017882  
; GENERAL INFORMATION:  
; APPLICANT: Neisestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955, 636A  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

NAME/KEY: MOD RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-27

Query Match 82.3%; Score 158; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 6.7e-20;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ANAFLXLRDGLXRXCKXQCSFXXARIFKDAKRTKLFWISY 44

## RESULT 3

US-08-955-636-26  
Sequence 26, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-26

Query Match 81.8%; Score 157; DB 3; Length 44;  
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Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 ANAFLXLRGSLXRXCKXQCSFXXARIFKDAKRTKLFWISY 44

## RESULT 4

US-08-955-636-3  
Sequence 3, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-3

Query Match 80.7%; Score 155; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2.2e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 ANAFLXLRPGSLXRXCKXQCSFXXARIFKDAKRTKLFWISY 44

RESULT 5  
US-08-293-778-24  
Sequence 24, Application US/08293778  
Patent No. 5580560  
GENERAL INFORMATION:  
APPLICANT: Nicolaesen, Else M.  
APPLICANT: Bjorn, Soren E.  
APPLICANT: Wiberg, Finn C.  
APPLICANT: Woodbury, Richard  
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,778  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,509  
FILING DATE:  
APPLICATION NUMBER: DK 3235/87  
FILING DATE: 25-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/434,149  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129, 224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 80.7%; Score 155; DB 1; Length 406;  
Best Local Similarity 72.7%; Pred. No. 2.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFXXAFIFKDAKRTKLFWISY 44  
Db 1 ANAFLYLRLPGSLYRYCKYQCSFYARIFKDAKRTKLFWISY 44

RESULT 6  
US-08-295-411-5

Sequence 5, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-295-411-5  
Query Match 80.7%; Score 155; DB 1; Length 406;  
Best Local Similarity 72.7%; Pred. No. 2.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Db 1 ANAFLLXLRNGSLKRCXKQCFXAFXIFKDXARTLFWISY 44  
1 ANAFLELRPGSLERCKEQCFEAREIFKDAERTLFWISY 44  
RESULT 7  
US-08-955-471-5  
Sequence 5, Application US/08955471  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 North Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,471  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/295,411  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII Light Chain"  
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Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
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RESULT 8  
PCT-US92-10242-5  
Sequence 5, Application PC/TUS9210242  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 North Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA

TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 568751th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,471  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/295,411  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
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OTHER INFORMATION: /note= "Factor VII Light Chain"  
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US-08-955-471-5  
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Db 1 ANAFLLXLRNGSLKRCXKQCFXAFXIFKDXARTLFWISY 44  
1 ANAFLELRPGSLERCKEQCFEAREIFKDAERTLFWISY 44  
RESULT 8  
PCT-US92-10242-5  
Sequence 5, Application PC/TUS9210242  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 North Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA

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: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/10242
: FILING DATE: 19921118
: CLASSIFICATION:
: PRIORITY INFORMATION:
: APPLICATION NUMBER: US 07/793,989
: FILING DATE: 18-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SCR0472P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152
: OTHER INFORMATION: /note= "Factor VII Light Chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 153..406
: OTHER INFORMATION: /note= "Factor VII Heavy Chain"
: PCT-US92-10242-5

Query Match 80.7%; Score 155; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 2.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRXCKXQCSFXAXFIPDXARTKLFWISY 44
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RESULT 9
US-08-475-845-2
: Sequence 2, Application US/08475845
: Patent No. 5788965
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stuart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
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: PRIORITY INFORMATION:
: APPLICATION NUMBER: 08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY INFORMATION:
: APPLICATION NUMBER: 07/662,920
: FILING DATE: 28-FEB-1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 13952-8-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-475-845-2

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Best Local Similarity 72.7%; Pred. No. 2.5e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRXCKXQCSFXAXFIPDXARTKLFWISY 44
Db 39 ANAFLELRPGSLERECKEQCSFEAREIFPDARTKLFWISY 82

RESULT 10
US-08-327-690-2
: Sequence 2, Application US/08327690
: Patent No. 5817788
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stuart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
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: APPLICATION NUMBER: US/08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY INFORMATION:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920
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FILING DATE: 28-FEB-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-327-690-2

Query Match 80.7%; Score 155; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 2.5e-18;  
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Db 39 ANAFLELRPGSLERECKEQCSFEAREIFKDAERTKLTWISY 82

RESULT 11  
US-08-660-289-2  
Sequence 2, Application US/08660289  
Patent No. 5833982  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,289  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,845  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-660-289-2

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Best Local Similarity 72.7%; Pred. No. 2.5e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXKXCKXXQCSFXAFIFKDXARTKLTWISY 44  
Db 39 ANAFLELRPGSLERECKEQCSFEAREIFKDAERTKLTWISY 82

RESULT 12  
US-08-537-807-2  
Sequence 2, Application US/08537807  
Patent No. 5861374  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
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FILING DATE:  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05779  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 08/065,725  
FILING DATE: 21-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
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US-08-537-807-2

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Sequence 2, Application US/08871003  
Patent No. 5997864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.

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; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
;
; COMPUTER READABLE FORM:
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; FILING DATE:
; CLASSIFICATION: 514
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; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
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; MOLECULE TYPE: protein
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; Sequence 2, Application US/08464233
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; APPLICATION NUMBER: US/08/464,233
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; FILING DATE: 24-OCT-1994
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; FILING DATE: 21-MAY-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
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; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
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; APPLICATION NUMBER: 08/660,289
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION:

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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 3          | 93    | 48.4        | 419    | 9  | US-10-182-263-4    |
| 4          | 93    | 48.4        | 419    | 9  | US-10-182-263-5    |
| 5          | 92    | 47.9        | 419    | 9  | US-10-182-263-6    |
| 6          | 82    | 42.7        | 419    | 9  | US-10-182-263-1    |
| 7          | 82    | 42.7        | 419    | 9  | US-09-978-917A-4   |
| 8          | 82    | 42.7        | 461    | 9  | US-10-182-263-2    |
| 9          | 82    | 42.7        | 461    | 9  | US-09-978-917A-2   |
| 10         | 75    | 39.1        | 415    | 10 | US-09-118-748-2    |
| 11         | 75    | 39.1        | 461    | 9  | US-10-132-829-5    |
| 12         | 75    | 39.1        | 461    | 10 | US-09-884-901-3    |
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| 14         | 66    | 34.4        | 209    | 9  | US-09-759-130B-312 |
| 15         | 66    | 34.4        | 226    | 9  | US-09-759-130B-310 |
| 16         | 51    | 26.6        | 95     | 9  | US-09-759-130B-356 |
| 17         | 51    | 26.6        | 208    | 9  | US-09-759-130B-355 |
| 18         | 51    | 26.6        | 225    | 9  | US-09-759-130B-353 |
| 19         | 44.5  | 23.2        | 729    | 9  | US-10-145-396-11   |

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| 21 | 43.5 | 22.7 | 730 | 9  | US-10-145-396-12    | Sequence 12, Appli |
| 22 | 43.5 | 22.7 | 730 | 10 | US-09-780-053-2     | Sequence 2, Appli  |
| 23 | 40   | 20.8 | 88  | 10 | US-09-811-284-194   | Sequence 194, App  |
| 24 | 40   | 20.8 | 115 | 9  | US-09-883-152-21    | Sequence 21, Appli |
| 25 | 40   | 20.8 | 115 | 9  | US-09-986-480-192   | Sequence 192, App  |
| 26 | 40   | 20.8 | 130 | 9  | US-09-986-480-345   | Sequence 345, App  |
| 27 | 40   | 20.8 | 292 | 10 | US-09-764-864-1261  | Sequence 1261, Ap  |
| 28 | 39   | 20.3 | 240 | 9  | US-09-782-504-4     | Sequence 4, Appli  |
| 29 | 39   | 20.3 | 254 | 9  | US-10-104-019-21    | Sequence 21, Appli |
| 30 | 39   | 20.3 | 273 | 9  | US-09-764-868-968   | Sequence 968, App  |
| 31 | 39   | 20.3 | 873 | 9  | US-10-200-154-2     | Sequence 2, Appli  |
| 32 | 39   | 20.3 | 873 | 9  | US-09-954-043-2     | Sequence 2, Appli  |
| 33 | 38.5 | 20.1 | 111 | 10 | US-09-899-896-7     | Sequence 109, App  |
| 34 | 38   | 19.8 | 47  | 10 | US-09-739-254-109   | Sequence 109, App  |
| 35 | 38   | 19.8 | 47  | 10 | US-09-904-615-109   | Sequence 109, App  |
| 36 | 38   | 19.8 | 176 | 9  | US-10-078-770-106   | Sequence 106, App  |
| 37 | 38   | 19.8 | 286 | 9  | US-10-195-142-12    | Sequence 12, Appli |
| 38 | 38   | 19.8 | 333 | 9  | US-09-738-626-5683  | Sequence 5683, Ap  |
| 39 | 38   | 19.8 | 339 | 9  | US-10-195-142-4     | Sequence 4, Appli  |
| 40 | 38   | 19.8 | 400 | 9  | US-10-078-770-114   | Sequence 114, App  |
| 41 | 38   | 19.8 | 447 | 10 | US-09-815-242-13490 | Sequence 13490, A  |
| 42 | 38   | 19.8 | 447 | 10 | US-09-815-242-13612 | Sequence 13612, A  |
| 43 | 38   | 19.8 | 447 | 10 | US-09-735-564-2     | Sequence 2, Appli  |
| 44 | 38   | 19.8 | 594 | 9  | US-10-195-142-10    | Sequence 10, Appli |
| 45 | 38   | 19.8 | 608 | 10 | US-09-908-664-5     | Sequence 5, Appli  |

## ALIGNMENTS

RESULT 1  
US-10-109-498-1  
; Sequence 1, Application US/10109498  
; Publication No. US20030044908A1  
; GENERAL INFORMATION:  
; APPLICANT: Persson, Egon  
; TITLE OF INVENTION: Coagulation Factor VII Derivatives  
; FILE REFERENCE: 6286,200-US  
; CURRENT APPLICATION NUMBER: US/10/109,498  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/281,261  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: PA 2001 00477  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(406)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-109-498-1

Query Match 80.7%; Score 155; DB 9; Length 406;  
Best local similarity 95.5%; Pred. No. 1.2e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXKLRLNGSLRXCKXXCFXXAFIFKDXRTKLFWISY 44  
Db 1 ANAFLLXKLRLNGSLRXCKXXCFXXAFIFKDXRTKLFWISY 44

RESULT 2  
US-10-182-263-3  
; Sequence 3, Application US/10182263  
; Publication No. US20030022354A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlitz, Bruce E  
; APPLICANT: Jones, Bryan E

```

; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          48.4%; Score 93; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.3e-08;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSFXAXFIFKDAKRTKLFW 41
||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 3
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          48.4%; Score 93; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.3e-08;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSFXAXFIFKDAKRTKLFW 41
||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 4
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          48.4%; Score 93; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.3e-08;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSFXAXFIFKDAKRTKLFW 41
||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 5
US-10-182-263-6
; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          47.9%; Score 92; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLXLRNGSLKRXCKXQCSFXAXFIFKDAKRTKLFW 41
||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ANSFLELRHGSLERECEIEICDFEAKEIFEDVDDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-182-263-1

Query Match  
Best Local Similarity 42.7%; Score 82; DB 9; Length 419;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRXCKXXQCSFXA FXIFKDXARTKLEFW 41  
Db 1 ANSFLELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 41

RESULT 7

US-09-978-917A-4  
Sequence 4, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219us310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978, 917A  
CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-917A-4

Query Match  
Best Local Similarity 42.7%; Score 82; DB 9; Length 419;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRXCKXXQCSFXA FXIFKDXARTKLEFW 41  
Db 1 ANSFLELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 41

RESULT 8

US-10-182-263-2  
Sequence 2, Application US/10182263  
Publication No. US20030022354A1

GENERAL INFORMATION:  
APPLICANT: Getlitz, Bruce E  
APPLICANT: Jones, Bryan E  
APPLICANT: Grinnell, Brian W  
TITLE OF INVENTION: PROTEIN C DERIVATIVES  
FILE REFERENCE: X-13611  
CURRENT APPLICATION NUMBER: US/10/182, 263  
CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: 60/189199  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-182-263-2

Query Match  
Best Local Similarity 42.7%; Score 82; DB 9; Length 461;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRXCKXXQCSFXA FXIFKDXARTKLEFW 41  
Db 43 ANSFLELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 83

RESULT 9

US-09-978-917A-2  
Sequence 2, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219us310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978, 917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(42)  
FEATURE:  
NAME/KEY: CHAIN  
LOCATION: (43)...(461)  
US-09-978-917A-2

Query Match  
Best Local Similarity 42.7%; Score 82; DB 9; Length 461;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRNGSLXRXCKXXQCSFXA FXIFKDXARTKLEFW 41  
Db 43 ANSFLELRHSSLERECIEECDFEEAKEIFQNVDDTLAFW 83

RESULT 10

US-09-118-748-2  
Sequence 2, Application US/09118748A  
Patent No. US20020031799A1

GENERAL INFORMATION:  
APPLICANT: Stafford, Darrel W.  
APPLICANT: Chang, Jindl  
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting  
TITLE OF INVENTION: Activity  
FILE REFERENCE: 5470-183  
CURRENT APPLICATION NUMBER: US/09/118, 748A  
CURRENT FILING DATE: 1998-07-17  
EARLIER APPLICATION NUMBER: 60/053, 571  
EARLIER FILING DATE: 1997-07-21

NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-118-748-2

Query Match  
Best Local Similarity 39.1%; Score 75; DB 10; Length 415;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSFXA FXIFKDXARTKLEFWISY 44  
Db 12 GNLRECEMEKCSFEERAEVFEVTERTEFFWKQY 45

RESULT 11  
US-10-132-829-5  
Sequence 5, Application US/10132829  
Publication No. US20030044982A1

GENERAL INFORMATION:  
APPLICANT: Chien, Kenneth R  
APPLICANT: Hoshijima, Masahiko  
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII  
TITLE OF INVENTION: with vesicle vector  
FILE REFERENCE: 6627-PA1170

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; CURRENT APPLICATION NUMBER: US/10/132.829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          39.1%; Score 75; DB 9; Length 461;
Best Local Similarity 41.2%; Pred. No. 2.4e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Cy 11 GSLXKCKXXCQCFXAFIFDAXRTKLFWISY 44
Db 58 GNLERECMEBKCSFEAREVFENTERTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOEW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-901-3

Query Match          39.1%; Score 75; DB 10; Length 461;
Best Local Similarity 41.2%; Pred. No. 2.4e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Cy 11 GSLXKCKXXCQCFXAFIFDAXRTKLFWISY 44
Db 58 GNLERECMEBKCSFEAREVFENTERTEFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirscht, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          34.4%; Score 66; DB 9; Length 96;
Best Local Similarity 38.2%; Pred. No. 0.00018;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Cy 11 GSLXKCKXXCQCFXAFIFDAXRTKLFWISY 44
Db 46 GNLERECNEELCNVEAREIFVDEDKTIAFWQY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirscht, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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;; PRIOR APPLICATION NUMBER: US 09/608,452  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/393,996  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US 09/602,871  
;; PRIOR FILING DATE: 2000-06-23  
;; PRIOR APPLICATION NUMBER: US 09/420,707  
;; PRIOR FILING DATE: 1999-10-19  
;; NUMBER OF SEQ ID NOS: 460  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 312  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-759-130B-312

Query Match 34.4%; Score 66; DB 9; Length 209;  
Best Local Similarity 38.2%; Pred. No. 0.00041;  
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 11 GSLRXCKXXQCSPFXAXIFKDXRTKLFWISY 44  
DB 46 GNLERECNEELCNVEARELIFVDEKTIATFMOEY 79

RESULT 15

US-09-759-130B-310  
;; Sequence 310, Application US/09759130B  
;; Publication No. US2003002279A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Millennium Pharmaceuticals, Inc.  
;; APPLICANT: McCarthy, Sean A  
;; APPLICANT: Fraser, Christopher C  
;; APPLICANT: Sharp, John D  
;; APPLICANT: Barnes, Thomas S  
;; APPLICANT: Kirtel, Susan J  
;; APPLICANT: Mackay, Charles R  
;; APPLICANT: Myers, Paul S  
;; APPLICANT: Leiby, Kevin R  
;; APPLICANT: Wighton, Nicolas  
;; APPLICANT: Goodearl, Andrew  
;; APPLICANT: Holtzman, Douglas A  
;; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
;; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
;; TITLE OF INVENTION: USRS  
;; FILE REFERENCE: MP100-5350N1M  
;; CURRENT APPLICATION NUMBER: US/09/759,130B  
;; CURRENT FILING DATE: 2002-09-16  
;; PRIOR APPLICATION NUMBER: US 09/479,249  
;; PRIOR FILING DATE: 2000-01-07  
;; PRIOR APPLICATION NUMBER: US 09/559,497  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: US 09/578,063  
;; PRIOR FILING DATE: 2000-05-24  
;; PRIOR APPLICATION NUMBER: US 09/333,159  
;; PRIOR FILING DATE: 1999-06-14  
;; PRIOR APPLICATION NUMBER: US 09/596,194  
;; PRIOR FILING DATE: 2000-07-14  
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;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US 09/602,871  
;; PRIOR FILING DATE: 2000-06-23  
;; PRIOR APPLICATION NUMBER: US 09/420,707  
;; PRIOR FILING DATE: 1999-10-19  
;; NUMBER OF SEQ ID NOS: 460  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 310  
;; LENGTH: 226  
;; TYPE: PRT

;; ORGANISM: Homo sapiens  
US-09-759-130B-310

Query Match 34.4%; Score 66; DB 9; Length 226;  
Best Local Similarity 38.2%; Pred. No. 0.00045;  
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 11 GSLRXCKXXQCSPFXAXIFKDXRTKLFWISY 44  
DB 63 GNLERECNEELCNVEARELIFVDEKTIATFMOEY 96

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OM protein - protein search, using sw model

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194.803 Million cell updates/sec

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Perfect score: 192  
Sequence: 1 ANAFLLXLRNGSLXRCCKXX.....XXAFXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
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- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
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- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.\*
- 25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep.\*
- 26: /cgn2\_6/ptodata/2/paa/US102\_COMB.pep.\*
- 27: /cgn2\_6/ptodata/2/paa/US103\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 155   | 80.7        | 44     | 13 | US-08-955-636-3      |
| 2          | 155   | 80.7        | 44     | 17 | US-09-302-239-3      |
| 3          | 155   | 80.7        | 44     | 18 | US-09-497-591-3      |
| 4          | 155   | 80.7        | 152    | 21 | US-09-791-537-150941 |
| 5          | 155   | 80.7        | 406    | 3  | US-07-793-989-5      |
| 6          | 155   | 80.7        | 406    | 21 | US-09-782-587B-1     |

|    |       |      |     |    |                      |                    |
|----|-------|------|-----|----|----------------------|--------------------|
| 7  | 155   | 80.7 | 406 | 21 | US-09-782-587B-3     | Sequence 3, Appli  |
| 8  | 155   | 80.7 | 406 | 25 | US-10-109-498-1      | Sequence 1, Appli  |
| 9  | 155   | 80.7 | 406 | 26 | US-10-255-032-1      | Sequence 1, Appli  |
| 10 | 155   | 80.7 | 444 | 4  | US-08-065-725-2      | Sequence 2, Appli  |
| 11 | 155   | 80.7 | 444 | 5  | US-08-164-666-2      | Sequence 2, Appli  |
| 12 | 155   | 80.7 | 444 | 21 | US-09-791-537-50628  | Sequence 50628, A  |
| 13 | 155   | 80.7 | 461 | 23 | US-09-948-933-335    | Sequence 333, App  |
| 14 | 155   | 80.7 | 466 | 14 | US-09-009-822-14     | Sequence 14, Appli |
| 15 | 155   | 80.7 | 466 | 21 | US-09-791-537-100272 | Sequence 100272, A |
| 16 | 155   | 80.7 | 466 | 21 | US-10-017-132-2      | Sequence 2, Appli  |
| 17 | 155   | 80.7 | 466 | 27 | US-60-042-427-18     | Sequence 18, Appli |
| 18 | 155   | 80.7 | 483 | 23 | US-09-948-933-351    | Sequence 351, App  |
| 19 | 155   | 80.7 | 654 | 27 | US-60-230-435-1959   | Sequence 1959, App |
| 20 | 155   | 80.7 | 676 | 27 | US-60-230-435-1650   | Sequence 1650, App |
| 21 | 144   | 75.0 | 42  | 3  | US-07-621-647-2      | Sequence 2, Appli  |
| 22 | 135   | 70.3 | 42  | 17 | US-09-383-667-7      | Sequence 7, Appli  |
| 23 | 129.5 | 67.4 | 42  | 5  | US-08-134-373-1      | Sequence 1, Appli  |
| 24 | 121   | 63.0 | 44  | 13 | US-08-955-636-4      | Sequence 4, Appli  |
| 25 | 121   | 63.0 | 44  | 17 | US-09-302-239-4      | Sequence 4, Appli  |
| 26 | 121   | 63.0 | 44  | 18 | US-09-497-591-4      | Sequence 4, Appli  |
| 27 | 121   | 63.0 | 443 | 21 | US-09-791-537-12664  | Sequence 12664, A  |
| 28 | 121   | 63.0 | 444 | 21 | US-09-791-537-84459  | Sequence 84459, A  |
| 29 | 113   | 58.9 | 407 | 21 | US-09-791-537-94571  | Sequence 94571, A  |
| 30 | 110   | 57.3 | 446 | 21 | US-09-791-537-1837   | Sequence 1837, App |
| 31 | 110   | 57.3 | 446 | 21 | US-09-791-537-82360  | Sequence 82360, A  |
| 32 | 103.5 | 53.9 | 42  | 5  | US-08-134-373-2      | Sequence 2, Appli  |
| 33 | 101   | 52.6 | 490 | 21 | US-09-791-537-96398  | Sequence 96398, A  |
| 34 | 99.5  | 51.8 | 42  | 5  | US-08-134-373-3      | Sequence 3, Appli  |
| 35 | 96    | 50.0 | 460 | 21 | US-09-791-537-86032  | Sequence 86032, A  |
| 36 | 96    | 50.0 | 461 | 21 | US-09-791-537-29340  | Sequence 29340, A  |
| 37 | 95    | 49.5 | 140 | 21 | US-09-791-537-41938  | Sequence 41938, A  |
| 38 | 95    | 49.5 | 140 | 27 | US-60-213-800-410    | Sequence 410, App  |
| 39 | 95    | 49.5 | 149 | 27 | US-60-213-800-354    | Sequence 354, App  |
| 40 | 95    | 49.5 | 437 | 20 | US-09-671-346-2      | GENERAL INFORMA    |
| 41 | 95    | 49.5 | 437 | 20 | US-09-671-346-3      | GENERAL INFORMA    |
| 42 | 95    | 49.5 | 440 | 21 | US-09-760-484-494    | Sequence 494, App  |
| 43 | 95    | 49.5 | 440 | 26 | US-10-211-366-899    | Sequence 899, App  |
| 44 | 95    | 49.5 | 440 | 26 | US-10-216-899-261    | Sequence 261, App  |
| 45 | 95    | 49.5 | 440 | 26 | US-10-217-651-359    | Sequence 359, App  |

## ALIGNMENTS

RESULT 1  
US-08-955-636-3  
; Sequence 3, Application US/08955636  
; GENERAL INFORMATION:  
; APPLICANT: Neisestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955, 636  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
; US-08-955-636-3

Query Match 80.7%; Score 155; DB 13; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2.5e-18;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ANAFLLXLRNGSLXRCCKXXQCSFXXAFXIFKDXRTKLFWISY 44  
Db 1 ANAFLLXLRNGSLXRCCKXXQCSFXXAFXIFKDXRTKLFWISY 44

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RESULT 2
US-09-302-239-3
; Sequence 3, Application US/09302239
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/302,239
; CURRENT FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3
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Query Match      80.7%; Score 155; DB 17; Length 44;
Best Local Similarity 95.5%; Pred. No. 2.5e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db      1 ANAFLLXLRPGSLXRXCKXQCSFYXARXIFKDAKRTKLFWISY 44
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US-09-497-591-3
; Sequence 3, Application US/09497591
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531-016001
; CURRENT APPLICATION NUMBER: US/09/497,591
; CURRENT FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: 09/302,239
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: 08/955,636
; EARLIER FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3
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Query Match      80.7%; Score 155; DB 18; Length 44;
Best Local Similarity 95.5%; Pred. No. 2.5e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy      1 ANAFLLXLRNGSLXRXCKXQCSFYXAFIFKDAKRTKLFWISY 44
Db      1 ANAFLLXLRPGSLXRXCKXQCSFYXARXIFKDAKRTKLFWISY 44
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RESULT 4
US-09-791-537-150941
; Sequence 150941, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
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; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 151055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 150941
; LENGTH: 152
; TYPE: PRT
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; ORGANISM: pdb 1DANL
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(7)
; OTHER INFORMATION: X is an unknown amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: X is an unknown amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: X is an unknown amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(20)
; OTHER INFORMATION: X is an unknown amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(26)
; OTHER INFORMATION: X is an unknown amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (35)..(35)
; OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-150941
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Query Match      80.7%; Score 155; DB 21; Length 152;
Best Local Similarity 95.5%; Pred. No. 8.3e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db      1 ANAFLLXLRPGSLXRXCKXQCSFYXARXIFKDAKRTKLFWISY 44
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RESULT 5
US-07-793-989-5
; Sequence 5, Application US/07793989
; GENERAL INFORMATION:
; APPLICANT: Griffith, John H.
; APPLICANT: Westers, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Office of Patent Counsel, The Scripps
; ADDRESS: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/793,989
FILING DATE: 19911118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRA472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-07-793-989-5
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Query Match      80.7%; Score 155; DB 3; Length 406;
Best Local Similarity 72.7%; Pred. No. 2.1e-17;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Qy 1 ANAFLLXLRNGSLRXCKXXQCSFXXAFKIDAXRTKLFWISY 44
Db 1 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTKLFWISY 44
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RESULT 6
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAU
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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NAME/KEY: MOD_RES
LOCATION: (19)..(20)
OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
NAME/KEY: MOD_RES
LOCATION: (25)..(26)
OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
NAME/KEY: MOD_RES
LOCATION: (29)
OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
NAME/KEY: MOD_RES
LOCATION: (35)
OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1
```

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Query Match      80.7%; Score 155; DB 21; Length 406;
Best Local Similarity 95.5%; Pred. No. 2.1e-17;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 1 ANAFLLXLRNGSLRXCKXXQCSFXXAFKIDAXRTKLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXQCSFXXARXIFKDAERTKLFWISY 44
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RESULT 7
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAU
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3
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Query Match      80.7%; Score 155; DB 21; Length 406;
Best Local Similarity 72.7%; Pred. No. 2.1e-17;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Qy 1 ANAFLLXLRNGSLRXCKXXQCSFXXAFKIDAXRTKLFWISY 44
Db 1 ANAFLELRPGSLRECKECCSFEEAREIFKDAERTKLFWISY 44
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RESULT 8
US-10-109-498-1
; Sequence 1, Application US/10109498
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match          80.7%; Score 155; DB 25; Length 406;
Best Local Similarity 95.5%; Pred. No. 2.1e-17;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFYXAXIFPDAXRTKLFWISY 44
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Db 1 ANAFLXLRPGSLXRXCKXQCSFYXAXIFPDAXRTKLFWISY 44

RESULT 9
US-10-255-032-1
; Sequence 1, Application US/10255032
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-255-032-1

Query Match          80.7%; Score 155; DB 26; Length 406;
Best Local Similarity 95.5%; Pred. No. 2.1e-17;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFYXAXIFPDAXRTKLFWISY 44
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Db 1 ANAFLXLRPGSLXRXCKXQCSFYXAXIFPDAXRTKLFWISY 44

RESULT 10
US-08-065-725-2
; Sequence 2, Application US/08065725
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/065,725
; FILING DATE: 21-MAY-1993
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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-065-725-2

Query Match          80.7%; Score 155; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 2.3e-17;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRNGSLXRXCKXQCSFYXAXIFPDAXRTKLFWISY 44
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Db 39 ANAFLLELRPGSLERECKEQQCSFEAREIFPDAXRTKLFWISY 82

RESULT 11
US-08-164-666-2
; Sequence 2, Application US/08164666
; GENERAL INFORMATION:
; APPLICANT: Berkner
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven W. Parmelee
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,666
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,920
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-164-666-2
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Oy 1 ANAFLLXLRNGSLRXCKXQCSFXXAFIFKDAERTKLFWISY 44  
Db 39 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 82

RESULT 12  
US-09-791-537-50628  
; Sequence 50628, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 50628  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-50628

Query Match 80.7%; Score 155; DB 21; Length 444;  
Best Local Similarity 72.7%; Pred. No. 2.4e-17;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRNGSLRXCKXQCSFXXAFIFKDAERTKLFWISY 44  
Db 39 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 82

RESULT 13  
US-09-948-933-335  
; Sequence 335, Application US/09948933  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF  
; FILE REFERENCE: CL000787  
; CURRENT APPLICATION NUMBER: US/09/948,933  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,399  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 6404  
; SOFTWARE: FaestSeq for Windows Version 4.0  
; SEQ ID NO 335  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Human  
US-09-948-933-335

Query Match 80.7%; Score 155; DB 23; Length 461;  
Best Local Similarity 72.7%; Pred. No. 2.4e-17;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRNGSLRXCKXQCSFXXAFIFKDAERTKLFWISY 44  
Db 56 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 99

RESULT 14  
US-09-009-822-14  
; Sequence 14, Application US/09009822  
; GENERAL INFORMATION:  
; APPLICANT: Thorpe, Philip E.  
; APPLICANT: King, Steven W.  
; APPLICANT: Gao, Boning  
; TITLE OF INVENTION: TISSUE FACTOR METHODS AND COMPOSITIONS

; TITLE OF INVENTION: FOR COAGULATION AND TUMOR TREATMENT  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,822  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/042,427  
; FILING DATE: 27-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,205  
; FILING DATE: 27-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,920  
; FILING DATE: 22-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hieber, David W.  
; REGISTRATION NUMBER: 41,071  
; REFERENCE/DOCKET NUMBER: UTSD:517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 466 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-009-822-14

Query Match 80.7%; Score 155; DB 14; Length 466;  
Best Local Similarity 72.7%; Pred. No. 2.4e-17;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRNGSLRXCKXQCSFXXAFIFKDAERTKLFWISY 44  
Db 61 ANAFLEELRPGSLERCKECCSFEEAREIFKDAERTKLFWISY 104

RESULT 15  
US-09-791-537-100272  
; Sequence 100272, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 100272  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-100272

Query Match 80.7%; Score 155; DB 21; Length 466;  
Best Local Similarity 72.7%; Pred. No. 2.4e-17;

Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 ANAFLLXXLRNGSLXRXCKXQCSFXAXFXIFKDAARITLFWISY 44  
Db 61 ANAFLEELRPGSLRECKEKEQCSFEAREIFKDAERTKLFWISY 104

Search completed: March 20, 2003, 14:14:46  
Job time : 146.812 secs



DR WPI; 1999-288309/24.  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 86.9%; Score 166; DB 20; Length 44;  
Best Local Similarity 97.7%; Pred. No. 5,2e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFLLXLRDGLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
Db 1 ANAFLLXLRDGLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
RESULT 2  
AA18310  
ID AA18310 standard; peptide; 44 AA.  
AC AA18310;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KM therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
XX  
PN WO9920767-A1.  
XX  
PD 29-APR-1999.  
XX  
PF 20-OCT-1998; 98WO-US22152.  
XX  
PR 23-OCT-1997; 97US-0955636.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Neiseetuen GL;  
XX  
DR WPI; 1999-288309/24.  
XX  
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX

CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 84.8%; Score 162; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 2,4e-19;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFLLXLRDGLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
Db 1 ANAFLLXLRDGLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
RESULT 3  
AA18305  
ID AA18305 standard; peptide; 44 AA.  
AC AA18305;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Human factor VII GLA domain.  
XX  
KW GLA domain; vitamin K-dependent protein; clotting disorder;  
KM therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
XX  
PN WO9920767-A1.  
XX  
PD 29-APR-1999.  
XX  
PF 20-OCT-1998; 98WO-US22152.  
XX  
PR 23-OCT-1997; 97US-0955636.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Neiseetuen GL;  
XX  
DR WPI; 1999-288309/24.  
XX  
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
PS Disclosure; Page 15; 86pp; English.  
XX  
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 83.2%; Score 159; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 7,4e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 ANAFLLXLRDGLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
Db 1 ANAFLLXLRDGLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44

```

RESULT 4
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
XX AAB36395;
AC
XX
XX 27-FEB-2001 (first entry)
DT
XX
XX Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
DE
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
XX Homo sapiens.
OS
XX
XX MO200066753-A2.
PN
XX
XX 09-NOV-2000.
PD
XX
XX 28-APR-2000; 2000WO-US11416.
PF
XX
XX 29-APR-1999; 99US-0302239.
PR
XX
XX (MINU ) UNIV MINNESOTA.
PA
XX
XX Nelsestuen GL;
PI
XX
XX MPI; 2001-007226/01.
DR
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
XX
XX Disclosure; Page 12; 81pp; English.
PS
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
XX
SQ Sequence 44 AA;

```

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Query Match 83.2%; Score 159; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 7,4e-19;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

OY 1 ANAFLLXLRDGLRCKXKXQCSFEXAEXIFKDXARTLFWISY 44
DB 1 ANAFLLXLRDGLRCKXKXQCSFEXAEXIFKDXARTLFWISY 44

```

```

RESULT 5
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
XX AAB84870;
AC
XX
XX 31-JUL-2001 (first entry)
DT
XX

```

```

DE Mutant blood coagulant factor VII (FVII-31).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 311..317
FT /note="Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
PD
XX
XX 24-AUG-1999; 99JP-0237610.
PF
XX
XX 24-AUG-1999; 99JP-0237610.
PR
XX
XX (KAGA ) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
PA
XX
XX MPI; 2001-310677/33.
DR
XX
XX N-PSDB; AAH19463.
DR
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
XX Claim 14; Page 20-21; 29pp; Japanese.
PS
XX
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX
SQ Sequence 401 AA;

```

```

Query Match 83.2%; Score 159; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 6.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

OY 1 ANAFLLXLRDGLRCKXKXQCSFEXAEXIFKDXARTLFWISY 44
DB 1 ANAFLELRGSLRECKEQCSFEAREIFKQARTLFWISY 44

```

```

RESULT 6
AAB84871
ID AAB84871 standard; Protein; 401 AA.
XX
XX AAB84871;
AC
XX
XX 31-JUL-2001 (first entry)
DT
XX
XX Mutant blood coagulant factor VII (FVII-39).
DE
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutein.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 235..239
FT /note="Wild-type Val-Pro-Gly-Thr-Thr substituted by
FT Asp-Arg-Lys-Thr-Leu"
FT Misc-difference 311..317
FT /note="Wild-type Leu-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX
XX JP2001061479-A.
XX

```

```
PD 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 83.2%; Score 159; DB 22; Length 401;
Best local similarity 72.7%; Pred. No. 6.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRLDGLXRXCKXQCSPFXAEXIFKDAARTKLFWISY 44
Db 1 ANAFLLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 7
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX
XX AAR35764;
XX
XX 24-SEP-1993 (first entry)
XX
XX Factor VII (VII).
XX
XX PC, protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX exosite; catalytic activity.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Region 1..152
XX Region /note= "Factor VII light chain"
XX Region 153..406
XX Peptide /note= "Factor VII heavy chain"
XX Peptide 374..388
XX Peptide /note= "exosite 1"
XX Peptide 290..310
XX Peptide /note= "exosite 2"
XX Peptide 290..310
XX Peptide /note= "pref. PC polypeptide; claim 2, page 136"
XX Peptide 374..388
XX Peptide /note= "pref. PC polypeptide; claim 2, page 136"
XX Peptide 289..304
XX Peptide /note= "pref. PC polypeptide; claim 4, page 137"
XX Peptide 290..304
XX Peptide /note= "pref. PC polypeptide; claim 4, page 137"
XX Peptide 245..266
XX /note= "claim 9, page 138-139 describes an antibody
XX that reacts with Factor VII; fragments
XX 289-304, 290-304, 290-310, 374-388 and
XX 400-414 but not with fragment 245-266"
XX
XX PN WO9309804-A.
```

```
PD 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US10242.
XX
XX 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Griffiin JH, Masters RM;
XX
XX WPI; 1993-182244/22.
XX
XX Serine protease derived polypeptide(s) and anti-peptide
XX antibodies - for inhibiting coagulation and assaying for the
XX presence of serine protease in fluid samples
XX
XX Disclosure; Page 133-135; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit
XX coagulation (they prevent binding of serine protease to natural
XX substrates), esp. when admin. to give an intravascular blood
XX concn. of 0.1-100 (pref. 0.5-10) microm.
XX NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
XX in the specification but have not yet been added to the SEQUENCE
XX LISTING.
XX
XX Sequence 406 AA;
SQ
Query Match 83.2%; Score 159; DB 14; Length 406;
Best local similarity 72.7%; Pred. No. 7e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXLRLDGLXRXCKXQCSPFXAEXIFKDAARTKLFWISY 44
Db 1 ANAFLLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
AAM14509
ID AAM14509 standard; protein; 406 AA.
XX
XX AAM14509;
XX
XX 14-MAY-1997 (first entry)
XX
XX Modified blood coagulation Factor VII (R290S).
XX
XX Blood coagulation; factor 7; mutacin; mutation; modification;
XX Chromocytopenia; von Willebrand's disease; plasma substitute.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 6
XX Modified-site /label= OTHER
XX Modified-site /note= "gamma-carboxyglutamic acid"
XX Modified-site 7
XX Modified-site /label= OTHER
XX Modified-site /note= "gamma-carboxyglutamic acid"
XX Modified-site 14
XX Modified-site /label= OTHER
XX Modified-site /note= "gamma-carboxyglutamic acid"
XX Modified-site 16
XX /note= "gamma-carboxyglutamic acid"
XX Modified-site 19
XX /label= OTHER
XX Modified-site /note= "gamma-carboxyglutamic acid"
XX Modified-site 20
XX /label= OTHER
XX /note= "gamma-carboxyglutamic acid"
XX
XX Disulfide-bond 17..22
```



|    |                          |  |  |
|----|--------------------------|--|--|
| FT | Modified-site            | 25   | /label= OTHER  |
| FT |                          | /note= "gamma-carboxylutamic acid"                 |  |
| FT | Modified-site            | 26   | /label= OTHER  |
| FT |                          | /note= "gamma-carboxylutamic acid"                 |  |
| FT | Modified-site            | 29   | /label= OTHER  |
| FT |                          | /note= "gamma-carboxylutamic acid"                 |  |
| FT | Cleavage-site            | 32..33   | /note= "proteolytic site"  |
| FT | Modified-site            | 35   | /label= OTHER  |
| FT |                          | /note= "gamma-carboxylutamic acid"                 |  |
| FT | Cleavage-site            | 38..39   | /note= "proteolytic site"  |
| FT |                          | /note= "proteolytic site"                          |  |
| FT | Cleavage-site            | 42..43   | /note= "proteolytic site"  |
| FT |                          | /note= "proteolytic site"                          |  |
| FT | Cleavage-site            | 44..45   | /note= "proteolytic site"  |
| FT |                          | /note= "proteolytic site"                          |  |
| FT | Disulfide-bond           | 50..61   |  |
| FT | Disulfide-bond           | 55..70   |  |
| FT | Modified-site            | 63   | /label= OTHER  |
| FT |                          | /note= "beta-hydroxy-aspartic acid"                |  |
| FT | Disulfide-bond           | 72..81   |  |
| FT | Disulfide-bond           | 91..102  |  |
| FT | Disulfide-bond           | 98..112  |  |
| FT | Disulfide-bond           | 114..127   |  |
| FT | Disulfide-bond           | 135..162   |  |
| FT | Cleavage-site            | 143..144   | /note= "proteolytic site"  |
| FT | Modified-site            | 145  | /note= "glycosylation site"  |
| FT |                          | /note= "glycosylation site"                        |  |
| FT | Disulfide-bond           | 159..164   |  |
| FT | Disulfide-bond           | 178..194   |  |
| FT | Active-site              | 193  |  |
| FT | Active-site              | 242  |  |
| FT | Active-site              | 344  |  |
| FT | Cleavage-site            | 290..291   |  |
| FT |                          | /note= "proteolytic site in unmodified factor VII" |  |
| FT | Misc-difference          | 290  | /note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond" |
| FT | Disulfide-bond           | 310..329   |  |
| FT | Cleavage-site            | 315..316   | /note= "proteolytic site"  |
| FT | Modified-site            | 322  | /note= "glycosylation site"  |
| FT |                          | /note= "glycosylation site"                        |  |
| FT | Disulfide-bond           | 340..368   |  |
| FT | Cleavage-site            | 341..342   | /note= "proteolytic site"  |
| FT |                          | /note= "proteolytic site"                          |  |
| FT | Cleavage-site            | 392..393   | /note= "proteolytic site"  |
| FT |                          | /note= "proteolytic site"                          |  |
| FT | Cleavage-site            | 396..397   | /note= "proteolytic site"  |
| FT |                          | /note= "proteolytic site"                          |  |
| FT | Cleavage-site            | 402..403   | /note= "proteolytic site"  |
| XX |                          |  |  |
| XX | US5580560-A.             |  |  |
| XX |                          |  |  |
| XX | 03-DEC-1996.             |  |  |
| XX |                          |  |  |
| XX | 13-NOV-1989;             | 89US-0434149.                                      |  |
| XX |                          |  |  |
| XX | 09-AUG-1993;             | 93US-0104509.                                      |  |
| PR | 13-NOV-1989;             | 89US-0434149.                                      |  |
| PR | 12-JUN-1992;             | 92US-0898248.                                      |  |
| PR | 22-AUG-1994;             | 94US-0293778.                                      |  |
| XX |                          |  |  |
| XX | (NOVO ) NOVO-NORDISK AS. |  |  |

|          |   |                                      |               |             |
|----------|---|--------------------------------------|---------------|-------------|
| PI       | Bjorn SE  | Nicolaissen EM,                      | Wiberg FC,    | Woodbury R; |
| DR       | WP1: 1997-033523/03.  |                                      |               |             |
| XX       |   |                                      |               |             |
| XX       | Mutated human factor VII or VIIa proteins - with amino acid         |                                      |               |             |
| PT       | substitutions to improve proteolytic stability                      |                                      |               |             |
| XX       |   |                                      |               |             |
| PS       | Example 3; Page -; 28pp; English.                                   |                                      |               |             |
| XX       |   |                                      |               |             |
| CC       | Modified human factor VII or VIIa proteins are stabilised against   |                                      |               |             |
| CC       | proteolytic cleavage by substitution of one of the residues Lys32,  |                                      |               |             |
| CC       | Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and     |                                      |               |             |
| CC       | Lys341 by an amino acid that provides a proteolytically more stable |                                      |               |             |
| CC       | peptide bond, provided that Lys32 is replaced by Gln, Glu, His,     |                                      |               |             |
| CC       | Gly, Thr, Ala or Ser. The modified proteins are useful for treating |                                      |               |             |
| CC       | bleeding disorders such as thrombocytopenia and von Willebrand's    |                                      |               |             |
| CC       | disease. They are also suitable for addition to plasma substitutes. |                                      |               |             |
| CC       | The present sequence is a specific example of a modified factor VII |                                      |               |             |
| CC       | protein.  |                                      |               |             |
| XX       |   |                                      |               |             |
| SQ       | Sequence  | 406 AA;                              |               |             |
|          | Query Match   | 83.2%; Score 159; DB 18; Length 406; |               |             |
|          | Best Local Similarity   | 72.7%; Pred. No. 7e-18;              |               |             |
|          | Matches   | 32; Conservative                     | 0; Mismatches | 12; Indels  |
|          |   |                                      | 0; Gaps       | 0;          |
| OY       | 1 ANAFLLXLRDGLKRXCKXKQCSFFXAEIPEKDAKRTLFWISY 44                     |                                      |               |             |
|          |   |                                      |               |             |
| DB       | 1 ANAFLEELRPGSLERECKEQCSFEAREIEFDKARTLFWISY 44                      |                                      |               |             |
|          |   |                                      |               |             |
|          |   |                                      |               |             |
| RESULT 9 |   |                                      |               |             |
| AAW14510 |   |                                      |               |             |
| ID       | AAW14510  | standard; protein; 406 AA.           |               |             |
| XX       |   |                                      |               |             |
| AC       | AAW14510;   |                                      |               |             |
| XX       |   |                                      |               |             |
| DT       | 14-MAY-1997   | (first entry)                        |               |             |
| XX       |   |                                      |               |             |
| DE       | Modified blood coagulation Factor VII (R315S).                      |                                      |               |             |
| XX       |   |                                      |               |             |
| KM       | Blood coagulation; factor 7; mutsin; mutation; modification;        |                                      |               |             |
| KW       | thrombocytopenia; von Willebrand's disease; plasma substitute.      |                                      |               |             |
| XX       |   |                                      |               |             |
| OS       | Homo sapiens.   |                                      |               |             |
| OS       | Synthetic.  |                                      |               |             |
| XX       |   |                                      |               |             |
| PH       | Key   | Location/Qualifiers                  |               |             |
| PH       | Modified-site   | 6                                    |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Modified-site   | 7                                    |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Modified-site   | 14                                   |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Modified-site   | 16                                   |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Modified-site   | 19                                   |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Modified-site   | 20                                   |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Disulfide-bond  | 17..22                               |               |             |
| FT       | Modified-site   | 25                                   |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |
| FT       | Modified-site   | 26                                   |               |             |
| FT       |   | /label= OTHER                        |               |             |
| FT       |   | /note= "gamma-carboxyglutamic acid"  |               |             |

```
FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33
FT /note= "proteolytic site"
FT Modified-site 35
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 38..39
FT /note= "proteolytic site"
FT Cleavage-site 42..43
FT /note= "proteolytic site"
FT Cleavage-site 44..45
FT /note= "proteolytic site"
FT Disulfide-bond 50..61
FT Disulfide-bond 55..70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72..81
FT Disulfide-bond 91..102
FT Disulfide-bond 98..112
FT Disulfide-bond 114..127
FT Disulfide-bond 135..162
FT Cleavage-site 143..144
FT /note= "proteolytic site"
FT Modified-site 145
FT /note= "glycosylation site"
FT Disulfide-bond 159..164
FT Disulfide-bond 178..194
FT Active-site 193
FT Active-site 242
FT Active-site 344
FT Cleavage-site 290..291
FT /note= "proteolytic site"
FT Disulfide-bond 310..329
FT Cleavage-site 315..316
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 315
FT /note= "native Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide
FT bond"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340..368
FT Cleavage-site 341..342
FT /note= "proteolytic site"
FT Cleavage-site 392..393
FT /note= "proteolytic site"
FT Cleavage-site 396..397
FT /note= "proteolytic site"
FT Cleavage-site 402..403
FT /note= "proteolytic site"
XX
XX US5580560-A.
XX
XX 03-DEC-1996.
XX
XX 13-NOV-1989; 89US-0434149.
XX
XX 09-AUG-1993; 93US-0104509.
XX 13-NOV-1989; 89US-0434149.
XX 12-JUN-1992; 92US-0898248.
XX 22-AUG-1994; 94US-0293778.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid
XX substitutions to improve proteolytic stability
PT
```

```
XX
XX Example 4; Page -, 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32,
XX Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
XX Lys341 by an amino acid that provides a proteolytically more stable
XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating
XX bleeding disorders such as thrombocytopenia and von Willebrand's
XX disease. They are also suitable for addition to plasma substitutes.
XX The present sequence is a specific example of a modified factor VII
XX protein.
XX
XX Sequence 406 AA;
XX
XX Query Match 83.2%; Score 159; DB 18; Length 406;
XX Best Local Similarity 72.7%; Pred. No. 7e-18;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 ANAFLXLRDGLRXCKXQCXFXAXEIPKAXRTYLFWISY 44
XX ||||| ||||| ||||| ||||| |||||
XX Db 1 ANAFLELRPGSLRECKEQCFEAREIRPKDAERTYLFWISY 44
XX
XX RESULT 10
XX AAU77745
XX ID AAU77745 standard; protein; 406 AA.
XX
XX AC AAU77745;
XX
XX DT 05-JUN-2002 (first entry)
XX
XX DE Human factor VIIa active site mutant.
XX
XX KW Factor VIIa; human; shock heat treatment; protein stability;
XX KW protein manufacture; protein conformation; mutant; muten.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Active-site 193
XX FT /note= "Member of the factor VIIa catalytic triad"
XX FT Active-site 242
XX FT /note= "Member of the factor VIIa catalytic triad"
XX FT Active-site 344
XX FT /note= "Member of the factor VIIa catalytic triad"
XX FT Misc-difference 344
XX FT /label= Gly, Met, Thr
XX FT /note= "Preferably Ala, wild type Ser"
XX
XX W020017741-A1.
XX
XX BD 18-OCT-2001.
XX
XX XX 06-APR-2001; 2001WO-DK00234.
XX
XX PF 06-APR-2000; 2000DK-0000573.
XX PR 17-APR-2000; 2000US-197650P.
XX
XX XX (NOVO ) NOVO NORDISK AS.
XX
XX PI Mathiesen F;
XX
XX DR WPI; 2001-657162/75.
XX
XX XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX PT involves a shock heat treatment -
XX XX Disclosure; Page -, 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
CC
```

CC shock heat treatment of the polypeptide. The method is useful in a  
 CC pharmaceutical composition, in the industrial or large scale method of  
 CC manufacturing a polypeptide, also as a unit operation during preparation,  
 CC purification, recovery and/or formulation of polypeptides. The shock heat  
 CC treatment improves the protein stability without substantial loss of  
 CC biological activity. The method can be applied to change polypeptide  
 CC conformation in a very fast and non-invasive manner. The polypeptide  
 CC formed is stable. The method is also useful for decreasing the  
 CC association of the polypeptide. This sequence represents a modified  
 CC human factor VIIa protein, mutated at the catalytic site, described  
 CC in the invention.  
 CC Note: This sequence does not appear in the specification but has  
 CC been obtained using information given in the invention.

CC Sequence 406 AA:

Query Match 83.2%; Score 159; DB 22; Length 406;  
 Best Local Similarity 72.7%; Pred. No. 7e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLRXKXKQCSFXXAEXIFKDXRRTKLFWISY 44  
 1 ANAFLELRPSGLRCKEPCQCFEAREIFKDXRRTKLFWISY 44

RESULT 11

AAM52171

ID AAM52171 standard; Protein; 406 AA.

XX AAM52171;

DT 07-FEB-2002 (first entry)

XX Human FVII SEQ ID NO 1.

XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
 KM cardant; hepatotrophic; cerebroprotective; haemophilia; liver disease;  
 KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.

XX Homo sapiens.

XX Location/Qualifiers

FT Key

FT Misc-difference 6

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 7

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 14

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 16

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 19

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 20

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 25

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 26

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 29

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Misc-difference 35

FT /label= GIU, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT Modified-site 52

FT /note= "OTHER = gamma carboxyglutamic acid"

FT /note= "O-glycosylated"

FT Modified-site 60

FT /note= "O-glycosylated"

FT Modified-site 145

FT /note= "N-glycosylated"

FT Cleavage-site 152..153

FT /note= "proteolytic cleavage site converting FVII zymogen

FT to an activated form, comprising two chains

FT linked by a single disulphide bridge"

FT Modified-site 322

FT /note= "N-glycosylated"

PN WO200158935-A2.

XX 16-AUG-2001.

XX 12-FEB-2001; 2001WO-DK00094.

XX 11-FEB-2000; 2000DK-0000218.

XX 18-OCT-2000; 2000DK-0001558.

XX (MAXY-) MAXYGEN APS.

XX Andersen KV, Pedersen AH, Bornas C;

XX WPI; 2001-581807/65.

XX N-PADB; AAI99982.

XX New conjugate, useful for treating Factor VIIa related diseases or

XX disorders such as haemophilia, liver disease, myocardial infarction and

XX deep-vein thrombosis, comprises non-polypeptide group covalently

XX attached to polypeptide group -

XX Claim 1; Page 81-83; 89pp; English.

XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)

XX polypeptide conjugates, comprising at least one non-polypeptide group

XX covalently attached to a polypeptide, where the amino acid sequence of

XX polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at

XX least one amino acid residue containing an attachment group for the

XX non-polypeptide group has been introduced or removed. The FVIIa

XX conjugates have haemostatic, thrombolytic, cardant, hepatotrophic and

XX cerebroprotective activity and are useful for treating FVIIa/TF-related

XX diseases or disorders such as haemophilia, liver disease, myocardial

XX infarction, thrombotic stroke and deep-vein thrombosis. The conjugates

XX have increased functional in vivo half life and/or increased plasma half

XX life, increased bioavailability and or reduced sensitivity to proteolytic

XX degradation. Consequently medical treatment using the conjugates has a

XX number of advantages over currently available such as longer duration

XX between injections.

XX Sequence 406 AA:

QY 1 ANAFLLXLRDGLRXKXKQCSFXXAEXIFKDXRRTKLFWISY 44

1 ANAFLELRPSGLRCKEPCQCFEAREIFKDXRRTKLFWISY 44

RESULT 12

AAM52172

ID AAM52172 standard; Protein; 406 AA.

XX AAM52172;

DT 07-FEB-2002 (first entry)

XX Mammalian expressed human FVII SEQ ID NO 3.

XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;

XX

KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;  
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Modified-site 52 /note= "O-glycosylated"  
 FT Modified-site 60 /note= "O-glycosylated"  
 FT Modified-site 145 /note= "N-glycosylated"  
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"  
 FT Modified-site 322 /note= "N-glycosylated"  
 FT W0200158935-A2.  
 XX 16-AUG-2001.  
 PD 12-FEB-2001; 2001WO-DK0094.  
 XX 11-FEB-2000; 2000DK-0000218.  
 PR 18-OCT-2000; 2000DK-0001558.  
 XX (MAXY-) MAXYGEN APS.  
 PA Andersen KV, Pedersen AH, Bornaes C;  
 XX WPI; 2001-581807/65.  
 DR N-PSDB; AA199983.  
 XX New conjugate, useful for treating Factor VIIa related diseases or  
 PT disorders such as haemophilia, liver disease, myocardial infarction and  
 PT deep-vein thrombosis, comprises non-polypeptide group covalently  
 PT attached to polypeptide group -  
 XX  
 PS Disclosure; Page 85-86; 89pp; English.  
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
 CC polypeptide conjugates, comprising at least one non-polypeptide group  
 CC covalently attached to a polypeptide, where the amino acid sequence of  
 CC polypeptide differs from that of the wildtype FVIIa (AAM52181) in that at  
 CC least one amino acid residue containing an attachment group for the  
 CC non-polypeptide group has been introduced or removed. The FVIIa  
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and  
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
 CC diseases or disorders such as haemophilia, liver disease, myocardial  
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
 CC have increased functional in vivo half life and/or increased plasma half  
 CC life, increased bioavailability and or reduced sensitivity to proteolytic  
 CC degradation. Consequently medical treatment using the conjugates has a  
 CC number of advantages over currently available such as longer duration  
 CC between injections.  
 CC  
 SQ Sequence 406 AA;  
 Query Match 83.2%; Score 159; DB 22; Length 406;  
 Best Local Similarity 72.7%; Pred. No. 7e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ANAFPLXLRDGLRXCKXGSEFXAXEIPDARRTLFWISY 44  
 DB 1 ANAFLEELRPSGLERECKEBCSEFARERIFDARERTLFWISY 44  
 RESULT 13  
 ID AAM52181  
 XX AAM52181 standard; Protein, 406 AA.

AC AAM52181;  
 XX 07-FEB-2002 (first entry)  
 DT Human FVII mutant T106N.  
 XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
 KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;  
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;  
 XX mutein.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 6 /label= GIU, OTHER  
 FT Modified-site 7 /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 14 /label= GIU, OTHER  
 FT Modified-site 16 /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 19 /label= GIU, OTHER  
 FT Modified-site 20 /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 25 /label= GIU, OTHER  
 FT Modified-site 26 /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 29 /label= GIU, OTHER  
 FT Modified-site 35 /label= GIU, OTHER  
 FT Modified-site 52 /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 60 /note= "O-glycosylated"  
 FT Modified-site 106 /note= "O-glycosylated"  
 FT Modified-site 145 /note= "O-glycosylated"  
 FT Modified-site 152..153 /note= "O-glycosylated"  
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"  
 FT Modified-site 322 /note= "N-glycosylated"  
 FT W0200158935-A2.  
 XX 16-AUG-2001.  
 PD 12-FEB-2001; 2001WO-DK0094.  
 XX 11-FEB-2000; 2000DK-0000218.  
 PR 18-OCT-2000; 2000DK-0001558.  
 XX (MAXY-) MAXYGEN APS.  
 PA Andersen KV, Pedersen AH, Bornaes C;  
 XX WPI; 2001-581807/65.  
 DR N-PSDB; AA199983.  
 XX New conjugate, useful for treating Factor VIIa related diseases or  
 PT disorders such as haemophilia, liver disease, myocardial infarction and  
 PT deep-vein thrombosis, comprises non-polypeptide group covalently  
 PT attached to polypeptide group -  
 XX  
 PS Disclosure; Page 85-86; 89pp; English.  
 CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
 CC polypeptide conjugates, comprising at least one non-polypeptide group  
 CC covalently attached to a polypeptide, where the amino acid sequence of  
 CC polypeptide differs from that of the wildtype FVIIa (AAM52181) in that at  
 CC least one amino acid residue containing an attachment group for the  
 CC non-polypeptide group has been introduced or removed. The FVIIa  
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and  
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
 CC diseases or disorders such as haemophilia, liver disease, myocardial  
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
 CC have increased functional in vivo half life and/or increased plasma half  
 CC life, increased bioavailability and or reduced sensitivity to proteolytic  
 CC degradation. Consequently medical treatment using the conjugates has a  
 CC number of advantages over currently available such as longer duration  
 CC between injections.  
 CC  
 SQ Sequence 406 AA;  
 Query Match 83.2%; Score 159; DB 22; Length 406;  
 Best Local Similarity 72.7%; Pred. No. 7e-18;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ANAFPLXLRDGLRXCKXGSEFXAXEIPDARRTLFWISY 44  
 DB 1 ANAFLEELRPSGLERECKEBCSEFARERIFDARERTLFWISY 44  
 RESULT 13  
 ID AAM52181  
 XX AAM52181 standard; Protein, 406 AA.

DR WPI; 2001-581807/65.

XX New conjugate, useful for treating Factor VIIa related diseases or

PT disorders such as haemophilia, liver disease, myocardial infarction and

PT deep-vein thrombosis, comprises non-polypeptide group covalently

PT attached to polypeptide group -

XX Example 3; Page -: 89pp; English.

PS

XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)

CC polypeptide conjugates, comprising at least one non-polypeptide group

CC covalently attached to a polypeptide, where the amino acid sequence of

CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at

CC least one amino acid residue containing an attachment group for the

CC non-polypeptide group has been introduced or removed. The FVIIa

CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and

CC cerebroprotective activity and are useful for treating FVIIa/TF-related

CC diseases or disorders such as haemophilia, liver disease, myocardial

CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates

CC have increased functional in vivo half life and/or increased plasma half

CC life, increased bioavailability and or reduced sensitivity to proteolytic

CC degradation. Consequently medical treatment using the conjugates has a

CC number of advantages over currently available such as longer duration

CC between injections. The present sequence is that of a human FVII mutant,

CC having an addition in vivo glycosylation site and tested for its

CC amidolytic activity.

CC Note: The present sequence is not shown in the specification but is

CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1

CC (AAM52171).

CC

XX Sequence 406 AA;

SO

Query Match 83.2%; Score 159; DB 22; Length 406;

Best Local Similarity 95.5%; Pred. No. 7e-18;

Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLRCKXXQCSFXXAEXIFKDXRTRKLFMISY 44

Db 1 ANAFLLXLRDGLRCKXXQCSFXXAEXIFKDXRTRKLFMISY 44

RESULT 14

AAM52182

ID AAM52182 standard; Protein; 406 AA.

XX

AC AAM52182;

XX

DT 07-FEB-2002 (first entry)

XX

DE Human FVII mutant K143N/N145T.

XX

XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;

KM cardiant; hepatotrophic; cerebroprotective; haemophilia, liver disease;

KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;

KM mutain.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

XX Location/Qualifiers

FH Key

FT Misc-difference 6

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 7

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 14

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 16

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 19

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 20

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 25

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 26

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 29

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Misc-difference 35

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Modified-site 52

FT /note= "OTHER = gamma carboxyglutamic acid"

FT

FT Modified-site 60

FT /note= "O-glycosylated"

FT

FT Modified-site 143

FT /note= "O-glycosylated"

FT

FT Misc-difference 145

FT /note= "Wild-type Lys substituted by Asn"

FT

FT Misc-difference 152..153

FT /note= "Wild-type Asn substituted by Thr"

FT

FT Cleavage-site 322

FT /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"

FT

FT Modified-site 322

FT /note= "N-glycosylated"

FT

XX W0200158935-A2.

XX

XX 16-AUG-2001.

XX

XX 12-FEB-2001; 2001WO-DK00094.

XX

XX 11-FEB-2000; 2000DK-0000218.

PR 18-OCT-2000; 2000DK-0001558.

XX

XX (MAXY-) MAXYGEN APS.

XX

XX Andersen KV, Pedersen AH, Bornaes C;

PI

XX WPI; 2001-581807/65.

DR

XX

XX New conjugate, useful for treating Factor VIIa related diseases or

PT disorders such as haemophilia, liver disease, myocardial infarction and

PT deep-vein thrombosis, comprises non-polypeptide group covalently

PT attached to polypeptide group -

XX

XX Example 3; Page -: 89pp; English.

PS

XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)

CC polypeptide conjugates, comprising at least one non-polypeptide group

CC covalently attached to a polypeptide, where the amino acid sequence of

CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at

CC least one amino acid residue containing an attachment group for the

CC non-polypeptide group has been introduced or removed. The FVIIa

CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and

CC cerebroprotective activity and are useful for treating FVIIa/TF-related

CC diseases or disorders such as haemophilia, liver disease, myocardial

CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates

CC have increased functional in vivo half life and/or increased plasma half

CC life, increased bioavailability and or reduced sensitivity to proteolytic

CC degradation. Consequently medical treatment using the conjugates has a

CC number of advantages over currently available such as longer duration

CC between injections. The present sequence is that of a human FVII mutant,

CC having an addition in vivo glycosylation site and tested for its

CC amidolytic activity.

CC Note: The present sequence is not shown in the specification but is

CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1

```

CC      (AAM52171) .
XX
SQ      Sequence      406 AA;

Query Match      83.2%; Score 159; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 7e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ANAFLXLRDGLRXCCKXCSPFXAEXIFKDAKRTKLFWISY 44
        |||
        1 ANAFLXLRPGSLRXCCKXCSPFXARXIFKDAKRTKLFWISY 44

Db
RESULT 15
AAM52183
ID      AAM52183 standard; Protein; 406 AA.
XX
AC      AAM52183;
XX
DT      07-FEB-2002 (first entry)
XX
DE      Human FVII mutant V253N.
XX
KM      Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
KM      cardiant; hepatocrophic; cerebroprotective; haemophilia; liver disease;
KM      myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KM      mutern.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FH      Misc-difference 6 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      7
FT      Misc-difference 7 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      14
FT      Misc-difference 14 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      16
FT      Misc-difference 16 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      19
FT      Misc-difference 19 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      20
FT      Misc-difference 20 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      25
FT      Misc-difference 25 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      26
FT      Misc-difference 26 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      29
FT      Misc-difference 29 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      35
FT      Misc-difference 35 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      52
FT      Modified-site 52 /note= "OTHER = gamma carboxyglutamic acid"
FT      60
FT      Modified-site 60 /note= "O-glycosylated"
FT      145
FT      Modified-site 145 /note= "O-glycosylated"
FT      152..153
FT      Cleavage-site 152..153 /note= "N-glycosylated"
FT      253
FT      Misc-difference 253 /note= "proteolytic cleavage site converting FVII zymogen
        to an activated form, comprising two chains
        linked by a single disulphide bridge"

```

```

FT      FT      Modified-site 322 /note= "wild-type Val substituted by Asn"
FT      /note= "N-glycosylated"
XX
XX      WO200158935-A2.
XX
XX      16-AUG-2001.
XX
XX      12-FEB-2001; 2001WO-DK00094.
XX
XX      11-FEB-2000; 2000DK-0000218.
XX      18-OCT-2000; 2000DK-0001558.
XX
XX      (MAXY-) MAXYGEN APPS.
XX
XX      Andersen KV, Pedersen AH, Bornaes C;
XX      WPI; 2001-581807/65.
XX
XX      New conjugate, useful for treating Factor VIIa related diseases or
XX      disorders such as haemophilia, liver disease, myocardial infarction and
XX      deep-vein thrombosis, comprises non-polypeptide group covalently
XX      attached to polypeptide group -
XX
XX      Example 3; Page -; 89pp; English.
XX
XX      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX      polypeptide conjugates, comprising at least one non-polypeptide group
XX      covalently attached to a polypeptide, where the amino acid sequence of
XX      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
XX      least one amino acid residue containing an attachment group for the
XX      non-polypeptide group has been introduced or removed. The FVIIa
XX      conjugates have haemostatic, thrombolytic, cardiant, hepatocrophic and
XX      cerebroprotective activity and are useful for treating FVIIa/TF-related
XX      diseases or disorders such as haemophilia, liver disease, myocardial
XX      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX      have increased functional in vivo half life and/or increased plasma half
XX      life, increased bioavailability and/or reduced sensitivity to proteolytic
XX      degradation. Consequently medical treatment using the conjugates has a
XX      number of advantages over currently available such as longer duration
XX      between injections. The present sequence is that of a human FVII mutant,
XX      having an addition in vivo glycosylation site and tested for its
XX      amidolytic activity.
XX
XX      Note: The present sequence is not shown in the specification but is
XX      derived from the human wild-type FVII sequence shown in SEQ ID NO 1
XX      (AAM52171).
XX
SQ      Sequence      406 AA;

Query Match      83.2%; Score 159; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 7e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ANAFLXLRDGLRXCCKXCSPFXAEXIFKDAKRTKLFWISY 44
        |||
        1 ANAFLXLRPGSLRXCCKXCSPFXARXIFKDAKRTKLFWISY 44

Db

```

Search completed: March 19, 2003, 14:51:08  
 Job time : 32.4375 secs

GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10ASP28GLU

Perfect score: 191  
Sequence: 1 ANAFLXLRDGLXLRXCXX.....XXAEXIFKAXRKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 159   | 83.2        | 466    | 1 KFHU7  | coagulation factor  |
| 2          | 125   | 65.4        | 443    | 2 I46932 | coagulation factor  |
| 3          | 115   | 60.2        | 407    | 1 KFB07  | coagulation factor  |
| 4          | 102   | 53.4        | 461    | 1 JX0210 | protein C (activat  |
| 5          | 100   | 52.4        | 461    | 1 S18994 | protein C (activat  |
| 6          | 97    | 50.8        | 488    | 1 EXHU   | coagulation factor  |
| 7          | 97    | 50.8        | 492    | 1 EXBO   | coagulation factor  |
| 8          | 91    | 47.6        | 456    | 1 KXBO   | protein C (activat  |
| 9          | 91    | 47.6        | 482    | 1 EXRT   | coagulation factor  |
| 10         | 87    | 45.5        | 475    | 1 EXCH   | coagulation factor  |
| 11         | 84    | 44.0        | 461    | 1 KXHU   | protein C (activat  |
| 12         | 83    | 43.5        | 462    | 1 TBHU   | thrombin (EC 3.4.2  |
| 13         | 81    | 42.4        | 416    | 1 KFB0   | coagulation factor  |
| 14         | 79    | 41.4        | 617    | 2 S10511 | thrombin (EC 3.4.2  |
| 15         | 79    | 41.4        | 618    | 2 A35827 | thrombin (EC 3.4.2  |
| 16         | 78    | 40.8        | 461    | 1 KFHU   | coagulation factor  |
| 17         | 73    | 38.2        | 452    | 1 A30351 | coagulation factor  |
| 18         | 73    | 38.2        | 459    | 2 J00419 | coagulation factor  |
| 19         | 63    | 34.0        | 642    | 2 S53433 | plasma protein S p  |
| 20         | 63    | 33.0        | 642    | 2 TBBO   | thrombin (EC 3.4.2  |
| 21         | 61    | 31.9        | 396    | 1 KXBO2  | plasma protein Z -  |
| 22         | 61    | 31.9        | 675    | 1 KXBO5  | plasma protein Z p  |
| 23         | 60    | 31.4        | 642    | 2 S53434 | plasma protein S p  |
| 24         | 60    | 31.4        | 676    | 1 KKHUS  | plasma protein S p  |
| 25         | 59    | 30.9        | 646    | 2 S38819 | plasma protein S -  |
| 26         | 58.5  | 30.6        | 676    | 2 G96763 | probable MAP kinase |
| 27         | 58    | 30.4        | 675    | 1 KXRTS  | plasma protein S p  |
| 28         | 56    | 29.3        | 422    | 1 KKHUZ  | plasma protein Z p  |
| 29         | 52.5  | 27.5        | 594    | 2 D84859 | probable MAP kinase |

#### ALIGNMENTS

RESULT 1  
KFH07  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text\_change 08-Dec-2000  
C:Accession: A28322; A23819; A31186; B31186; S63524  
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insoley, M.Y.; Hagen, F.S.; Murrie  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent  
A:Reference number: A28322; PMID:87260948; PMID:3037537  
A:Accession: A28322  
A:Molecule type: DNA  
A:Residues: 1-466 <OH>  
A:Cross-references: GB:U02933; NID:g180333; PIN:AAA51983.1; PID:g180334  
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A:Title: Characterization of a cDNA coding for human factor VII.  
A:Reference number: A23819; PMID:86205965; PMID:3486420  
A:Accession: A23819  
A:Molecule type: mRNA  
A:Residues: 1-466 <HAG>  
A:Cross-references: GB:M1332; NID:g182799; PIDN:AAA86040.1; PID:g182801  
R:Thim, L.; Björn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.;  
Biochemistry 27, 7705-7793, 1988  
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a fr  
A:Reference number: A90539; PMID:89088153; PMID:3264725  
A:Accession: A31186  
A:Molecule type: Protein  
A:Residues: 61-212 <THI>  
A:Accession: B31186  
A:Molecule type: Protein  
A:Residues: 213-466 <TH>  
R:Björn, S.; Foster, D.C.; Thim, L.; Wibeberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen  
J. Biol. Chem. 266, 11051-11057, 1991  
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at  
Eur. J. Biochem. 234, 293-300, 1995  
A:Contents: annotation; carbohydrate binding sites  
R:Persson, E.; Petersen, L.C.  
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy  
A:Reference number: S63524; PMID:86096752; PMID:8596655  
A:Accession: S63524  
A:Molecule type: Protein  
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>  
C:Genetics:  
A:Gene: GDB:F7  
A:Cross-references: GDB:119897; OMIM:227500  
A:Map position: 13q34-13q34  
A:Intons: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser  
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-60/Domain: propeptide #status predicted <PRO>  
F:45-104/Domain: Gla domain homology <GLA>  
F:61-213/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F:110-141/Domain: EGF homology <EG1>  
F:151-187/Domain: EGF homology <EG2>  
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:213-447/Domain: trypsin homology <TRY>  
F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,  
F:112,120/Binding site: carboxylate (Ser) (covalent) #status experimental  
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
F:205,382/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:212-213/Cleavage site: Arg-Ile (coagulation factor Xla) #status experimental  
F:253,302,404/Active site: His, Asp, Ser #status predicted  
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 83.2%; Score 159; DB 1; Length 466;  
Best Local Similarity 72.7%; Pred. No. 1.3e-19;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFIXLRDGLKXCKXQCSFYXAEKIFDAXRTKLFWISY 44  
Db 61 ANAFLEELRPGSLRECKEELCSFEAREIFPDARTKLFWISY 104

RESULT 2  
coagulation factor VII - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
C:Accession: I46932  
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
A:Reference number: I46932; MUID:93190306; PMID:8383365  
A:Accession: I46932  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-443 <BRO>  
A:Cross-references: GB:S56300; NID:g266294; PID:g266295  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
F:24-83/Domain: Gla domain homology <GLA>  
F:89-120/Domain: EGF homology <EG1>  
F:130-166/Domain: EGF homology <EG2>  
F:192-425/Domain: trypsin homology <TRY>

Query Match 65.4%; Score 125; DB 2; Length 443;  
Best Local Similarity 54.5%; Pred. No. 1.1e-13;  
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANAFIXLRDGLKXCKXQCSFYXAEKIFDAXRTKLFWISY 44  
Db 40 ANSFLEELRPGSLRECKEELCSFEAREVFPSTERTKQFWISY 83

RESULT 3  
coagulation factor VIIa (EC 3.4.21.21) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
C:Accession: A31979; C20274  
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
J. Biol. Chem. 263, 14868-14877, 1988  
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.  
A:Reference number: A31979; MUID:89008362; PMID:3049594  
A:Accession: A31979  
A:Molecule type: protein  
A:Residues: 1-407 <TKA>  
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Accession: C20274  
A:Molecule type: protein  
A:Residues: 58-62, 'X', 64-68 <MCM>  
A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid  
R:Haee, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.  
J. Biochem. 104, 867-868, 1988  
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX  
A:Reference number: A44556; MUID:89213999; PMID:33149637  
A:Contents: annotation  
A>Note: structure and location of covalently bound carboxylate  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor  
A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid  
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F:1-44/Domain: Gla domain homology (fragment) <GLA>  
F:50-81/Domain: EGF homology <EG1>  
F:91-127/Domain: EGF homology <EG2>  
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:153-387/Domain: trypsin homology <TRY>  
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/1  
F:52/Binding site: carboxylate (Ser) (covalent) #status experimental  
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental  
F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:152-153/Cleavage site: Arg-Ile (coagulation factor Xla) #status experimental  
F:193,242,344/Active site: His, Asp, Ser #status predicted  
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 60.2%; Score 115; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 5.4e-12;  
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy 1 ANAFIXLRDGLKXCKXQCSFYXAEKIFDAXRTKLFWISY 44  
Db 1 ANGFLEELRPGSLRECKEELCSFEAREIFRNERBTQFWISY 44

RESULT 4  
JX0210  
protein C (activated) (EC 3.4.21.69) precursor - mouse  
N:Alternate names: vitamin K-dependent serine proteinase  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: JX0210  
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
J. Biochem. 111, 491-495, 1992  
A:Title: Isolation and characterization of a mouse protein C cDNA.  
A:Reference number: JX0210; MUID:92316897; PMID:1618739  
A:Accession: JX0210  
A:Molecule type: mRNA  
A:Residues: 1-461 <TRD>  
A:Cross-references: GB:D10445; NID:g220385; PID:BAA01235.1; PID:g220386  
A:Experimental source: liver  
A:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that regulates blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:27-85/Domain: Gla domain homology <GLA>  
F:34-41/Domain: propeptide #status predicted <PRO>  
F:42-196,199-461/Product: protein C #status predicted <PRC>  
F:42-196/Domain: light chain #status predicted <PCr>  
F:91-130/Domain: EGF homology <EG1>  
F:139-174/Domain: EGF homology <EG2>  
F:199-461/Domain: heavy chain #status predicted <PCH>  
F:199-211/Domain: activation peptide #status predicted <ACT>  
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>



F:212-445/Domain: trypsin homology <TRY>  
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
 F:214,290,355/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 53.4%; Score 102; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 1.1e-09;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLXRXCKXQCSFYXAEKIFKDAARTKLFWISY 44  
 42 ANSFLEVRGSLERECMERICDFEEAOEIFQWVEDTLAWIKY 85

## RESULT 5

S18994  
 protein C (activated) (EC 3.4.21.69) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
 C:Accession: S18994; S24312  
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
 A:Description: The cDNA cloning and mRNA expression of rat protein C.  
 A:Reference number: S18994

A:Accession: S18994

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <OKA>

C:Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963

R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.

Biochim. Biophys. Acta 1131, 329-332, 1992

A:Title: The cDNA cloning and mRNA expression of rat protein C.

A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <OKA>

C:Cross-references: EMBL:X64336; NID:G56962; PIDN:CAA45617.1; PID:G56963

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase

F:1-33/Domain: signal sequence #status predicted <SIG>

F:27-85/Domain: Gla domain homology <Gla>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-61/Domain: EGF homology <EGF>

F:91-130/Domain: EGF homology <EGF>

F:139-174/Domain: EGF homology <EG2>

F:213-445/Domain: trypsin homology <TRY>

F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:121-130,139-150,146-159,161-174,182-319,238-255,373-387,398-426/Disulfide bonds: #stat

F:215,291,355/Binding site: carbohydrate (asn) (covalent) #status predicted

F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 52.4%; Score 100; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 2.5e-09;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLXRXCKXQCSFYXAEKIFKDAARTKLFWISY 44  
 42 ANSFLEVRGSLERECMERICDFEEAOEIFQWVEDTLAWIKY 85

RESULT 6  
 EXHU  
 coagulation factor Xa (BC 3.4.21.6) precursor [validated] - human  
 N:Alternate names: Stuart factor

C:Species: Homo sapiens (man)  
 C:Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
 C:Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00  
 R:leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
 Biochemistry 25, 5098-5102, 1986

A:Title: Gene for human Factor X, a blood coagulation factor whose gene organization is e

A:Reference number: A24478; MUID:87026600; PMID:3768336

A:Accession: A24478

A:Molecule type: DNA

A:Residues: 1-488 <LEV>

A:Cross-references: GB:L29433; GB:M4327; NID:G459809; PIDN:AAA52764.1; PID:G182831

R:Wessler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.O.; Church, W.R.

Gene 99, 291-294, 1991

A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag

A:Reference number: J00917; MUID:91216473; PMID:1902434

A:Accession: J00917

A:Molecule type: mRNA

A:Residues: 1-488 <MES>

A:Cross-references: GB:M57285; NID:G182389; PIDN:AAA52421.1; PID:G182390

R:Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A:Title: Liver-specific expression of the gene coding for human factor X, a blood coagul

A:Reference number: A42485; MUID:92218390; PMID:1313796

A:Accession: A42485

A:Molecule type: DNA

A:Residues: 1-15 <MTA>

A:Experimental source: Liver

A:Note: Sequence extracted from NCBI backbone (NCBIN:93780, NCBIPI:93787)

R:Kau, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A:Reference number: A25853; MUID:86221713; PMID:3011603

A:Accession: A25853

A:Molecule type: mRNA

A:Residues: 19-284, 'E', 289-488 <RAU>

A:Cross-references: GB:M2613; NID:G180335; PIDN:AAA51984.1; PID:G180336

R:Rung, M.R.; Hay, C.W.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulat

A:Reference number: A22208; MUID:85216545; PMID:2582420

A:Accession: A22208

A:Molecule type: mRNA

A:Residues: 13-441, 'S', 443-488 <FUN>

A:Cross-references: GB:K0194; NID:G182840; PIDN:AAA52490.1; PID:G182841

R:leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A:Title: Characterization of a cDNA coding for human factor X.

A:Reference number: A21284; MUID:84222026; PMID:6587384

A:Accession: A21284

A:Molecule type: mRNA

A:Residues: 13-284, 'E', 289-488 <LE2>

A:Cross-references: GB:K01886

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howard, W.N.; Kwa, E.Y.; Weinst

Biochemistry 22, 2875-2884, 1983

A:Title: Complete amino acid sequence of the light chain of human blood coagulation fact

A:Reference number: A20362; MUID:83257207; PMID:6671167

A:Accession: A20362

A:Molecule type: protein

A:Residues: 41-179 <MCW>

R:inoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A:Reference number: S39414; MUID:94062825; PMID:8243461

A:Accession: S39415

A:Molecule type: protein

A:Residues: 183-234 <INO>

A:Note: glycosylation sites

A:Note: Identification and characterization of beta-hydroxyaspartic acid

R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.U.; Hamsabhushanam, K.; Lyman, G.

Gene 84, 517-519, 1989

A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human f

A:Reference number: I54051; MUID:90128299; PMID:2612918

A:Accession: I54051

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-23 <RSS>

A:Cross-references: GB:M32297; NID:G183860; PIDN:AAA52636.1; PID:G553330

R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blar

J. Mol. Biol. 232, 947-966, 1993  
 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A49458; MUID:93360277; PMID:8355279  
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 C:Genetics:  
 A:Gene: GDB:F10  
 A:Cross-references: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Interons: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A:Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-234/Domain: activation peptide #status experimental <APT>  
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:235-462/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
 F:57-62/Disulfide bonds: #status predicted  
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/  
 F:193/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:224-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 50.8%; Score 97; DB 1; Length 488;  
 Best Local Similarity 38.6%; Pred. No. 8.8e-09;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLDGSLRXKXKXOCSEFXAXEIPDAXRTKLFWSY 44  
 Db 41 ANSFLEEMKKGHLREKMEFTCSYEAREVFEDSDKTFPMNKY 84

RESULT 7  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Rung, M.R.; Campbell, R.M.; Macgillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; MUID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FUN>  
 A:Cross-references: GB:X00673; NID:g192; PID:CAA25286.1; PID:g193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Tiltani, K.  
 Biochemistry 19, 659-667, 1980  
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, 'N', 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:8330813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Tiltani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:7605069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <T>  
 A:Note: carboxylate binding sites and disulfide bonds were determined  
 R:Peterson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Ohlin, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; MUID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A:Note: beta-hydroxyaspartic acid site  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196, 199-209, 216-233 <INO>  
 A:Note: carboxylate binding sites  
 R:Tiltani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; De  
 Biochemistry 11, 4899-4903, 1972  
 A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
 A:Reference number: A12453; MUID:73053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Tiltani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to f  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic  
 A:Reference number: A38024; MUID:84185716; PMID:6546920  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of two  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), or  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with str  
 C:Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin  
 C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:41-160/Product: coagulation factor X heavy chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-482/Product: coagulation factor X heavy chain #status experimental <APT>  
 F:183-233/Domain: activation peptide #status experimental <ACT>  
 F:234-482/Product: coagulation factor Xa heavy chain #status experimental <HCH>  
 F:234-461/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #st  
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status pr  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat

F:240-245,260-276,389-403,414-442/Dileufide bonds: #status experimental  
F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 50.8%; Score 97; DB 1; Length 492;

Best Local Similarity 40.9%; Pred. No. 8.8e-09; Mismatches 19; Indels 0; Gaps 0;

Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLRCKXXQCSFXXAEXIFKDXARTKLFMISY 44

DB 41 ANSLFEEVKQGNLERECLEACSLSEARVFDHAEQTDFFMSKY 84

#### RESULT 8

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N/Alternate names: autoprothrombin IIA; plasma protein C

C/Species: Bos primigenius taurus (cattle)

C/Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999

C/Accession: A26250; A18385; A18386; A00928

R/Long: G.L.; Balagaje, R.M.; Macgillivray, R.T.A.

A/Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A/Reference number: A26250; PMID:85014826; PMID:6091100

A/Accession: A26250

A/Molecule type: mRNA

A/Residues: 1-456 <LON>

R/Fernlund, P.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982

A/Title: Amino acid sequence of the light chain of bovine protein C.

A/Reference number: A18385; PMID:83007325; PMID:6896876

A/Accession: A18385

A/Molecule type: protein

A/Residues: 40-194 <PER>

A/Note: 82-Lys was also found

R/Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983

A/Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.

A/Reference number: A19316; PMID:83169769; PMID:6572939

A/Accession: A19316

A/Content: annotation; revision to residue 110

R/Stenflo, J.; Fernlund, P.

J. Biol. Chem. 257, 12180-12190, 1982

A/Title: Amino acid sequence of the heavy chain of bovine protein C.

A/Reference number: A18386; PMID:83007326; PMID:6896877

A/Accession: A18386

A/Molecule type: protein

A/Residues: 197-454; 'PV' <STE>

R/Esmon, N.L.; DeBault, L.E.; Esmon, C.T.

J. Biol. Chem. 258, 5548-5553, 1983

A/Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F

A/Reference number: A37541; PMID:83213513; PMID:6304092

F:211-440/Domain: trypsin homology <TRY>

F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #statu

F:136,289,350/Binding site: carbonyl (Asn) (covalent) #status predicted

F:252,298,397/Active site: His, Asp, Ser #status predicted

F:366/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 47.6%; Score 91; DB 1; Length 456;

Best Local Similarity 40.9%; Pred. No. 9.1e-08; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLRCKXXQCSFXXAEXIFKDXARTKLFMISY 44

DB 40 ANSLFEEVKQGNLERECLEACSLSEARVFDHAEQTDFFMSKY 83

#### RESULT 9

coagulation factor Xa (EC 3.4.21.6) precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000

C/Accession: S49075; JC4670; PS0191; PS0190; 162745

R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.

Thromb. Res. 80, 63-73, 1995

A/Title: Evidence for competition between vitamin K-dependent clotting factors for intrac

A/Reference number: A58498; PMID:96093366; PMID:8578539

A/Accession: S49075

A/Molecule type: mRNA

A/Residues: 1-482 <STA1>

A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601

A/Note: submitted to the EMBL Data Library, June 1994

R/Scanton, C.; Ross, P.; Hutson, S.; Wallin, R.

Gene 169, 269-273, 1996

A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.

A/Reference number: JC4670; PMID:96194815; PMID:8647460

A/Accession: JC4670

A/Molecule type: mRNA

A/Residues: 1-482 <STA2>

A/Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601

A/Experimental source: Cos-1 cell

R/Enjyoji, K.; Miyazaki, K.; Kato, H.

J. Biochem. 109, 890-898, 1991

A/Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas

A/Reference number: PS0190; PMID:92041742; PMID:1718949

A/Accession: PS0191

A/Molecule type: protein

A/Residues: 41-58; 'X', 60-65 <ENU1>

A/Accession: PS0190

A/Molecule type: protein

A/Residues: 183-186; 'X', 188-207 <ENU2>

R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.

Eur. J. Haematol. 52, 162-168, 1994

A/Title: Analysis of the partial nucleotide sequences and deduced primary structures of t

A/Reference number: I46196; PMID:94222160; PMID:8168596

A/Accession: 162745

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 295-383; 'G', 385-455 <MUR>

A/Cross-references: GB:D21215; NID:G415309; PIDN:BA04756.1; PID:G455396

C/Function:

A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr

A/Pathway: blood coagulation

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-40/Domain: propeptide #status predicted <PRO>

F:25-84/Domain: Gla domain homology <GLA>

F:41-179/Domain: EGF homology <EGF>

F:90-121/Domain: EGF homology <EG1>

F:129-164/Domain: EGF homology <EG2>

F:183-482/Domain: coagulation factor X heavy chain #status predicted <HCH>

F.1183-231/Domain: activation peptide #status predicted <AP>  
 F.1232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F.1232-460/Domain: trypsin homology <TRY>  
 F.1567-47,54,56,55,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F.1567-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,368-402,411  
 F.1103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F.1187/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F.1208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F.1218/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F.1231-233/Cleavage site: Arg-Ile (coagulation factor IX) #status predicted  
 F.1274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 47.6%; Score 91; DB 1; Length 482;  
 Best Local Similarity 38.6%; Pred. No. 9.6e-08;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

1 ANAFLLXLRDGLSRKCKXQCSFXXAXEIFKDAKRTKLFWISY 44  
 DB 41 ANSFPEIKKGNLRECEVEICSFEEAREVFEDNKTTFMKY 84

RESULT 10  
 EXCH  
 coagulation factor Xa (BC 3.4.21.6) precursor - chicken  
 N/Alternate names: virus-activating proteinase  
 C/Species: Gallus gallus (chicken)  
 C/Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text\_change 16-Jun-1999  
 C/Accession: S15838; S20380; S20381  
 R/Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na  
 FEBS Lett. 283, 281-285, 1991  
 A>Title: Primary structure of the virus activating protease from chick embryo. Its identit  
 A/Reference number: S15838; MUID:91257322; PMID:2044767  
 A/Accession: S15838  
 A>Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-475 <SUZ>  
 A/Cross-references: DDBJ: D00844; NID: G222869; PIDN: BAA00724.1; PID: G222870  
 FEBS Lett. 296, 274-278, 1992  
 A/Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib  
 A/Reference number: S20380; MUID: 92164779; PMID: 1537403  
 A/Accession: S20380  
 A/Molecule type: protein  
 A/Residues: 41-55 <G02>  
 A/Accession: S20381  
 A/Molecule type: protein  
 A/Residues: 241-246, 'X', 248-251, 'X', 253-261 <G0T>  
 C/Function:  
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A/Pathway: blood coagulation  
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F.121-40/Domain: signal sequence #status predicted <SIG>  
 F.125-84/Domain: propeptide #status predicted <PRO>  
 F.141-185/Product: coagulation factor X light chain #status experimental <LCR>  
 F.129-121/Domain: EGF homology <EG1>  
 F.129-167/Domain: EGF homology <EG2>  
 F.186-475/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F.1241-475/Product: activation peptide #status predicted <AP>  
 F.1241-468/Domain: trypsin homology <TRY>  
 F.1567-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42  
 F.1195,207,228,225/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F.1282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 45.5%; Score 87; DB 1; Length 475;  
 Best Local Similarity 36.4%; Pred. No. 4.7e-07;  
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

1 ANAFLLXLRDGLSRKCKXQCSFXXAXEIFKDAKRTKLFWISY 44

```

Db      41 ANSFLEEMKQGNTERECNEBRCSEKEAREAFEDNTEEFWNIV 84
|||||::||::||::||::||::||::||::||::||::||::||::||::||
RESULT 11
KXHU
protein C (activated) (EC 3.4.21.69) precursor - human
Name alternate names: autoprothrombin IIA; plasma protein C
C[Species]: Homo sapiens (man)
C[Date]: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C[Accession]: A22331; A25426; J21781; A23789; A00927
R[Foster]: D.C.; Yoshitake, S.; Davie, E.W
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A[Title]: The nucleotide sequence of the gene for human protein C.
A[Reference number]: A22331; MUID:85270390; PMID:2591887
A[Accession]: A22331
A:Molecule type: DNA
A:Residues: 1-461 <FOS1>
A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R[Plutsky, J.; Hosking, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A[Title]: Evolution and organization of the human protein C gene.
A[Reference number]: A25426; MUID:86120978; PMID:3511471
A[Accession]: A25426
A:Molecule type: DNA
A:Residues: 1-445,'L', 446-461 <PLU>
A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
R[Foster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A[Title]: Characterization of a cDNA coding for human protein C.
A[Reference number]: A21781; MUID:84272714; PMID:6589623
A[Accession]: A21781
A:Molecule type: mRNA
A:Residues: 'Q', 107-461 <FOS2>
A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
R[Beckmann, R.J.; Schmidt, R.U.; Satterre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A[Title]: The structure and evolution of a 461 amino acid human protein C precursor and its
A[Reference number]: A23789; MUID:85269639; PMID:2991859
A[Accession]: A23789
A:Molecule type: mRNA
A:Residues: 1-461 <BEC>
A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
R[Milletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A[Title]: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
A[Reference number]: AA4605; MUID:90293094; PMID:1594179
A[Contents]: annotation; carbohydrate binding sites; activation peptide
A[Note]: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R[Harris, R.J.; Lång, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A[Title]: O-linked fucose is present in the first epidermal growth factor domain of factor
A[Reference number]: AA4606; MUID:92184750; PMID:1544894
A[Contents]: annotation; beta-hydroxyaspartic acid
C[Comment]: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also fe
C[Comment]: Protein C is synthesized in the liver as a single chain precursor, which is c]
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C[Genetics]:
A:Gene: GDB:PROC
A:Cross-references: GDB:120317; OMIM:176860
A:Map position: 2q13-q21
A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C[Superfamily]: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C[keywords]: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding,
F:1-32/Domain: signal sequence #status predicted <SIG>
F:27-86/Domain: Gla domain homology <Gla>
F:33-42/Domain: propeptide #status predicted <Pro>
F:43-197/Product: protein C light chain #status predicted <LC>
F:92-133/Domain: EGF homology <EG1>
F:140-175/Domain: EGF homology <EG2>
F:200-461/Product: protein C heavy chain #status predicted <HC>
F:200-211/Domain: activation peptide #status experimental <APT>
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F:212-445/Domain: trypsin homology <TRY>  
 F:48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D  
 F:106-111/Disulfide bonds: #status predicted  
 F:110/Binding site: carboxylate (Thr) (covalent) #status absent  
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:139,290,355/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
 F:253,299,402/Active site: His, Asp, Ser #status predicted  
 F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 44.0%; Score 84; DB 1; Length 461;  
 Best Local Similarity 43.9%; Pred. No. 1.5e-06;  
 Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLRLDGLRKKXKQCSFXAXEYFKDAXRKLFW 41  
 Db 43 ANSFLELRHSSLERECIEECIDFEAKKEIFQNVDTLAFW 83

RESULT 12

thrombin (EC 3.4.21.5) precursor [validated] - human  
 N:Alternate names: coagulation factor II  
 N:Contains: prothrombin  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Nov-1980 #sequence, revision 22-Jul-1994 #text change 08-Dec-2000  
 C:Accession: A29351; A00914; B00914; A37549; A37550; I51952  
 R:Degen, S.J.F.; Davie, E.W.  
 Biochemistry 26, 6165-6177, 1987  
 A>Title: Nucleotide sequence of the gene for human prothrombin.  
 A:Reference number: A29351; MUID:88077877; PMID:2825773  
 A:Accession: A29351  
 A:Molecule type: DNA  
 A:Residues: 1-622 <DEG>  
 A:Cross-references: GB:M17262; GB:M33691; NID:9558069; PIDN:AA63054.1; PID:G339641  
 R:Degen, S.J.F.; Macgillivray, R.T.A.; Davie, E.W.  
 Biochemistry 22, 2087-2097, 1983  
 A>Title: Characterization of the complementary deoxyribonucleic acid and gene coding for  
 A:Reference number: A00914; MUID:83231469; PMID:6305407  
 A:Accession: A00914  
 A:Molecule type: mRNA  
 A:Residues: 8-163; 'N',165-622 <DE2>  
 A:Cross-references: GB:J00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344  
 A:Accession: B00914  
 A:Molecule type: DNA  
 A:Residues: 188-311 <DE3>  
 R:Walz, D.A.; Hewett-Emlert, D.; Seegers, W.H.  
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977  
 A:Reference number: A37549; MUID:77193964; PMID:266717  
 A:Accession: A37549  
 A:Molecule type: protein  
 A:Residues: 44-118; 'N',120; 'S',122-163; 'I',165-175; 'A',177-182; 'T',184-193; 'NW',196-308;  
 R:Butkowski, R.U.; Elion, J.; Downing, M.R.; Mann, K.G.  
 J. Biol. Chem. 252, 4942-4957, 1977  
 A>Title: Primary structure of human prothrombin 2 and alpha-thrombin.  
 A:Reference number: A37550; MUID:77207112; PMID:873923  
 A:Accession: A37550  
 A:Molecule type: protein  
 A:Residues: 315-334; 'N',336-348; 'N',350-368; 'N',370-397; 'N',399-413; 'N',415-484; 'N',486-  
 R:Rabbit, M.U.; Blashill, A.; Furie, B.; Furie, B.C.  
 J. Biol. Chem. 261, 13210-13215, 1986  
 A:Reference number: A37551; MUID:87008532; PMID:3759958  
 A:Contents: annotation; activation cleavages  
 R:McGillivray, R.T.; Irwin, D.M.; Guanto, E.R.; Stone, J.C.  
 Ann. N. Y. Acad. Sci. 485, 73-79, 1986  
 A>Title: Recombinant genetic approaches to functional mapping of thrombin.  
 A:Reference number: I51952; MUID:87182874; PMID:3471151  
 A:Accession: I51952  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2; 'RI',5-100 <RES>  
 A:Cross-references: GB:M33011; NID:G190723; PIDN:AAA60220.1; PID:G190724

C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds  
 C:Comment: can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain  
 ter 314-Arg, are released in natural blood clotting.  
 C:Comment: The cleavage after Arg-196, observed in vitro, does not occur in plasma.  
 C:Comment: The gamma-carboxyglutamic acid residues bind calcium ions, result from the carboxy  
 ent interaction with the negatively charged phospholipid membrane surface.  
 C:Comment: The prothrombin precursor is synthesized in the liver.  
 C:Genetic:  
 A:Gene: GDB:F2  
 A:Cross-references: GDB:119894; OMIM:176930  
 A:Map position: 11p11-11q12  
 A:Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/  
 C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology  
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-43/Domain: propeptide #status predicted <PRO>  
 F:28-87/Domain: Gla domain homology <GLA>  
 F:44-622/Domain: prothrombin #status experimental <MAT>  
 F:44-622/Product: activation peptide #status experimental <APY>  
 F:108-186/Domain: kringe homology <KR1>  
 F:213-291/Domain: kringe homology <KR2>  
 F:328-363/Product: thrombin light chain #status experimental <LCH>  
 F:364-622/Product: thrombin heavy chain #status experimental <HCH>  
 F:364-613/Domain: trypsin homology <TRY>  
 F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status  
 F:111,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:336-482,536-550,564-594/Disulfide bonds: #status predicted  
 F:331-407/Disulfide bonds: #status experimental  
 F:406,462/Active site: His, Asp #status predicted  
 F:416/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:568/Active site: Ser #status experimental

Query Match 43.5%; Score 83; DB 1; Length 622;  
 Best Local Similarity 36.4%; Pred. No. 3e-06;  
 Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ANAFLLRLDGLRKKXKQCSFXAXEYFKDAXRKLFWISY 44  
 Db 44 ANTFLEVRKGNLERECVEETCSYEAFEALESSTATDVFAKY 87

RESULT 13

KFBO  
 coagulation factor IXA (EC 3.4.21.22) precursor - bovine  
 N:Alternate names: Christmas factor  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #text change 16-Jul-1999  
 C:Accession: A14757; B20274; I45891; A00923  
 R:Katayama, K.; Ericson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4950-4994, 1979  
 A>Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac  
 A:Reference number: A14757; MUID:80056619; PMID:291916  
 A:Accession: A14757  
 A:Molecule type: protein  
 A:Residues: 1-63; 'T',65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Accession: B20274  
 A:Molecule type: protein  
 A:Residues: 59-63; 'X',65-69 <MCX>  
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
 Nature 299, 178-180, 1982  
 A>Title: Molecular cloning of the gene for human anti-haemophilic factor IX.  
 A:Reference number: I45891; MUID:82272386; PMID:6287289  
 A:Accession: I45891  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 52-139 <CHO>  
 A:Cross-references: GB:J00007; NID:G163053; PIDN:AAA30520.1; PID:G163054



GenCore version 5.1.4.p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)  
328.082 Million cell updates/sec

Title: 10ASP28GLU  
Perfect score: 191  
Sequence: 1 ANAFLLXLDGSLXRCXKX.....XXAELIFKDXRRKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length DB | ID         | Description         |
|------------|-------|-------------|-----------|------------|---------------------|
| 1          | 159   | 83.2        | 466       | FA7_HUMAN  | P08709 homo sapien  |
| 2          | 125   | 65.4        | 444       | FA7_RABIT  | P88139 corycolagus  |
| 3          | 115   | 60.2        | 407       | FA7_BOVIN  | P2457 bos taurus    |
| 4          | 114   | 59.7        | 446       | FA7_MOUSE  | P07375 mus musculus |
| 5          | 102   | 53.4        | 461       | PRTC_MOUSE | P33587 mus musculus |
| 6          | 101   | 52.9        | 459       | PRTC_PIG   | P31392 sus scrofa   |
| 7          | 100   | 52.4        | 461       | PRTC_PIG   | P31392 sus scrofa   |
| 8          | 97    | 50.8        | 488       | FA10_HUMAN | P00742 homo sapien  |
| 9          | 97    | 50.8        | 490       | FA10_RABIT | P09045 corycolagus  |
| 10         | 97    | 50.8        | 492       | FA10_BOVIN | P00743 bos taurus   |
| 11         | 95    | 49.7        | 218       | TMG1_HUMAN | O14668 homo sapien  |
| 12         | 91    | 47.6        | 456       | PRTC_BOVIN | P00745 bos taurus   |
| 13         | 88    | 46.1        | 231       | TMG3_HUMAN | P25155 gallus galli |
| 14         | 87    | 45.5        | 475       | FA10_CHICK | P25155 gallus galli |
| 15         | 85    | 44.5        | 458       | PRTC_RABIT | P28661 corycolagus  |
| 16         | 84    | 44.0        | 461       | PRTC_HUMAN | P04070 homo sapien  |
| 17         | 83    | 43.5        | 622       | THRB_HUMAN | P00733 homo sapien  |
| 18         | 81    | 42.4        | 416       | FA9_BOVIN  | P00741 bos taurus   |
| 19         | 79    | 41.4        | 376       | FA10_TROCA | P01428 troglodychis |
| 20         | 79    | 41.4        | 617       | THRB_RAT   | P18292 rattus norv  |
| 21         | 79    | 41.4        | 618       | THRB_MOUSE | P19221 rattus norv  |
| 22         | 78    | 40.8        | 461       | FA9_HUMAN  | P00740 homo sapien  |
| 23         | 76    | 39.8        | 202       | TMG2_HUMAN | O14669 homo sapien  |
| 24         | 73    | 38.2        | 452       | FA9_CANFA  | P19540 canis famli  |
| 25         | 73    | 38.2        | 459       | FA9_MOUSE  | P16294 mus musculus |
| 26         | 69.5  | 36.4        | 226       | TMG4_HUMAN | P08266 homo sapien  |
| 27         | 63    | 33.0        | 625       | THRB_BOVIN | P00734 bos taurus   |
| 28         | 61    | 31.9        | 396       | PRTZ_BOVIN | P00744 bos taurus   |
| 29         | 61    | 31.9        | 675       | PRTS_BOVIN | P07224 bos taurus   |
| 30         | 60    | 31.4        | 649       | PRTS_MACMU | O28520 macaca mula  |
| 31         | 60    | 31.4        | 676       | PRTS_HUMAN | P07225 homo sapien  |
| 32         | 59    | 30.9        | 646       | PRTS_RABIT | P88118 corycolagus  |
| 33         | 58    | 30.4        | 675       | PRTS_RAT   | P58813 rattus norv  |

|    |      |      |      |   |            |                     |
|----|------|------|------|---|------------|---------------------|
| 34 | 56   | 29.3 | 400  | 1 | PRTZ_HUMAN | P22891 homo sapien  |
| 35 | 51   | 26.7 | 675  | 1 | PRTS_MOUSE | O08761 mus musculus |
| 36 | 45.5 | 23.8 | 356  | 1 | MURB_BUCAL | P57153 buchnera ap  |
| 37 | 45   | 23.6 | 879  | 1 | YN55_YEAST | P42837 saccharomyc  |
| 38 | 44   | 23.0 | 413  | 1 | NCAP_TINRV | P19691 infectious   |
| 39 | 42.5 | 22.3 | 133  | 1 | OUTS_ERWCH | P01567 erwania chr  |
| 40 | 42.5 | 22.3 | 322  | 1 | YOLJ_CABEL | P09292 caenorhabd1  |
| 41 | 42   | 22.0 | 263  | 1 | PFLA_STRMU | O68575 streptococc  |
| 42 | 41.5 | 21.7 | 1290 | 1 | BXB_CLOBO  | P10844 streptidum   |
| 43 | 41   | 21.5 | 814  | 1 | TOP1_SCHPO | P07799 schizosacch  |
| 44 | 40.5 | 21.2 | 878  | 1 | SYV_METDA  | O58413 methanococc  |
| 45 | 40   | 20.9 | 71   | 1 | LEA2_CAVPO | O91X13 cavia porce  |

## ALIGNMENTS

RESULT 1  
ID FA7\_HUMAN STANDARD; PRT; 466 AA.  
AC P08709: 014339;  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).  
GN F7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
ON NCBI\_Taxid=9606;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86205965; PubMed=3486420;  
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kistel W., Kurachi K., Davie E.W.;  
RA "Characterization of a cDNA coding for human factor VII."; Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=87260948; PubMed=3037537;  
RX O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;  
RA "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation."; Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
RN [3]  
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.  
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=89088153; PubMed=3264725;  
RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;  
RA "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."; Biochemistry 27:7785-7793(1988).  
RL [5]  
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
RX MEDLINE=91250411; PubMed=1904059;  
RA Bjorn S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kistel W.;  
RA "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine."; J. Biol. Chem. 266:11051-11057(1991).  
RL [6]  
RN STRUCTURE OF CARBOHYDRATE ON SER-112.  
RX MEDLINE=90062160; PubMed=2511201;



RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [17]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Knigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RL Nature 380:41-46(1996).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=9825787;  
 RA Zhang E., St. Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a Bp1 mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gipeert G.P., Forssen S., Stenflo J.,  
 RA Driksen T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Roderigo G., Casanato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=9337811; PubMed=8364544;  
 RA Marchetti G., Ferrari M., Patrascchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 RT (15His and 33Ser) in the human coagulation factor VII gene.";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamaya O., Kempball-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lunley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;  
 RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Caetanman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294His-->Val) and X (334Ser-->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";  
 RL Thromb. Haemost. 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arpini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS W-283, K-325, V-358, Q-364, E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Caetanman G., Pinotti M., Ferraresi P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tanary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,  
 RA Zatzov R., Seligsohn U.;  
 RT "A1244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN [21]  
 RP VARIANTS ALA124 THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerif C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:5189-S191(1998).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-lle bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PM: THE VITAMIN K-DEPENDENT. ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -1- PHARMACEUTICAL: Available under the names Nistase or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in



Query Match 83.2%; Score 159; DB 1; Length 466;  
 Best Local Similarity 72.7%; Pred. No. 2.4e-20;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLKRCCKXXQCSFXXAEXIFPKDARTKLFMISY 44  
 Db 61 ANAFLELRPGSLERCKEKCQSFEEAREIFPKDARTKLFMISY 104

RESULT 2  
 ID -FA7 RABIT STANDARD; PRT; 444 AA.  
 AC P98139; P79224;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin conversion accelerator).  
 GN F7.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93190306; PubMed=8383365;  
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";  
 RL Thromb. Res. Suppl. 69:231-238(1993).  
 RN [2]  
 RP REVISION TO 395.  
 RC TISSUE=Liver;  
 RA Ruiz S.R., Blajchman M.A., Clarke B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR XA AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAITIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC -----  
 CC EMBL; U77477; AAB37326.1; -.  
 CC HSSP; P08709; IFAK.  
 DR HSSP; S01.215; -.  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin\_1.  
 DR Pfam; PF00594; gla\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00001; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_1like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00187; EGF\_CA; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR HydroLase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 21  
 FT PROPEP 22 39  
 FT CHAIN 40 191  
 FT CHAIN 192 444  
 FT DOMAIN 45 74  
 FT DOMAIN 85 121  
 FT DOMAIN 125 167  
 FT DOMAIN 192 444  
 FT SITE 191 192

FT ACT SITE 232 232  
 FT ACT SITE 281 281  
 FT ACT SITE 383 383  
 FT BINDING 377 377  
 FT DISULFID 56 61  
 FT DISULFID 89 100  
 FT DISULFID 94 109  
 FT DISULFID 111 120  
 FT DISULFID 130 141  
 FT DISULFID 137 151  
 FT DISULFID 153 166  
 FT DISULFID 174 301  
 FT DISULFID 198 203  
 FT DISULFID 217 233  
 FT DISULFID 349 368  
 FT DISULFID 379 407  
 FT MOD RES 45 45  
 FT MOD RES 46 46  
 FT MOD RES 53 53  
 FT MOD RES 55 55  
 FT MOD RES 58 58  
 FT MOD RES 59 59  
 FT MOD RES 64 64  
 FT MOD RES 65 65  
 FT MOD RES 68 68  
 FT MOD RES 74 74  
 FT MOD RES 102 102  
 FT CARBOHYD 211 211  
 FT CARBOHYD 242 242  
 FT CARBOHYD 306 306  
 SQ SEQUENCE 444 AA; 49011 MW; 0481ABCFE5427F8 CRC64;

Query Match 65.4%; Score 125; DB 1; Length 444;  
 Best Local Similarity 54.5%; Pred. No. 2.3e-14;  
 Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLKRCCKXXQCSFXXAEXIFPKDARTKLFMISY 44  
 Db 40 ANAFLELRPGSLERCKEKCQSFEEAREIFPKDARTKLFMISY 83

RESULT 3

FA7\_BOVIN  
ID\_FA7\_BOVIN STANDARD; PRT; 407 AA.  
AC P22457;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
RX MEDLINE=9913;  
RP [1]  
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.,  
RT "Bovine factor VII. Its purification and complete amino acid sequence."  
RT J. Biol. Chem. 263:14868-14877(1988).  
RN [2]  
RP MEDLINE=89213999; PubMed=3149637;  
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."  
RT J. Biochem. 104:867-868(1988).  
RN [3]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RA MEDLINE=91344709; PubMed=2129367;  
RX Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."  
RT Adv. Exp. Med. Biol. 281:121-131(1990).  
RL -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC PIR: A31979; A31979.  
DR HSSP; P08709; 1BF9.  
DR MEROPS; S01.215; -.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF-2.  
DR InterPro; IPR001881; EGF-Ga.  
DR InterPro; IPR001438; EGF-II.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00089; trypsin\_1.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PRO0722; CHYMOTRYPSIN.  
DR PRINTS; PRO0010; EGFBLD.  
DR PRINTS; PRO0001; GLABLOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.

DR SMART; SM00059; GLA\_1.  
DR SMART; SM00020; tryp\_spec; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01866; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS02400; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.  
KW EGF-like domain; Repeat.  
FT CHAIN 1 152  
FT CHAIN 153 407  
FT DOMAIN 6 35  
FT DOMAIN 46 82  
FT DOMAIN 87 128  
FT DOMAIN 153 407  
FT SITE 152 153  
FT ACT SITE 193 193  
FT ACT SITE 242 242  
FT ACT SITE 344 344  
FT BINDING 338 338  
FT DISULFID 17 22  
FT DISULFID 50 61  
FT DISULFID 55 70  
FT DISULFID 72 81  
FT DISULFID 91 102  
FT DISULFID 98 112  
FT DISULFID 114 127  
FT DISULFID 135 262  
FT DISULFID 159 164  
FT DISULFID 178 194  
FT DISULFID 310 329  
FT DISULFID 340 368  
FT MOD\_RES 6 7  
FT MOD\_RES 7 7  
FT MOD\_RES 14 14  
FT MOD\_RES 16 16  
FT MOD\_RES 19 19  
FT MOD\_RES 20 20  
FT MOD\_RES 25 25  
FT MOD\_RES 26 26  
FT MOD\_RES 29 29  
FT MOD\_RES 35 35  
FT MOD\_RES 52 52  
FT CARBOHYD 145 145  
FT CARBOHYD 203 203  
FT SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;  
Query Match 60.2%; Score 115; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 1.3e-12;  
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;  
QY 1 ANAFPLXLRDGLXRXCKXQCSFXXAEXIFKDXARTLFWISY 44  
DB 1 ANGFLELLPGLSLRECHRELLCSFPEAHEIFRNERRTQFVVS 44  
RESULT 4  
FA7\_MOUSE STANDARD; PRT; 446 AA.  
ID\_FA7\_MOUSE P70375;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7 OR CF7  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97127167; PubMed=8972017;  
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine blood  
 coagulation factor VII gene."  
 RL Thromb. Haemost. 76:957-964(1996).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS  
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR  
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U66079; AAC3796.1; -.  
 DR HSSP; P08709; IBF9.  
 DR MEROPS; S01.215; -.  
 DR MCD; MGI.1109325; F7.  
 DR InterPro; IPR000152; Aex\_hydroxy1.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF\_1like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_Blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Vitr\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM000179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_1like; 1.  
 DR SMART; SM00069; GLA\_1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PSS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KM EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL; 1  
 FT PROPEP; 25  
 FT CHAIN; 42  
 FT DOMAIN; 47  
 FT DOMAIN; 87

FT DOMAIN 128 169 EGF-LIKE 2.  
 FT DOMAIN 194 446 SERINE PROTEASE.  
 FT SITE 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,  
 FT ACT SITE 234 234 FACTOR IXa, OR THROMBIN) (BY SIMILARITY).  
 FT ACT SITE 283 283 BY SIMILARITY.  
 FT ACT SITE 283 283 BY SIMILARITY.  
 FT ACT SITE 385 385 BY SIMILARITY.  
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 96 111 BY SIMILARITY.  
 FT DISULFID 113 122 BY SIMILARITY.  
 FT DISULFID 132 143 BY SIMILARITY.  
 FT DISULFID 139 153 BY SIMILARITY.  
 FT DISULFID 155 168 BY SIMILARITY.  
 FT DISULFID 176 303 BY SIMILARITY.  
 FT DISULFID 200 205 BY SIMILARITY.  
 FT DISULFID 219 235 BY SIMILARITY.  
 FT DISULFID 351 370 BY SIMILARITY.  
 FT DISULFID 381 409 BY SIMILARITY.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45CB936E CRC64;

Query Match 59.7%; Score 114; DB 1; Length 446;  
 Best Local Similarity 54.5%; Pred. No. 2, 1e-12;  
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAEFLXXLRDGSIXRCKKXQCSFXAXEXIFKDXRKLWISY 44  
 Db 42 ANSLBELWPGSLERECNEBCSFEEAREIFKSPERTKQFIIV 85

RESULT 5  
 PRTC\_MOUSE STANDARD; PRT; 461 AA.  
 AC P33587; O35498;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)  
 DE (Antiproteohembin IIA) (Anticoagulant protein C) (Blood coagulation  
 factor XIV).  
 GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=92316897; PubMed=1618739;  
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;  
 RT "Isolation and characterization of a mouse protein C cDNA."  
 RT J. Biochem. 111:491-495(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RX MEDLINE=98152576; PubMed=9493582;  
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine gene encoding



OX NCBI\_TaxID=9823;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=21121490; PubMed=11229814;  
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,  
 RA Kim H.K.W.;  
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional  
 RT protein modeling of membrane binding sites and comparative anatomy of  
 RT domains";  
 RL Cell Mol. Life Sci. 58:148-159(2001).  
 CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that  
 CC regulates blood coagulation by inactivating factors Va and VIIIa  
 CC in the presence of calcium ions and phospholipids.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIa.  
 CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved  
 CC into a light chain and a heavy chain held together by a disulfide  
 CC bond. The enzyme is then activated by thrombin, which cleaves a  
 CC tetradecapeptide from the amino end of the heavy chain; this  
 CC reaction, which occurs at the surface of endothelial cells, is  
 CC strongly promoted by thrombomodulin.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu  
 CC residues allows the modified protein to bind calcium.  
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
 CC another site, beyond the GLA domain. This GLA-independent binding  
 CC site is necessary for the recognition of the  
 CC thrombin-thrombomodulin complex.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF191307; AMG28380.1; -.  
 DR HSSP; P04070; 1PCU.  
 DR MEROPS; S01.218; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001381; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PR00008; EGF\_2.  
 DR Pfam; PR00089; trypsin; 1.  
 DR PRINTS; PR00722; Chymotrypsin.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00181; EGF\_2.  
 DR SMART; SM00001; EGF\_like; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01166; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Blood coagulation; Glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 41 BY SIMILARITY.  
 FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.

FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY  
 FT SIMILARITY).  
 FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY  
 FT SIMILARITY).  
 FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).  
 FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY  
 FT SIMILARITY).  
 FT DOMAIN 96 131 EGF-LIKE 1.  
 FT DOMAIN 135 175 EGF-LIKE 2.  
 FT DOMAIN 214 459 SERINE PROTEASE.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 112 112 HYDROXYLATION (BY SIMILARITY).  
 FT ACT\_SITE 255 255 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 301 301 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 400 400 CHARGE RELAY SYSTEM.  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 110 BY SIMILARITY.  
 FT DISULFID 100 105 BY SIMILARITY.  
 FT DISULFID 104 119 BY SIMILARITY.  
 FT DISULFID 121 130 BY SIMILARITY.  
 FT DISULFID 139 150 BY SIMILARITY.  
 FT DISULFID 146 159 BY SIMILARITY.  
 FT DISULFID 161 174 BY SIMILARITY.  
 FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 240 256 BY SIMILARITY.  
 FT DISULFID 371 385 BY SIMILARITY.  
 FT DISULFID 396 424 BY SIMILARITY.  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;  
 Query Match 52.9%; Score 101; DB 1; Length 459;  
 Best Local Similarity 45.5%; Pred. No. 4.2e-10;  
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 ANAFLLXLRDGLRCKXXQCSFXAXEJFKDAXRTLFWISY 44  
 Db 42 ANSFLELRPSLSRECKEFCDFEARELFFONTENTMARWSKY 85  
 ID PRTC RAT STANDARD; PRT; 461 AA.  
 AC P1354;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (BC 3.4.21.69)  
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistat; TISSUE=liver;  
 RX MEDLINE=9329550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C";  
 RL Biochim. Biophys. Acta 1131:329-332(1992).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, X64336; CA445617.1; -.  
 DR PIR, S18994; S18994.  
 DR PIR, S24312; S24312.  
 DR HSSP, P04070; 1PCU.  
 DR MEROPS, S01.218; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VltK\_dep\_GLA.  
 DR Pfam, PF00008; EGF\_2.  
 DR Pfam, PF00089; trypsin, 1.  
 DR Pfam, PF00594; gla, 1.  
 DR PRINTS, PR00722; CHYMOTRYPSIN.  
 DR PRINTS, PR00001; GLABLOOD.  
 DR SMART, SM00179; EGF\_CA, 1.  
 DR SMART, SM00001; EGF\_Like, 1.  
 DR SMART, SM00069; GLA, 1.  
 DR SMART, SM00020; Tryp\_Spc, 1.  
 DR PROSITE, PS00010; ASX\_HYDROXYL, 1.  
 DR PROSITE, PS00022; EGF\_1, 1.  
 DR PROSITE, PS01186; EGF\_2, 2.  
 DR PROSITE, PS01187; EGF\_CA, 1.  
 DR PROSITE, PS00011; GLU\_CARBOXYLATION, 1.  
 DR PROSITE, PS00240; TRYPSIN\_DOM, 1.  
 DR PROSITE, PS00134; TRYPSIN\_HIS, 1.  
 DR PROSITE, PS00135; TRYPSIN\_SER, 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 32  
 FT PROPEP 3 41  
 FT CHAIN 42 196  
 FT CHAIN 199 461  
 FT PEPTIDE 199 212  
 FT PROTEIN C LIGHT CHAIN (BY SIMILARITY).  
 FT PROTEIN C HEAVY CHAIN (BY SIMILARITY).  
 FT ACTIVATION PEPTIDE (BY SIMILARITY).

FT SITE 212 213  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 213 461  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 254 300  
 FT ACT\_SITE 402 402  
 FT ACT\_SITE 402 402  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 320  
 FT DISULFID 239 255  
 FT DISULFID 373 387  
 FT DISULFID 398 426  
 FT CARBOHYD 215 215  
 FT CARBOHYD 291 291  
 FT CARBOHYD 355 355  
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDAC05 CRC64;  
 Query Match 52.4%; Score 100; DB 1; Length 461;  
 Best local Similarity 45.5%; Pred. No. 6.3e-10;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 ANAPLXLRLDGLKRXCKXCCSPFXAEXIPKDXARTLFWISY 44  
 DB 42 ANSFLAEVYRAGSLEREKMEIEICDFEEAOEITFQNEVDTLAFWIKY 85  
 RESULT 8  
 P10 HUMAN STANDARD; PRT; 488 AA.  
 AC P00742; Q14340;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91216473; PubMed=1902434;  
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;  
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding  
 RT human coagulation factor X";  
 RL Gene 99:291-294(1991).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026600; PubMed=3768336;  
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;  
 RT "Gene for human factor X: a blood coagulation factor whose gene  
 RT organization is essentially identical with that of factor IX and  
 RT protein C.";  
 RL Biochemistry 25:5098-5102(1986).  
 RN [3]  
 RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420.  
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RN [4]  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA.";  
 RL Gene 41:311-314(1986).  
 RN [5]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howard W.N.,  
 RA Kna E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884(1983).  
 RN [6]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [7]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [8]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hameedhannam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279; Tulinsey A., Park C.H., Bode W.,  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsey A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: K03194; AAA52490.1; -;  
 DR EMBL: M57285; AAA52421.1; -;  
 DR EMBL: L29433; AAA52764.1; -;  
 DR EMBL: L00390; AAA52764.1; JOINED.  
 DR EMBL: L00391; AAA52764.1; JOINED.  
 DR EMBL: L00392; AAA52764.1; JOINED.  
 DR EMBL: L00393; AAA52764.1; JOINED.  
 DR EMBL: L00394; AAA52764.1; JOINED.  
 DR EMBL: L00395; AAA52764.1; JOINED.  
 DR EMBL: M22613; AAA51984.1; -;  
 DR EMBL: M01886; AAA52486.1; -;  
 DR EMBL: M33297; AAA52636.1; -;  
 DR PIR: A00824; EXHU.  
 DR PIR: A25853; A25853.  
 DR PIR: A24478; A24478.  
 DR PDB: 1HCG; 08-MAY-95.  
 DR PDB: 1FAK; 29-OCT-97.  
 DR PDB: 1FXY; 17-JUN-98.  
 DR PDB: 1XKA; 23-MAR-99.  
 DR PDB: 1XKB; 23-MAR-99.  
 DR MEROPS: S01.216; -;  
 DR GlycoSiteDB: P00742; -;  
 DR Genew: HGNC:3528; F10.  
 DR MIM: 134530; -;  
 DR MIM: 227600; -;  
 DR InterPro: IPR000152; Aex\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF 2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_Blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; Vltk\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin\_1.  
 DR Pfam: PF00594; gla\_1.  
 DR PRINTS: PR00722; GYBMOIRYPSIN.  
 DR SMART: SM00179; EGF\_CA\_1.  
 DR SMART: SM00001; EGF-like\_1.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; TRYF\_SPC\_1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA\_1.  
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM\_1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER\_1.  
 DR GlycoProtein: Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;

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KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 40
FT CHAIN 41 179
FT CHAIN 183 488
FT PROPEP 183 234
FT CHAIN 235 488
FT DOMAIN 86 122
FT DOMAIN 125 165
FT DOMAIN 235 488
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 56 56
FT MOD_RES 59 59
FT MOD_RES 60 60
FT MOD_RES 65 65
FT MOD_RES 66 66
FT MOD_RES 69 69
FT MOD_RES 72 72
FT MOD_RES 79 79
FT MOD_RES 103 103
FT CARBOHYD 199 211
FT CARBOHYD 221 221
FT CARBOHYD 231 231
FT ACT_SITE 276 276
FT ACT_SITE 322 322
FT ACT_SITE 419 419
FT DISULFID 90 101
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

Query Match 50.8%; Score 97; DB 1; Length 488;
Best Local Similarity 38.6%; Pred. No. 2.3e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFPLXLRDGLRXKXCKXQCFXAXEYFKDARKTLFWISY 44
Db 41 ANSFLEMKKGHLRECMETCSYEBAREVFEEDSDXTNFEWY 84

RESULT 9
FA10_RABIT STANDARD; PRT; 490 AA.
AC 019045;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor) .
GN F10.
OS Oryctolagus cuniculus (Rabbit) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; PubMed=9101642;
RA Pendurthi U.R., Anderson K.D., James H.L.;
RL "Characterization of a full-length cDNA for rabbit factor X.";
RT "Thromb. Res. 85:503-514(1997)."
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Thr and then
CC Arg|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
```

```
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
CC -----
CC EMBL; AF003200; AAB62542.1; -
CC HSSP; P00742; IHCG.
CC MEROPS; S01.216; -.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR001254; Ser_protease_Try.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00089; trypsin; 1.
CC Pfam; PF00594; gla; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00001; EGF_Like; 1.
CC SMART; SM00059; GLA; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF 1; 1.
CC PROSITE; PS01186; EGF 2; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Glycoprotein; Hydroxylase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20
FT PROPEP 21 40
FT CHAIN 41 180
FT CHAIN 184 490
FT PROPEP 184 232
FT CHAIN 233 490
FT DOMAIN 86 165
FT DOMAIN 125 122
FT DOMAIN 233 490
FT MOD_RES 46 46
FT MOD_RES 47 47
FT MOD_RES 54 54
FT MOD_RES 56 56
FT MOD_RES 59 59
FT MOD_RES 60 60
FT MOD_RES 65 65
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FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 50.8%; Score 97; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 2.3e-09;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXRLRDSGLRXCKXCCSFXXEYIFKDXRTLFNYSY 44
Db 41 ANSFLEELKKNLRECEMENCSEYEALVEDEDEKTFEFNNKY 84

RESULT 10
FA10_BOVIN STANDARD; PRT; 492 AA.
ID FA10_BOVIN
AC P00743;
DT 21-JUN-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RA MEDLINE=84247315; PubMed=6330671;
RA Fung W.R., Campbell R.M., McGilivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RA MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor)."
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RA MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Risiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
```

```
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RA MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RA MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X."
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RA MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases."
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RA MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RA MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region."
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RA MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide."
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RA MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X."
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RA MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding."
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RA MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
```

RL J. Biol. Chem. 267:19642-19649(1992).

RP [13]

RX STRUCTURE BY NMR OF 41-126.

RA MEDLINE=96387194; PubMed=8794734;

RA Sunnerhagen M., Olah G.A., Stenflo J., Forssen S., Drakenberg T.,

RA Tiewhella J.;

RT "The relative orientation of G1a and EGF domains in coagulation

RT factor X is altered by Ca2+ binding to the first EGF domain. A

RT combined NMR-small angle X-ray scattering study.";

RL Biochemistry 35:11547-11559(1996).

CC -1 FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that

CC converts prothrombin to thrombin in the presence of factor Va,

CC calcium and phospholipid during blood clotting.

CC -1 CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then

CC Arg-|-Ile bonds in prothrombin to form thrombin.

CC -1 SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HEID TOGETHER BY 1 OR

CC MORE DISULFIDE BONDS.

CC -1 PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME

CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM.

CC -1 PTM: N- AND O-GLYCOSYLATED.

CC -1 PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

CC -1 MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO

CC ANOTHER SITE, BEYOND THE GLA DOMAIN.

CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1 SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

CC -----

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CC -----

DR EMBL; X00673; CAA25286.1; -.

DR PIR; A00925; EXBO.

DR PDB; IAP0; 31-JAN-94.

DR PDB; ICCP; 31-MAY-94.

DR PDB; 1WHE; 15-MAY-97.

DR PDB; 1WHF; 15-MAY-97.

DR MEROPS; S01.216; -.

DR GlycoSuiteDB; P00743; -.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR002383; GLA\_blood.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VltK\_dep\_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PF00594; glia; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF\_CA; 1.

DR SMART; SM00001; EGF\_like; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp\_Spc; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; 1.

DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01187; EGF\_CA; 1.

DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; 1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;

KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;

KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.

| FT | SIGNAL   | 1   | 23  | POTENTIAL.                               |
|----|----------|-----|-----|--|
| FT | PROPEP   | 24  | 40  | FACTOR X LIGHT CHAIN.                    |
| FT | CHAIN    | 41  | 180 | FACTOR X HEAVY CHAIN.                    |
| FT | PROPEP   | 183 | 492 | ACTIVATION PEPTIDE.                      |
| FT | CHAIN    | 234 | 233 | ACTIVATED FACTOR XA, HEAVY CHAIN.        |
| FT | PROPEP   | 476 | 492 | MAY BE REMOVED BUT IS NOT NECESSARY FOR  |
| FT | DOMAIN   | 86  | 122 | ACTIVATION.                              |
| FT | DOMAIN   | 125 | 165 | EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL). |
| FT | ACT_SITE | 234 | 492 | EGF-LIKE 2.                              |
| FT | ACT_SITE | 275 | 275 | SERINE PROTEASE.                         |
| FT | ACT_SITE | 321 | 321 | CHARGE RELAY SYSTEM.                     |
| FT | ACT_SITE | 418 | 418 | CHARGE RELAY SYSTEM.                     |
| FT | MOD_RES  | 46  | 46  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 47  | 47  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 54  | 54  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 56  | 56  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 59  | 59  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 60  | 60  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 65  | 65  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 66  | 66  | GAMMA-CARBOXYGLUTAMIC ACID.              |

Query Match 50.8%; Score 97; DB 1; Length 492;

Best Local Similarity 40.9%; Pred. No. 2.3e-09;

Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAPLXLRLDGLSLKRXCKXQCSFYXAEYFPAKARLFLWISY 44

Db 41 ANSFLIEVYQGNLREHCLEACSLSEAREVFEDARQDTDFMSKY 84

-----

RESULT 11

TMG1 HUMAN

AD 014668;

ID TMG1 HUMAN STANDARD; PRT; 218 AA.

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-

DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein

DE 1).

GN PRG1 OR TMG1 OR PRG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97404347; PubMed=9256434;

RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;

RT "Primary structure and tissue distribution of two novel proline-rich

RT gamma-carboxyglutamic acid proteins.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).

CC -1 TISSUE SPECIFICITY: Highly expressed in the spinal cord.

CC -1 PTM: Gla residues are produced after subsequent posttranslational

CC modifications of glutamic acid by a vitamin K-dependent gamma-

CC carboxylase.

CC -----

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CC -----

DR EMBL; AF009242; AAB67070.1; -.

DR HSSP; P00740; ICFH.

DR GeneW; HGNC:9469; PRG1.

DR MIM; 604428; -.

DR InterPro; IPR002383; GLA\_blood.

DR InterPro; IPR000294; VltK\_dep\_GLA.

```

DR Pfam; PF00594; glaf, 1.
DR SMART; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83
FT TRANSMEM 84 106
FT DOMAIN 107 218
FT DOMAIN 24 61
FT DOMAIN 131 135
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AE98 CRC64;

Query Match 49.7%; Score 95; DB 1; Length 218;
Best Local Similarity 38.6%; Pred. No. 2,3e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRDGLRCKXQCFXAXEIPDAXRTLFMTSY 44
Db 21 ANGFPEIRQGNIRECKEFCFPEARAEENNEKTEFMSTY 64

RESULT 12
PRTC BOVIN STANDARD; PRT: 456 AA.
AC P00745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balasajee R.M., McGillivray R.T.A.;
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN 2
RP SEQUENCE OF 40-194.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo J.;
RT "Amino acid sequence of the light chain of bovine protein C.";
RL J. Biol. Chem. 257:12170-12179(1982).
RN 3
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN 4
RP SEQUENCE OF 197-456.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
RT "Amino acid sequence of the heavy chain of bovine protein C.";
RL J. Biol. Chem. 257:12180-12190(1982).
RN 15
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmen N.L., Debault L.E., Esmen C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
domainless protein C.";
RL J. Biol. Chem. 258:5548-5553(1983).
RN 16
RP PROCESSING, AND CALCIUM-BINDING DATA.

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RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmen N.L., Laue T.M., Esmen C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02435; AAA30685.1; -.
DR PIR; A00928; KXBO.
DR HSSP; P04070; IPCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin_1.
DR Pfam; PF00594; glaf, 1.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hyaluronase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPEP 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RSS 45 45
FT MOD_RSS 46 46
FT MOD_RSS 53 53
MOD_RSS 53 53

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# OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(Without alignments)  
196.288 Million cell updates/sec

Title: 10ASP28GLU  
Perfect score: 191  
Sequence: 1 ANAFLLXLRDGLRXCKXX.....XXAEXIFKDXRKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

## Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 159   | 83.2        | 701    | 4     | Q96PQ8      |
| 2          | 114   | 59.7        | 446    | 11    | Q61109      |
| 3          | 102   | 53.4        | 460    | 11    | Q91WN8      |
| 4          | 96    | 50.3        | 460    | 11    | Q99PC6      |
| 5          | 91    | 47.6        | 466    | 6     | Q9TPR0      |
| 6          | 91    | 47.6        | 482    | 11    | Q63207      |
| 7          | 89    | 46.6        | 469    | 6     | Q9GMD9      |
| 8          | 89    | 46.6        | 481    | 11    | Q54740      |
| 9          | 89    | 46.6        | 481    | 11    | Q99132      |
| 10         | 89    | 46.6        | 481    | 11    | Q88947      |
| 11         | 83    | 43.5        | 100    | 4     | Q15253      |
| 12         | 81    | 42.4        | 449    | 6     | Q95ME8      |
| 13         | 78    | 40.8        | 456    | 4     | Q14316      |
| 14         | 78    | 40.8        | 461    | 6     | Q95ND7      |
| 15         | 78    | 40.8        | 461    | 6     | Q95ND6      |
| 16         | 76    | 39.8        | 179    | 4     | Q8TA63      |

|    |      |      |     |    |        |                     |
|----|------|------|-----|----|--------|---------------------|
| 17 | 76   | 39.8 | 198 | 11 | Q8R182 | Q8R182 mus musculus |
| 18 | 74   | 38.7 | 138 | 6  | Q28994 | Q28994 sus scrofa   |
| 19 | 70   | 36.6 | 433 | 13 | Q90YK1 | Q90YK1 brachydanio  |
| 20 | 65   | 34.0 | 98  | 13 | P82807 | P82807 notechis sc  |
| 21 | 65   | 34.0 | 648 | 6  | Q29094 | Q29094 sus scrofa   |
| 22 | 62   | 32.5 | 399 | 11 | Q9CQM3 | Q9CQM3 mus musculus |
| 23 | 61   | 31.9 | 608 | 13 | Q9PTW7 | Q9PTW7 struthio ca  |
| 24 | 60   | 31.4 | 650 | 4  | Q9NSD0 | Q9NSD0 homo sapien  |
| 25 | 60   | 31.4 | 650 | 4  | Q16519 | Q16519 homo sapien  |
| 26 | 58.5 | 30.6 | 431 | 10 | Q94EY5 | Q94EY5 arabidopsis  |
| 27 | 58.5 | 30.6 | 492 | 10 | Q9SMJ7 | Q9SMJ7 cicer ariet  |
| 28 | 58.5 | 30.6 | 543 | 10 | Q9MB23 | Q9MB23 arabidopsis  |
| 29 | 58.5 | 30.6 | 576 | 10 | Q9C9U4 | Q9C9U4 arabidopsis  |
| 30 | 58.5 | 30.6 | 589 | 10 | Q9LMS2 | Q9LMS2 arabidopsis  |
| 31 | 58   | 30.4 | 607 | 13 | Q91001 | Q91001 gallus gall  |
| 32 | 57.5 | 29.1 | 196 | 10 | Q04284 | Q04284 selaginella  |
| 33 | 56.5 | 29.6 | 459 | 10 | Q9SE22 | Q9SE22 oryza sativ  |
| 34 | 55.5 | 29.1 | 506 | 10 | Q9SPF0 | Q9SPF0 oryza sativ  |
| 35 | 55.5 | 29.1 | 506 | 10 | Q9SE23 | Q9SE23 oryza sativ  |
| 36 | 55.5 | 29.1 | 542 | 5  | Q8TE13 | Q8TE13 halocynthia  |
| 37 | 55.5 | 29.1 | 567 | 10 | Q8W4J2 | Q8W4J2 arabidopsis  |
| 38 | 54.5 | 28.5 | 510 | 10 | Q9WB22 | Q9WB22 arabidopsis  |
| 39 | 54.5 | 28.5 | 619 | 10 | Q9LVJ7 | Q9LVJ7 arabidopsis  |
| 40 | 53   | 27.7 | 25  | 11 | Q9QVH6 | Q9QVH6 ratcus sp.   |
| 41 | 52.5 | 27.5 | 588 | 10 | Q9LM33 | Q9LM33 arabidopsis  |
| 42 | 52.5 | 27.5 | 603 | 10 | Q91PG7 | Q91PG7 arabidopsis  |
| 43 | 52.5 | 27.5 | 606 | 10 | Q9SUG9 | Q9SUG9 arabidopsis  |
| 44 | 52.5 | 27.5 | 651 | 10 | Q8S218 | Q8S218 oryza sativ  |
| 45 | 51.5 | 27.0 | 575 | 10 | Q94E17 | Q94E17 oryza sativ  |

## ALIGNMENTS

RESULT 1  
Q96PQ8 PRELIMINARY; PRT; 701 AA.  
ID Q96PQ8  
AC Q96PQ8;  
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 20, last annotation update)  
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
DE Factor VII active site mutant immunocongulate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxId=9606;  
RX MEDLINE=21477448; PubMed=11593034;  
RA Hu Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
RT cells for immunotherapy in mouse models of prostatic cancer."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
DR EMBL; AF272774; AKS58686.1; -  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PR00008; EGF\_2.  
DR Pfam; PR00594; gla\_1.  
DR Pfam; PR00047; Ig\_2.  
DR Pfam; PR00089; trypsin; 1.  
DR SMART; SM00181; EGF\_2.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydroxylase; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94ACCEBA42CC992F CRC64;

Query Match 83.2%; Score 159; DB 4; Length 701;  
Best Local Similarity 72.7%; Pred. No. 6,6e-21;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXRXCKXQCSFXAXEYIFDAXRTKLFWISY 44  
Db 61 ANAFLELRPGSLERCKECCSFEEAREIFPDARTKLFWISY 104

## RESULT 2

ID 061109 PRELIMINARY; PRT; 446 AA.  
AC 061109;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Coagulation factor VII.  
GN F7 OR FVII.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96276538; PubMed=8701412;  
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
RA Castellino F.J.;  
RT "Characterization of a cDNA encoding murine coagulation factor VII.",  
RL Thromb. Haemost. 75:481-487(1996).  
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPsin FAMILY.  
DR EMBL; U4795; AAC52570.1; -.  
DR HSSP; P08709; 1PAK.  
DR MEROPS; S01.215; -.  
DR MGD; MGI:109325; F7.  
DR InterPro; IPR002086; Aldehyde\_dehydr.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; Gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PRO0722; CHYMOTRYPSIN.  
DR PRINTS; PRO0001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Repeat;  
KW Serine protease.  
SQ SEQUENCE 446 AA; 50318 MW; 482FDD09BEFDA6870 CRC64;

Query Match 59.7%; Score 114; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 1.1e-12;  
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRDGLXRXCKXQCSFXAXEYIFDAXRTKLFWISY 44  
Db 42 ANSLLEELWPGSLERCKECCSFEEAREIFKSPERTKQFIVY 85

## RESULT 3

ID 091WN8 PRELIMINARY; PRT; 460 AA.  
AC 091WN8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Similar to protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013896; AAH13896.1; -.  
DR MGD; MGI:97771; Proc.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; Gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydroxylase; Serine protease.  
SQ SEQUENCE 460 AA; 51818 MW; 0117E26E68FCC274 CRC64;

Query Match 53.4%; Score 102; DB 11; Length 460;  
Best Local Similarity 45.5%; Pred. No. 2e-10;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXRXCKXQCSFXAXEYIFDAXRTKLFWISY 44  
Db 42 ANSLLEELWPGSLERCKECCSFEEAREIFQNVEDTLAFIKY 85

RESULT 4

ID 099PC6 PRELIMINARY; PRT; 460 AA.  
AC 099PC6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anticoagulant protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL;  
Korf I.;



RT "Complete sequence of UC72A01."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL: AF318182; AK079181.1; -.  
 DR HSSP: P04070; IPCU.  
 DR MEROPS: S01.218; -.  
 DR MGD: MGI:97771; Proc.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VltK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00594; GLA\_1.  
 DR Pfam: PF00089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00001; EGF\_1like; 2.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; tryp\_spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA\_1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KM Hydroxylation; Repeat; Serine protease.  
 SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E93EDJ6 CRC64;  
 Query Match 50.3%; Score 96; DB 11; Length 460;  
 Best Local Similarity 43.2%; Pred. No. 2.7e-09;  
 Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 ANAFLLXLRDGLRCKXCKXCSFXAXEIPKDXRTKLFMISY 44  
 Db 42 ANSFLEWRPGLERECWEICDLEAQEIFQNVDTLAFWIKY 85  
 RESULT 5  
 Q9TTRO PRELIMINARY; PRT; 456 AA.  
 AC Q9TTRO;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Protein C precursor.  
 GN PROC.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunberg L.,  
 RT "Molecular characterization and chromosomal assignment of the canine  
 RT protein C gene."  
 RL Mamm. Genome 10:135-139 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93371952; PubMed=10443005;  
 RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breen B.,  
 RT "Analysis of canine protein C gene polymorphisms."  
 RL Anim. Genet. 30:237-238 (1999).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.

DR EMBL: AJ001979; CA05126.1; -.  
 DR HSSP: P04070; IPCU.  
 DR MEROPS: S01.218; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VltK\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00594; GLA\_1.  
 DR Pfam: PF00089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00001; EGF\_1like; 2.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; tryp\_spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA\_1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
 KM Hydroxylation; Repeat; Serine protease; Signal.  
 FT SIGNAL 1 42  
 FT CHAIN 1 192  
 FT CHAIN 193 194  
 FT CHAIN 195 456  
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C34E59FC CRC64;  
 Query Match 47.6%; Score 91; DB 6; Length 456;  
 Best Local Similarity 40.9%; Pred. No. 2.3e-08;  
 Matches 18; Conservative 6; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 ANAFLLXLRDGLRCKXCKXCSFXAXEIPKDXRTKLFMISY 44  
 Db 43 ANSFLEIRAGSLERECWEICDLEAQEIFQNVDTLAFWIKY 86  
 RESULT 6  
 Q63207 PRELIMINARY; PRT; 482 AA.  
 AC Q63207;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Factor X.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=96093366; PubMed=8578539;  
 RA Stanton C., Ross R.P., Hutson S., Wallin R.,  
 RT "Evidence for competition between vitamin K-dependent clotting factors  
 RT for intracellular processing by the vitamin K-dependent gamma-  
 RT carboxylase."  
 RL Thromb. Res. 80:63-73 (1995).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY.  
 DR EMBL: X79807; CAA56202.1; -.  
 DR HSSP: P00742; IXKA.  
 DR MEROPS: S01.216; -.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF\_2.

DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA-  
DR Pfam; PF00006; EGF\_2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease.  
SQ SEQUENCE 482 AA; 54265 MW; 0284678E354A698 CRC64;

Query Match 47.6%; Score 91; DB 11; Length 482;  
Best Local Similarity 38.6%; Pred. No. 2.5e-08;  
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLEXLRDGLRXCKXCKXCSFXAXEIRFDAXRTKLFWISY 44  
DB 41 ANSLFEEIKGNLRECEVEICSFEEAREVFEDDTKTNEFWNIY 84

## RESULT 7

OGGMD9 PRELIMINARY; PRT; 469 AA.  
AC OGGMD9;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Coagulation factor X.  
OS Ornithorhynchus anatinus (Duckbill platypus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.  
OX NCBI\_TaxId=9258;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21015017; PubMed=1132153;  
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;  
RT "Identification and structural analysis of four serine proteases in a  
RT monotreme, the platypus, Ornithorhynchus anatinus.";  
RL Immunogenetics 52:19-28(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPsin FAMILY.  
DR EMBL; AF275654; AAG00453.1; -.  
DR HSSP; P00742; 1XKB.  
DR MEROPS; S01.216; -.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR00294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00179; EGF\_CA; 1.

DR SMART; SM00001; EGF\_like; 2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 469 AA; 52196 MW; 4C66C23DD0758FEA CRC64;

Query Match 46.6%; Score 89; DB 6; Length 469;  
Best Local Similarity 36.4%; Pred. No. 5.7e-08;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAFLEXLRDGLRXCKXCKXCSFXAXEIRFDAXRTKLFWISY 44  
DB 41 ANSLFEEIKGNLRECEVEICSFEEAREVFEDDTKTNEFWNIY 84

## RESULT 8

OG54740 PRELIMINARY; PRT; 481 AA.  
AC OG54740;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Coagulation factor X precursor (EC 3.4.21.6).  
GN F10 OR FA10.  
OS Mus musculus (Mouse).  
OG Plasmid pbluescript.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=98454993; PubMed=9783672;  
RA Heidemann H.H., Kontermann R.E.;  
RT "Cloning and recombinant expression of mouse coagulation factor X.";  
RL Thromb. Res. 92:33-41(1998).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; AJ222677; CA010933.1; -.  
DR HSSP; P00742; 1XKA.  
DR MEROPS; S01.216; -.  
DR MGD; MGI:103107; F10.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR00294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;  
KW Repeat; Serine protease; Signal.  
FT SIGNAL 1 40  
FT CHAIN 41 481  
SQ SEQUENCE 481 AA; 53986 MW; CF702D5E5F9D7AE CRC64;

Query Match 46.6%; Score 89; DB 11; Length 481;  
Best Local Similarity 36.4%; Pred. No. 5.8e-08;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGSIXRCKXKXQCSFXAXEJFKDAXRTKLFWISY 44  
Db 41 ANSFFEEFKKGNLERECMEICSYEEVREIFEDDEKTKYWTXY 84

RESULT 9  
ID 099L32 PRELIMINARY; PRT; 481 AA.  
AC 099L32;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Coagulation factor X.  
GN P10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
CC EMBL; BC003877; AA03877.1; -.  
DR HSSP; P00742; 1XKA.  
DR MEROPS; S01.216; -.  
DR MGD; MGI:103107; P10.  
DR InterPro; IPR000152; Asx\_hydroxy1.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_11.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; GLA\_1.  
DR Pfam; PF00089; Trypsin\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00010; EGFBL00D.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM000181; EGF\_2.  
DR SMART; SM00001; EGF\_like; 2.  
DR SMART; SM00069; GLA\_1.  
DR SMART; SM00020; TRYPSIN\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
KW Serine protease; Signal.  
SQ SEQUENCE 481 AA; 54004 MW; BD88596C8A0B7E7F CRC64;

Query Match 46.6%; Score 89; DB 11; Length 481;  
Best Local Similarity 36.4%; Pred. No. 5.8e-08;

Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRDGSIXRCKXKXQCSFXAXEJFKDAXRTKLFWISY 44  
Db 41 ANSFFEEFKKGNLERECMEICSYEEVREIFEDDEKTKYWTXY 84

RESULT 10  
ID 088947 PRELIMINARY; PRT; 481 AA.  
AC 088947;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Coagulation factor X precursor.  
GN P10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;  
RX MEDLINE=98347933; PubMed=9684791;  
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,  
RA Castellino F.J., Rosen E.D.;  
RT "Cloning and characterization of a cDNA encoding murine coagulation factor X";  
RL Thromb. Haemost. 80:87-91(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129S/J;  
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;  
RT "Cloning and characterization of the Murine Factor X Gene";  
RL Thromb. Haemost. 0:0-0(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
CC EMBL; AF087644; AAC6345.1; -.  
DR EMBL; AF211347; AAF22980.1; -.  
DR HSSP; P00742; 1XKA.  
DR MEROPS; S01.216; -.  
DR MGD; MGI:103107; P10.  
DR InterPro; IPR000152; Asx\_hydroxy1.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_11.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; GLA\_1.  
DR Pfam; PF00089; Trypsin\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA\_1.  
DR SMART; SM00020; TRYPSIN\_SPC; 1.  
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DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;  
KW Serine protease; Signal.  
FT SIGNAL 1 40  
FT CHAIN 41 481  
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5E5F9D271E CRC64;



Query Match 40.8%; Score 78; DB 4; Length 456;  
Best Local Similarity 41.2%; Pred. No. 6.3e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;  
Qy 11 GSLRXCKXKXCSFXAXEIKFDXAKTKLFWISY 44  
Db 53 GNLERECMEKCSFEAREVENTERTTEFWKQY 86

RESULT 14  
Q95ND7 PRELIMINARY; PRT; 461 AA.  
AC Q95ND7;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Coagulation factor XI.  
GN F9.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=504;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and  
RT chimpanzees.";  
RL Genes Genet. Syst. 0:0-0(2001).  
DR EMBL; AB062470; BAB58885.1; JOINED.  
DR EMBL; AB062458; BAB58885.1; JOINED.  
DR EMBL; AB062460; BAB58885.1; JOINED.  
DR EMBL; AB062462; BAB58885.1; JOINED.  
DR EMBL; AB062464; BAB58885.1; JOINED.  
DR EMBL; AB062466; BAB58885.1; JOINED.  
DR EMBL; AB062468; BAB58885.1; JOINED.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS00186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolyase; Serine protease.  
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 40.8%; Score 78; DB 6; Length 461;  
Best Local Similarity 41.2%; Pred. No. 6.4e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;  
Qy 11 GSLRXCKXKXCSFXAXEIKFDXAKTKLFWISY 44  
Db 58 GNLERECMEKCSFEAREVENTERTTEFWKQY 91

RESULT 15  
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AC Q95ND6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Coagulation factor XI.  
GN F9.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=505;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and  
RT chimpanzees.";  
RL Genes Genet. Syst. 0:0-0(2001).  
DR EMBL; AB062471; BAB58886.1; JOINED.  
DR EMBL; AB062459; BAB58886.1; JOINED.  
DR EMBL; AB062461; BAB58886.1; JOINED.  
DR EMBL; AB062463; BAB58886.1; JOINED.  
DR EMBL; AB062465; BAB58886.1; JOINED.  
DR EMBL; AB062467; BAB58886.1; JOINED.  
DR EMBL; AB062469; BAB58886.1; JOINED.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF\_2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolyase; Serine protease.  
SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 40.8%; Score 78; DB 6; Length 461;  
Best Local Similarity 41.2%; Pred. No. 6.4e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;  
Qy 11 GSLRXCKXKXCSFXAXEIKFDXAKTKLFWISY 44  
Db 58 GNLERECMEKCSFEAREVENTERTTEFWKQY 91

Search completed: March 19, 2003, 15:13:29  
Job time : 47.3125 secs

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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10ASP28GLU  
Perfect score: 191  
Sequence: 1 ANAFLXLRDGLRXCKXX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
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| 1          | 166   | 86.9        | 44     | 3  | US-08-955-636-27 |
| 2          | 162   | 84.8        | 44     | 3  | US-08-955-636-26 |
| 3          | 159   | 83.2        | 44     | 3  | US-08-955-636-3  |
| 4          | 159   | 83.2        | 406    | 1  | US-08-293-778-24 |
| 5          | 159   | 83.2        | 406    | 1  | US-08-295-411-5  |
| 6          | 159   | 83.2        | 406    | 1  | US-08-955-471-5  |
| 7          | 159   | 83.2        | 406    | 5  | PCT-US92-10242-5 |
| 8          | 159   | 83.2        | 444    | 1  | US-08-475-845-2  |
| 9          | 159   | 83.2        | 444    | 2  | US-08-337-690-2  |
| 10         | 159   | 83.2        | 444    | 2  | US-08-660-289-2  |
| 11         | 159   | 83.2        | 444    | 2  | US-08-537-807-2  |
| 12         | 159   | 83.2        | 444    | 2  | US-08-871-003-2  |
| 13         | 159   | 83.2        | 444    | 2  | US-08-464-233-2  |
| 14         | 159   | 83.2        | 444    | 4  | US-09-189-607-2  |
| 15         | 159   | 83.2        | 444    | 4  | US-09-378-907-2  |
| 16         | 159   | 83.2        | 444    | 5  | PCT-US94-05779-2 |
| 17         | 159   | 83.2        | 466    | 1  | US-07-862-202A-4 |
| 18         | 159   | 83.2        | 466    | 1  | US-08-021-615A-4 |
| 19         | 159   | 83.2        | 466    | 4  | US-08-321-777-4  |
| 20         | 159   | 83.2        | 466    | 4  | US-09-009-217-14 |
| 21         | 159   | 83.2        | 466    | 4  | US-09-009-656-14 |
| 22         | 159   | 83.2        | 466    | 5  | PCT-US93-04493-4 |
| 23         | 156   | 81.7        | 44     | 3  | US-08-955-636-28 |
| 24         | 156   | 81.7        | 44     | 3  | US-08-955-636-30 |
| 25         | 153   | 80.1        | 44     | 3  | US-08-955-636-29 |
| 26         | 144   | 75.4        | 41     | 1  | US-08-229-280-4  |
| 27         | 123   | 64.4        | 44     | 3  | US-08-955-636-4  |

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| 28 | 106 | 55.5 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appl1  |
| 29 | 106 | 55.5 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appl1  |
| 30 | 106 | 55.5 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appl1  |
| 31 | 106 | 55.5 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appl1  |
| 32 | 106 | 55.5 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appl1  |
| 33 | 106 | 55.5 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appl1  |
| 34 | 106 | 55.5 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appl1  |
| 35 | 98  | 51.3 | 44  | 3 | US-08-955-636-35 | Sequence 35, Appl1 |
| 36 | 97  | 50.8 | 44  | 3 | US-08-955-636-18 | Sequence 18, Appl1 |
| 37 | 97  | 50.8 | 448 | 1 | US-08-295-411-3  | Sequence 3, Appl1  |
| 38 | 97  | 50.8 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appl1  |
| 39 | 97  | 50.8 | 448 | 2 | PCT-US92-1006-1  | Sequence 1, Appl1  |
| 40 | 97  | 50.8 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appl1  |
| 41 | 97  | 50.8 | 487 | 1 | US-08-469-486-53 | Sequence 53, Appl1 |
| 42 | 97  | 50.8 | 487 | 2 | US-08-469-658-53 | Sequence 53, Appl1 |
| 43 | 97  | 50.8 | 492 | 1 | US-08-469-486-2  | Sequence 2, Appl1  |
| 44 | 97  | 50.8 | 492 | 2 | US-08-469-658-2  | Sequence 2, Appl1  |
| 45 | 96  | 50.3 | 44  | 3 | US-08-955-636-22 | Sequence 22, Appl1 |

## ALIGNMENTS

RESULT 1  
US-08-955-636-27  
; Sequence 27, Application US/08955636A  
; Patent No. 6017882  
; GENERAL INFORMATION:  
; APPLICANT: Neissestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955,636A  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-27

Query Match 86.9%; Score 166; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 2.8e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXLRDGLRXCKXXQCSFXAEXIFKDXRTKLFWISY 44  
DB 1 ANAFLXLRDGLRXCKXXQCSFXAEXIFKDXRTKLFWISY 44

RESULT 2  
US-08-955-636-26  
; Sequence 26, Application US/08955636A  
; Patent No. 6017882  
; GENERAL INFORMATION:  
; APPLICANT: Neissestuen, Gary  
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
; FILE REFERENCE: 09531/002001  
; CURRENT APPLICATION NUMBER: US/08/955,636A  
; CURRENT FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-26

Query Match 84.8%; Score 162; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 1.2e-19;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
Db 1 ANAFLXLRDGLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44

## RESULT 3

US-08-955-636-3  
Sequence 3, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-3

Query Match 83.2%; Score 159; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 3.8e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
Db 1 ANAFLXLRDGLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44

## RESULT 4

US-08-293-778-24  
Sequence 24, Application US/08293778  
Patent No. 5580560  
GENERAL INFORMATION:  
APPLICANT: Nicolaissen, Elise M.  
APPLICANT: Bjorn, Soren E.  
APPLICANT: Wiberg, Finn C.  
APPLICANT: Woodbury, Richard  
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,778  
FILING DATE:  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/104,509  
FILING DATE:  
APPLICATION NUMBER: DK 3235/87  
FILING DATE: 25-JUN-1987  
PRIOR APPLICATION DATA: 149  
APPLICATION NUMBER: US 07/434,149  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129,224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 83.2%; Score 159; DB 1; Length 406;  
Best Local Similarity 72.7%; Pred. No. 3.8e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44  
Db 1 ANAFLXLRDGLXRXCKXQCSFYXAEIIFKDAKRTKLFWISY 44

## RESULT 5

US-08-295-411-5  
Sequence 5, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Office of Patent Counsel, The Scripps  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas



```

;
;   REGISTRATION NUMBER: 34,163
;   REFERENCE/DOCKET NUMBER: TSRI263.0C1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-554-2937
;   TELEFAX: 619-554-6312
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 406 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..152
;   OTHER INFORMATION: /note= "Factor VII Light Chain"
;
;   LOCATION: 153..406
;   OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
US-08-295-411-5

Query Match      83.2%; Score 159; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 3.8e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLKRXCKXKCCFXKXEXIFKDXRRTKLFMISY 44
Db 1 ANAFLEELRPSGLERCKEQQCFEAREIFKDAERTKLFMISY 44

RESULT 6
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffith, John H.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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;
;   LENGTH: 406 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Region
;   LOCATION: 1..152
;   OTHER INFORMATION: /note= "Factor VII Light Chain"
;
;   LOCATION: 153..406
;   OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
US-08-955-471-5

Query Match      83.2%; Score 159; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 3.8e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLKRXCKXKCCFXKXEXIFKDXRRTKLFMISY 44
Db 1 ANAFLEELRPSGLERCKEQQCFEAREIFKDAERTKLFMISY 44

RESULT 7
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffith, John H.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
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OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match      83.2%; Score 159; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 3,8e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRDGLXRXCKXQCSFXAXEIPKDAKRTKLFWISY 44
Db 1 ANAFLEELRPGSLERECKEQCSEAEAREIFKDAERTKLFWISY 44

RESULT 8
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2

Query Match      83.2%; Score 159; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 4,2e-18;
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Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRDGLXRXCKXQCSFXAXEIPKDAKRTKLFWISY 44
Db 39 ANAFLEELRPGSLERECKEQCSEAEAREIFKDAERTKLFWISY 82

RESULT 9
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match      83.2%; Score 159; DB 2; Length 444;
Best Local Similarity 72.7%; Pred. No. 4,2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRDGLXRXCKXQCSFXAXEIPKDAKRTKLFWISY 44
Db 39 ANAFLEELRPGSLERECKEQCSEAEAREIFKDAERTKLFWISY 82

RESULT 10
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
```

APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Knourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,289  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,845  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-660-289-2

Query Match 83.2%; Score 159; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.2e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFILXLRDGLRQXKXQCSFXXAEXIFKDXARTKLFWISY 44  
DB 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 11  
US-08-537-807-2  
Sequence 2, Application US/08537807  
Patent No. 5861374  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/537,807  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05779  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 08/065,725  
FILING DATE: 21-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 83.2%; Score 159; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.2e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFILXLRDGLRQXKXQCSFXXAEXIFKDXARTKLFWISY 44  
DB 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5997864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 83.2%; Score 159; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.2e-16;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXRXCKXOCSPFXAEXIFKDAKRTLFWISY 44  
39 ANAFLELRPGSLERCKEEOCSFEAREIFKDAKRTLFWISY 82

RESULT 13  
US-08-464-233-2  
Sequence 2, Application US/08464233  
Patent No. 6039944  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,233  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-233-2

Query Match 83.2%; Score 159; DB 3; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.2e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRDGLXRXCKXOCSPFXAEXIFKDAKRTLFWISY 44  
39 ANAFLELRPGSLERCKEEOCSFEAREIFKDAKRTLFWISY 82

Db 39 ANAFLELRPGSLERCKEEOCSFEAREIFKDAKRTLFWISY 82

RESULT 14  
US-09-189-607-2  
Sequence 2, Application US/09189607  
Patent No. 6168789  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,607  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/660,289  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-189-607-2

Query Match 83.2%; Score 159; DB 4; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.2e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXRXCKXOCSPFXAEXIFKDAKRTLFWISY 44  
39 ANAFLELRPGSLERCKEEOCSFEAREIFKDAKRTLFWISY 82

RESULT 15  
US-09-378-907-2  
Sequence 2, Application US/09378907  
Patent No. 6183743

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/
/  GENERAL INFORMATION:
/  APPLICANT: Hart, Charles B.
/  APPLICANT: Petersen, Lars C.
/  APPLICANT: Hedner, Ulla
/  APPLICANT: Rasmussen, Mirella E.
/  TITLE OF INVENTION: Modified Factor VII
/  NUMBER OF SEQUENCES: 4
/  CORRESPONDENCE ADDRESS:
/  ADDRESSEE: ZymoGenetics, Inc.
/  STREET: 1201 Eastlake Avenue East
/  CITY: Seattle
/  STATE: WA
/  COUNTRY: USA
/  ZIP: 98102
/  COMPUTER READABLE FORM:
/  MEDIUM TYPE: Floppy disk
/  COMPUTER: IBM PC compatible
/  OPERATING SYSTEM: PC-DOS/MS-DOS
/  SOFTWARE: Patent In Release #1.24
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER: US/09/378,907
/  FILING DATE:
/  CLASSIFICATION:
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: 08/871,003
/  FILING DATE:
/  CLASSIFICATION:
/  ATTORNEY/AGENT INFORMATION:
/  NAME: Sawislak, Deborah A
/  REGISTRATION NUMBER: 37,438
/  REFERENCE/DOCKET NUMBER: 90-07C7
/  INFORMATION FOR SEQ. ID NO: 2:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH: 444 amino acids
/  TYPE: amino acid
/  TOPOLOGY: linear
/  MOLECULE TYPE: protein
/  US-09-378-907-2

Query Match      83.2%; Score 159; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 4.2e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1  ANAFIXXLRDGLXRXGKXXGCSFXAXEXIFKDXRTKLFWISY 44
Db      39  ANAFLEELRPGSLERCKEQCSFEARELIFKDXRTKLFWISY 82
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Search completed: March 19, 2003, 15:16:13  
Job time : 10.75 secs

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GenCore version 5.1.4 p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds  
(without alignments)  
280.876 Million cell updates/sec

Title: 10ASP28GLU  
Perfect score: 191  
Sequence: 1 ANAFLLXLRDGLRCKKX.....XXAEXIFKDXRKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 159   | 83.2        | 406    | 9     | US-10-109-498-1    |
| 2          | 96    | 50.3        | 419    | 9     | US-10-182-263-6    |
| 3          | 95    | 49.7        | 419    | 9     | US-10-182-263-3    |
| 4          | 95    | 49.7        | 419    | 9     | US-10-182-263-4    |
| 5          | 95    | 49.7        | 419    | 9     | US-10-182-263-5    |
| 6          | 84    | 44.0        | 419    | 9     | US-10-182-263-1    |
| 7          | 84    | 44.0        | 419    | 9     | US-09-978-917A-4   |
| 8          | 84    | 44.0        | 461    | 9     | US-10-182-263-2    |
| 9          | 84    | 44.0        | 461    | 9     | US-09-978-917A-2   |
| 10         | 78    | 40.8        | 415    | 10    | US-09-118-748-2    |
| 11         | 78    | 40.8        | 461    | 9     | US-10-132-829-5    |
| 12         | 78    | 40.8        | 461    | 10    | US-09-884-901-3    |
| 13         | 69.5  | 36.4        | 96     | 9     | US-09-759-1308-313 |
| 14         | 69.5  | 36.4        | 209    | 9     | US-09-759-1308-310 |
| 15         | 69.5  | 36.4        | 226    | 9     | US-09-759-1308-310 |
| 16         | 54.5  | 28.5        | 95     | 9     | US-09-759-1308-356 |
| 17         | 54.5  | 28.5        | 208    | 9     | US-09-759-1308-355 |
| 18         | 54.5  | 28.5        | 225    | 9     | US-09-759-1308-353 |
| 19         | 49    | 25.7        | 273    | 9     | US-09-764-868-968  |

|    |      |      |      |    |                     |                   |
|----|------|------|------|----|---------------------|-------------------|
| 20 | 47   | 24.6 | 1266 | 9  | US-09-931-969A-2    | Sequence 2, Appl  |
| 21 | 47   | 24.6 | 1266 | 9  | US-10-079-699-2     | Sequence 2, Appl  |
| 22 | 47   | 24.6 | 1366 | 10 | US-09-757-781-63    | Sequence 63, Appl |
| 23 | 47   | 24.6 | 1356 | 10 | US-09-757-781-2     | Sequence 2, Appl  |
| 24 | 44   | 23.0 | 744  | 10 | US-09-862-179A-1    | Sequence 1, Appl  |
| 25 | 44   | 23.0 | 1337 | 10 | US-09-757-781-62    | Sequence 62, Appl |
| 26 | 42   | 22.0 | 608  | 10 | US-09-908-664-5     | Sequence 5, Appl  |
| 27 | 42   | 22.0 | 1237 | 9  | US-10-024-623-32    | Sequence 32, Appl |
| 28 | 42   | 22.0 | 1258 | 10 | US-09-922-543-1     | Sequence 12, Appl |
| 29 | 42   | 22.0 | 1274 | 10 | US-09-746-491-12    | Sequence 12, Appl |
| 30 | 41.5 | 21.7 | 440  | 9  | US-09-910-186A-8    | Sequence 8, Appl  |
| 31 | 41   | 21.5 | 88   | 10 | US-09-811-284-194   | Sequence 194, App |
| 32 | 41   | 21.5 | 447  | 10 | US-09-815-242-13490 | Sequence 13490, A |
| 33 | 41   | 21.5 | 447  | 10 | US-09-815-242-13612 | Sequence 13612, A |
| 34 | 41   | 21.5 | 447  | 10 | US-09-735-564-2     | Sequence 2, Appl  |
| 35 | 41   | 21.5 | 729  | 9  | US-10-145-396-11    | Sequence 11, Appl |
| 36 | 40.5 | 21.2 | 1149 | 9  | US-09-965-528-5     | Sequence 5, Appl  |
| 37 | 39   | 20.4 | 873  | 9  | US-10-200-154-2     | Sequence 2, Appl  |
| 38 | 39   | 20.4 | 873  | 10 | US-09-954-043-2     | Sequence 2, Appl  |
| 39 | 38.5 | 20.2 | 49   | 10 | US-09-764-864-1054  | Sequence 1054, Ap |
| 40 | 38.5 | 20.2 | 348  | 10 | US-09-982-610-18    | Sequence 18, Appl |
| 41 | 38.5 | 20.2 | 1298 | 10 | US-09-982-610-33    | Sequence 33, Appl |
| 42 | 38.5 | 20.2 | 1363 | 9  | US-09-375-248-2     | Sequence 2, Appl  |
| 43 | 38.5 | 20.2 | 1363 | 9  | US-09-375-248-19    | Sequence 19, Appl |
| 44 | 38   | 19.9 | 47   | 10 | US-09-739-254-109   | Sequence 109, App |
| 45 | 38   | 19.9 | 47   | 10 | US-09-904-615-109   | Sequence 109, App |

#### ALIGNMENTS

RESULT 1  
US-10-109-498-1  
; Sequence 1, Application US/10109498  
; Publication No. US20030044908A1  
; GENERAL INFORMATION:  
; APPLICANT: Persson, Egon  
; TITLE OF INVENTION: Coagulation Factor VII Derivatives  
; FILE REFERENCE: 6286.200-US  
; CURRENT APPLICATION NUMBER: US/10/109,498  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/281,261  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: PA 2001 00477  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(406)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
; US-10-109-498-1

Query Match 83.2%; Score 159, DB 9, Length 406;  
Best Local Similarity 95.5%; Pred. No. 1,4e-20;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLRCKKXQCSFXAEXIFKDXRKLFWISY 44  
Db 1 ANAFLLXLRDGLRCKKXQCSFXAEXIFKDXRKLFWISY 44

RESULT 2  
US-10-182-263-6  
; Sequence 6, Application US/10182263  
; Publication NO. US2003002354A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlitz, Bruce E  
; APPLICANT: Jones, Bryan E

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          50.3%; Score 96; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 3.2e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFIXLRDGLKRXCKXOCSEFXAEXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          49.7%; Score 95; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 4.8e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFIXLRDGLKRXCKXOCSEFXAEXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          49.7%; Score 95; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 4.8e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFIXLRDGLKRXCKXOCSEFXAEXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          49.7%; Score 95; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 4.8e-09;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFIXLRDGLKRXCKXOCSEFXAEXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLERECIEICDFEAKEIFEDVDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-182-263-1

Query Match 44.0%; Score 84; DB 9; Length 419;  
Best Local Similarity 43.9%; Pred. No. 4.6e-07;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKXQCSFXAXEIXFKDAXRTKLFW 41  
Db 1 ANSFLELRHSLERECIEICDFEAKEIFQNVDTLAFW 41

RESULT 7

US-09-978-917A-4  
Sequence 4, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219us310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978,917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-917A-4

Query Match 44.0%; Score 84; DB 9; Length 419;  
Best Local Similarity 43.9%; Pred. No. 4.6e-07;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKXQCSFXAXEIXFKDAXRTKLFW 41  
Db 1 ANSFLELRHSLERECIEICDFEAKEIFQNVDTLAFW 41

RESULT 8

US-10-182-263-2  
Sequence 2, Application US/10182263  
Publication No. US20030022354A1

GENERAL INFORMATION:  
APPLICANT: Getlitz, Bruce E  
APPLICANT: Jones, Bryan E  
APPLICANT: Grinnell, Brian W  
TITLE OF INVENTION: PROTEIN C DERIVATIVES  
FILE REFERENCE: X-13611  
CURRENT APPLICATION NUMBER: US/10/182,263  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: 60/181948  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: 60/189199  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-182-263-2

Query Match 44.0%; Score 84; DB 9; Length 461;  
Best Local Similarity 43.9%; Pred. No. 5.1e-07;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKXQCSFXAXEIXFKDAXRTKLFW 41  
Db 43 ANSFLELRHSLERECIEICDFEAKEIFQNVDTLAFW 83

RESULT 9

US-09-978-917A-2  
Sequence 2, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219us310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978,917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(42)  
FEATURE:  
NAME/KEY: CHAIN  
LOCATION: (43)...(461)  
US-09-978-917A-2

Query Match 44.0%; Score 84; DB 9; Length 461;  
Best Local Similarity 43.9%; Pred. No. 5.1e-07;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKXQCSFXAXEIXFKDAXRTKLFW 41  
Db 43 ANSFLELRHSLERECIEICDFEAKEIFQNVDTLAFW 83

RESULT 10

US-09-118-748-2  
Sequence 2, Application US/09118748A  
Patent No. US20020031799A1

GENERAL INFORMATION:  
APPLICANT: Staaford, Darrel W.  
APPLICANT: Chang, Jinli  
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting  
FILE REFERENCE: 5470-183  
CURRENT APPLICATION NUMBER: US/09/118,748A  
CURRENT FILING DATE: 1998-07-17  
EARLIER APPLICATION NUMBER: 60/053,571  
EARLIER FILING DATE: 1997-07-21  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-118-748-2

Query Match 40.8%; Score 78; DB 10; Length 415;  
Best Local Similarity 41.2%; Pred. No. 5.4e-06;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLRXCKXKXQCSFXAXEIXFKDAXRTKLFWISY 44  
Db 12 GNLRECEMEKCSFEARVFEVTERTTTFWKOY 45

RESULT 11

US-10-132-829-5  
Sequence 5, Application US/10132829  
Publication No. US20030044982A1

GENERAL INFORMATION:  
APPLICANT: Chien, Kenneth R  
APPLICANT: Hoshijima, Masahiko  
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII  
FILE REFERENCE: 6627-PAL170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          40.8%; Score 78; DB 9; Length 461;
Best Local Similarity 41.2%; Pred. No. 6.1e-06;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLRXCKXXCSEFXAXEIPFDXRTKLFWISY 44
DB 58 GNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US2002007678A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-901-3

Query Match          40.8%; Score 78; DB 10; Length 461;
Best Local Similarity 41.2%; Pred. No. 6.1e-06;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLRXCKXXCSEFXAXEIPFDXRTKLFWISY 44
DB 58 GNLERECMEKCSFEAREVFENTERTEFWKQY 91

RESULT 13
US-09-759-1308-313
; Sequence 313, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-1308-313

Query Match          36.4%; Score 69.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 3.7e-05;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY 2 NAF-LXXLRDGLRXCKXXCSEFXAXEIPFDXRTKLFWISY 44
DB 36 NRPDLFLTPGNLERECMEKCSFEAREVFENTERTEFWKQY 79

RESULT 14
US-09-759-1308-312
; Sequence 312, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 312  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-130B-312

Query Match 36.4%; Score 69.5; DB 9; Length 209;  
Best Local Similarity 36.4%; Pred. No. 8.7e-05;  
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY 2 NAF-LXXLRDGSIXRXCXXQCSFXAXEXIFKDXRTKLFWISY 44  
DB 36 NRPDLLEFTPGNLERECNEBELCNYEARREIFVDEDKTIAFWQEX 79

RESULT 15  
US-09-759-130B-310  
Sequence 310, Application US/09759130B  
Publication No. US2003002279A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: McCarthy, Sean A  
APPLICANT: Fraser, Christopher C  
APPLICANT: Sharp, John D  
APPLICANT: Barnes, Thomas S  
APPLICANT: Kirst, Susan J  
APPLICANT: Mackay, Charles R  
APPLICANT: Myers, Paul S  
APPLICANT: Leiby, Kevin R  
APPLICANT: Wrighton, Nicolas  
APPLICANT: Goodearl, Andrew  
APPLICANT: Holtzman, Douglas A  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USES.  
FILE REFERENCE: MP100-535OMNIM  
CURRENT APPLICATION NUMBER: US/09/759,130B  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: US 09/479,249  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/559,497  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 09/578,063  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/333,159  
PRIOR FILING DATE: 1999-06-14  
PRIOR APPLICATION NUMBER: US 09/596,194  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/342,364  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 310  
LENGTH: 226  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-759-130B-310

Query Match 36.4%; Score 69.5; DB 9; Length 226;  
Best Local Similarity 36.4%; Pred. No. 9.4e-05;  
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY 2 NAF-LXXLRDGSIXRXCXXQCSFXAXEXIFKDXRTKLFWISY 44  
DB 53 NRPDLLEFTPGNLERECNEBELCNYEARREIFVDEDKTIAFWQEX 96

Search completed: March 20, 2003, 13:30:10  
Job time : 9.375 secs

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DR WPI; 1999-288309/24.  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 85.9%; Score 165; DB 20; Length 44;  
Best Local Similarity 97.7%; Pred. No. 9.3e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFLXXLRDGLRXCKXXQCSFXXAFXIFDAXRTKLFWISY 44  
DB 1 ANAFLXXLRDGLRXCKXXQCSFXXAFXIFDAXRTKLFWISY 44  
RESULT 2  
AAV18311  
ID AAV18311 standard; peptide; 44 AA.  
XX  
AC AAV18311;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
XX therapy.  
XX  
KM Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
XX  
XX  
XX W09920767-A1.  
XX  
XX 29-APR-1999.  
XX  
XX 20-OCT-1998; 98WO-US22152.  
XX  
XX 23-OCT-1997; 97US-0955636.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX  
XX Nelsestuen GL;  
XX  
XX WPI; 1999-288309/24.  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;

CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 84.9%; Score 163; DB 20; Length 44;  
Best Local Similarity 97.7%; Pred. No. 2e-19;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFLXXLRDGLRXCKXXQCSFXXAFXIFDAXRTKLFWISY 44  
DB 1 ANAFLXXLRDGLRXCKXXQCSFXXAFXIFDAXRTKLFWISY 44  
RESULT 3  
AAV18310  
ID AAV18310 standard; peptide; 44 AA.  
XX  
AC AAV18310;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
XX therapy.  
XX  
KM Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
XX  
XX  
XX W09920767-A1.  
XX  
XX 29-APR-1999.  
XX  
XX 20-OCT-1998; 98WO-US22152.  
XX  
XX 23-OCT-1997; 97US-0955636.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX  
XX Nelsestuen GL;  
XX  
XX WPI; 1999-288309/24.  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 82.8%; Score 159; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 8.9e-19;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 ANAFLXXLRDGLRXCKXXQCSFXXAFXIFDAXRTKLFWISY 44  
DB 1 ANAFLXXLRDGLRXCKXXQCSFXXAFXIFDAXRTKLFWISY 44

```

RESULT 4
AAV18305
ID AAV18305 standard; peptide: 44 AA.
XX
AC AAV18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KM GLA domain; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX W09920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX
XX Sequence 44 AA;
XX
XX Query Match 81.2%; Score 156; DB 20; Length 44;
XX Best Local Similarity 95.5%; Pred. No. 2.8e-18;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1 ANAFLXLRDGLXKXCKXQCSFYXAFIFDXARTLFWISY 44
XX |||||
XX 1 ANAFLXLRPGSLXRXCKXQCSFYXARXIFDXARTLFWISY 44
XX |||||
XX
XX
XX RESULT 5
XX AAB36395
XX ID AAB36395 standard; peptide: 44 AA.
XX
XX AAB36395;
XX
XX 27-FEB-2001 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
XX gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
XX factor X; prothrombin; enhanced membrane binding affinity;
XX

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```

XX clot formation; thrombolytic; haemostatic; bleeding disorder;
XX thrombosis; clotting disorder; haemophilia A; haemophilia B;
XX liver disease.
XX
XX Homo sapiens.
XX
XX W020066753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
XX gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity.
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot
XX formation in a mammal, a factor VII or factor IX containing a modified
XX GLA domain is useful for increasing clot formation and for treating a
XX bleeding disorder, including thrombosis and clotting disorders such as
XX haemophilia A, haemophilia B and liver disease. The present sequence
XX represents a wild type human factor VII GLA domain sequence, given in
XX the exemplification of the present invention.
XX
XX
XX Sequence 44 AA;
XX
XX Query Match 81.2%; Score 156; DB 22; Length 44;
XX Best Local Similarity 95.5%; Pred. No. 2.8e-18;
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1 ANAFLXLRDGLXKXCKXQCSFYXAFIFDXARTLFWISY 44
XX |||||
XX 1 ANAFLXLRPGSLXRXCKXQCSFYXARXIFDXARTLFWISY 44
XX |||||
XX
XX
XX RESULT 6
XX AAB84870
XX ID AAB84870 standard; Protein: 401 AA.
XX
XX AAB84870;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-31).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 311..317
XX /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX

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```
PN JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX MPI: 2001-310677/33.
XX
XX N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX PS Claim 14; Page 20-21; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX SQ Sequence 401 AA;
XX
XX Query Match 81.2%; Score 156; DB 22; Length 401;
XX Best Local Similarity 72.7%; Pred. No. 2.6e-17;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 ANAFLLXLRDGSIXRCKXQCSFXXAFXIFDAXRTKLFWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 ANAFLEELRPGSLERCKEQCSFEARARIFDAXRTKLFWISY 44
XX
XX RESULT 7
XX AAB84871
XX ID AAB84871 standard; Protein; 401 AA.
XX
XX AC AAB84871;
XX
XX DT 31-JUL-2001 (first entry)
XX
XX DE Mutant blood coagulant factor VII (FVII-39).
XX
XX KM Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 235..239
XX FT /note="Wild-type Val-Pro-Gly-Thr-Thr substituted by
XX FT Asp-Arg-Lys-Thr-Leu"
XX FT Misc-difference 311..317
XX FT /note="Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX PN JP2001061479-A.
XX
XX PD 13-MAR-2001.
XX
XX PF 24-AUG-1999; 99JP-0237610.
XX
XX PR 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX MPI: 2001-310677/33.
XX
XX N-PSDB; AAH19464.
XX
XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
```

```
XX
XX PS Claim 16; Page 23-24; 29pp; Japanese.
XX
XX CC The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX SQ Sequence 401 AA;
XX
XX Query Match 81.2%; Score 156; DB 22; Length 401;
XX Best Local Similarity 72.7%; Pred. No. 2.6e-17;
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 ANAFLLXLRDGSIXRCKXQCSFXXAFXIFDAXRTKLFWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 ANAFLEELRPGSLERCKEQCSFEARARIFDAXRTKLFWISY 44
XX
XX Db 1 ANAFLEELRPGSLERCKEQCSFEARARIFDAXRTKLFWISY 44
XX
XX RESULT 8
XX AAR35764
XX ID AAR35764 standard; protein; 406 AA.
XX
XX AC AAR35764;
XX
XX DT 24-SEP-1993 (first entry)
XX
XX DE Factor VII (VII).
XX
XX KM PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;
XX exosite; catalytic activity.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Region 1..152
XX FT /note="Factor VII light chain"
XX FT Region 153..406
XX FT /note="Factor VII heavy chain"
XX FT Peptide 374..388
XX FT /note="exosite 1"
XX FT Peptide 290..310
XX FT /note="exosite 2"
XX FT Peptide 290..310
XX FT /note="pref. PC polypeptide; claim 2, page 136"
XX FT Peptide 374..388
XX FT /note="pref. PC polypeptide; claim 2, page 136"
XX FT Peptide 289..304
XX FT /note="pref. PC polypeptide; claim 4, page 137"
XX FT Peptide 290..304
XX FT /note="pref. PC polypeptide; claim 4, page 137"
XX FT Peptide 245..266
XX FT /note="claim 9, page 138-139 describes an antibody
XX FT that reacts with Factor VII; fragments
XX FT 289-304, 290-304, 290-310, 374-388 and
XX FT 400-414 but not with fragment 245-266"
XX
XX PN WO9309804-A.
XX
XX PD 27-MAY-1993.
XX
XX PF 18-NOV-1992; 92WO-US10242.
XX
XX PR 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Griffiin JH, Mesters RM;
XX
XX MPI; 1993-182244/22.
XX
XX PT Serine protease derived-polypeptide(s) and anti-peptide
```



FT /label= OTHER

CC Lys341 by an amino acid that provides a proteolytically more stable



XX SQ Sequence 406 AA; 81.2%; Score 156; DB 18; Length 406;  
 Query Match Best Local Similarity 72.7%; Pred. No. 2.7e-17;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 Oy 1 ANAFLLXLRDGLRXCKXOCSPFXAFIFKDAKRTLFWISY 44  
 1 ANAFLEELRPGSLRCKEBCQSFEEAREIFKDAKRTLFWISY 44  
 Db 1 ANAFLEELRPGSLRCKEBCQSFEEAREIFKDAKRTLFWISY 44

RESULT 11  
 AAU77745 ID AAU77745 standard; protein: 406 AA.  
 AAU77745;  
 05-JUN-2002 (first entry)  
 Human factor VIIa active site mutant.  
 DE Factor VIIa; human; shock heat treatment; protein stability;  
 KM protein manufacture; protein conformation; mutant; mutain.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Active-site 193 /note= "Member of the factor VIIa catalytic triad"  
 FT Active-site 242 /note= "Member of the factor VIIa catalytic triad"  
 FT Active-site 344 /note= "Member of the factor VIIa catalytic triad"  
 FT Misc-difference 344 /label= Gly, Met, Thr  
 FT /note= "Preferably Ala. Wild type Ser"  
 FT  
 XX WO200177141-A1.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-DK00234.  
 XX 06-APR-2000; 2000DK-0000573.  
 XX 17-APR-2000; 2000US-197650P.  
 XX (NOVO ) NOVO NORDISK AS.  
 XX Mathiesen F;  
 XX WPI; 2001-657162/75.  
 XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition  
 PT involves a shock heat treatment  
 PS Disclosure; Page -; 22pp; English.  
 XX The invention describes a method of stabilising a polypeptide involving  
 CC shock heat treatment of the polypeptide. The method is useful in a  
 CC pharmaceutical composition, in the industrial or large scale method of  
 CC manufacturing a polypeptide, also as a unit operation during preparation,  
 CC purification, recovery and/or formulation of polypeptides. The shock heat  
 CC treatment improves the protein stability without substantial loss of  
 CC biological activity. The method can be applied to change polypeptide  
 CC conformation in a very fast and non-invasive manner. The polypeptide  
 CC formed is stable. The method is also useful for decreasing the  
 CC association of the polypeptide. This sequence represents a modified  
 CC human factor VIIa protein, mutated at the catalytic site, described  
 CC in the invention.  
 CC Note: This sequence does not appear in the specification but has  
 CC been obtained using information given in the invention.

XX SQ Sequence 406 AA; 81.2%; Score 156; DB 22; Length 406;  
 Query Match Best Local Similarity 72.7%; Pred. No. 2.7e-17;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 Oy 1 ANAFLLXLRDGLRXCKXOCSPFXAFIFKDAKRTLFWISY 44  
 1 ANAFLEELRPGSLRCKEBCQSFEEAREIFKDAKRTLFWISY 44  
 Db 1 ANAFLEELRPGSLRCKEBCQSFEEAREIFKDAKRTLFWISY 44

RESULT 12  
 AAM52171 ID AAM52171 standard; Protein: 406 AA.  
 AAM52171;  
 07-FEB-2002 (first entry)  
 Human FVII SEQ ID NO 1.  
 DE Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
 KM cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease;  
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Misc-difference 6 /label= Glu, OTHER  
 FT Misc-difference 6 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 7 /label= Glu, OTHER  
 FT Misc-difference 14 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 14 /label= Glu, OTHER  
 FT Misc-difference 16 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 19 /label= Glu, OTHER  
 FT Misc-difference 19 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 20 /label= Glu, OTHER  
 FT Misc-difference 25 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 25 /label= Glu, OTHER  
 FT Misc-difference 26 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 29 /note= "OTHER = gamma carboxylutamic acid"  
 FT Misc-difference 35 /label= Glu, OTHER  
 FT Misc-difference 35 /note= "OTHER = gamma carboxylutamic acid"  
 FT Modified-site 52 /label= Glu, OTHER  
 FT Modified-site 60 /note= "O-glycosylated"  
 FT Modified-site 145 /note= "O-glycosylated"  
 FT Cleavage-site 152..153 /note= "N-glycosylated"  
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen  
 FT to an activated form, comprising two chains  
 FT linked by a single disulphide bridge"  
 FT Modified-site 322 /note= "N-glycosylated"  
 FT  
 XX WO200158935-A2.

XX 16-AUG-2001.  
PD  
XX  
XX 12-FEB-2001; 2001WO-DK00094.  
PF  
XX  
XX 11-FEB-2000; 2000DK-0000218.  
PR  
XX 18-OCT-2000; 2000DK-0001558.  
PR  
XX (MAXY-) MAXYGEN APS.  
PA  
XX  
XX Andersen KV, Pedersen AH, Bornaes C;  
PI  
XX WPI; 2001-581807/65.  
DR  
XX N-PSDB; AA19982.  
DR  
XX  
XX New conjugate, useful for treating Factor VIIa related diseases or  
PT disorders such as haemophilia, liver disease, myocardial infarction and  
PT deep-vein thrombosis, comprises non-polypeptide group covalently  
PT attached to polypeptide group -  
XX  
XX Claim 1; Page 81-83; 89pp; English.  
XX  
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.  
XX  
XX Sequence 406 AA;  
SQ  
Query Match 81.2%; Score 156; DB 22; Length 406;  
Best Local Similarity 95.5%; Pred. No. 2.7e-17;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 ANAFLXXLRDGSIXRXCKXXQCSFXXAFXIFKDXARTKLFWISY 44  
DB 1 ANAFLXXLRPGLRXCKXXQCSFXXARXIFKDXARTKLFWISY 44  
RESULT 13  
AAM52172  
ID AAM52172 standard; Protein; 406 AA.  
XX  
XX AAM52172;  
XX  
XX 07-FEB-2002 (first entry)  
DT  
XX  
XX Mammalian expressed human FVII SEQ ID NO 3.  
DE  
XX  
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;  
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 52  
FT /note= "O-glycosylated"  
FT 60  
FT /note= "O-glycosylated"  
FT Modified-site 145  
FT /note= "N-glycosylated"  
FT Cleavage-site 152..153

FT /note= "proteolytic cleavage site converting FVII zymogen  
FT to an activated form, comprising two chains  
FT linked by a single disulphide bridge"  
FT Modified-site 322  
FT /note= "N-glycosylated"  
PN W0200158935-A2.  
XX  
XX 16-AUG-2001.  
PD  
XX  
XX 12-FEB-2001; 2001WO-DK00094.  
PF  
XX  
XX 11-FEB-2000; 2000DK-0000218.  
PR  
XX 18-OCT-2000; 2000DK-0001558.  
PR  
XX (MAXY-) MAXYGEN APS.  
PA  
XX  
XX Andersen KV, Pedersen AH, Bornaes C;  
PI  
XX WPI; 2001-581807/65.  
DR  
XX N-PSDB; AA19983.  
DR  
XX  
XX New conjugate, useful for treating Factor VIIa related diseases or  
PT disorders such as haemophilia, liver disease, myocardial infarction and  
PT deep-vein thrombosis, comprises non-polypeptide group covalently  
PT attached to polypeptide group -  
XX  
XX Disclosure; Page 85-86; 89pp; English.  
XX  
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.  
XX  
XX Sequence 406 AA;  
SQ  
Query Match 81.2%; Score 156; DB 22; Length 406;  
Best Local Similarity 72.7%; Pred. No. 2.7e-17;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
OY 1 ANAFLXXLRDGSIXRXCKXXQCSFXXAFXIFKDXARTKLFWISY 44  
DB 1 ANAFLXELRPGSLERCKEQCSFEARIFKDXARTKLFWISY 44  
RESULT 14  
AAM52181  
ID AAM52181 standard; Protein; 406 AA.  
XX  
XX AAM52181;  
XX  
XX 07-FEB-2002 (first entry)  
DT  
XX  
XX Human FVII mutant T106N.  
DE  
XX  
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
KM cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;  
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;  
KM mutain.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
OS

|    |  |  |
|----|--|--|
| XX |  | Location/Qualifiers  |
| FH | Key  |  |
| FT | Misc-difference  | 6<br>/label= Glu, OTHER  |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 7<br>/label= Glu, OTHER  |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 14<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 16<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 19<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 20<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 25<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 26<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 29<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Misc-difference  | 35<br>/label= Glu, OTHER   |
| FT |  | /note= "OTHER = gamma carboxyglutamic acid"  |
| FT | Modified-site  | 52<br>/note= "O-glycosylated"  |
| FT |  | /note= "O-glycosylated"  |
| FT | Modified-site  | 60<br>/note= "O-glycosylated"  |
| FT |  | /note= "O-glycosylated"  |
| FT | Misc-difference  | 106<br>/note= "Wild-type Thr substituted by Asn"   |
| FT |  | /note= "N-glycosylated"  |
| FT | Modified-site  | 145<br>/note= "proteolytic cleavage site converting FVII zymogen<br>to an activated form, comprising two chains<br>linked by a single disulphide bridge" |
| FT | Cleavage-site  | 152, 153<br>/note= "N-glycosylated"  |
| FT |  | /note= "N-glycosylated"  |
| FN | WO200158935-A2.  |  |
| PD | 16-AUG-2001.   |  |
| PE | 12-FEB-2001; 2001WO-DK00094.   |  |
| PX | 11-FEB-2000; 2000DK-0000218.   |  |
| PR | 18-OCT-2000; 2000DK-0001558.   |  |
| PA | (MAXY-) MAXYGEN APS.   |  |
| PI | Anderseen KV, Pedersen AH, Bornaaes C;   |  |
| DR | WPI; 2001-581807/65.   |  |
| PT | New conjugate, useful for treating Factor VIIA related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis; comprises non-polypeptide group covalently attached to polypeptide group -  |  |
| PS | Example 3; Page -: 89pp; English.  |  |
| CC | The invention relates to novel Factor VII (FVII) or Factor VIIA (FVIIa) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIA (AAW52171) in that at |  |

| Query     | 1 ANAFIXLRDGLRXCKXCOCSPFXAXRFXDKMRTLFWISY 44                               | 81.2%; Score 156; DB 22; Length 406;            |
|-----------|--|---|
| Db        | 1 ANAFIXLRDGLRXCKXCOCSPFXAXRFXDKMRTLFWISY 44                               | Best Local Similarity 95.5%; Pred. No. 2,7e-17; |
|           | Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;                |   |
| RESULT 15 |  |   |
| AAM52182  |  |   |
| ID        | AAM52182 standard; Protein: 406 AA.  |   |
| XX        | AAM52182;  |   |
| XX        |  |   |
| DT        | 07-FEB-2002 (first entry)  |   |
| XX        |  |   |
| DE        | Human FVII mutant K143N/N145T.   |   |
| XX        |  |   |
| XX        | Factor VII; FVII; Factor VIIA; FVIIa; haemostatic; thrombolytic;           |   |
| KM        | cardiant; hepatocrotrophic; cerebroprotective; haemophilia; liver disease; |   |
| KW        | myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;    |   |
| KM        | mutin.   |   |
| XX        |  |   |
| OS        | Homo sapiens.  |   |
| OS        | Synthetic.   |   |
| XX        |  |   |
| XX        |  |   |
| FT        | Key  | location/Qualifiers                             |
| FT        | Misc-difference  | 6 /label= Glu, OTHER                            |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 7 /label= Glu, OTHER                            |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 14 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 16 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 19 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 20 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 25 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 26 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 29 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |
| FT        | Misc-difference  | 29 /label= Glu, OTHER                           |
| FT        |  | /note= "OTHER = gamma carboxyglutamic acid"     |



GenCore version 5.1.4.p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10ASP28PNE  
Perfect score: 192  
Sequence: 1 ANFLXLRDGLXRCCKX.....XXAFXPKDAXRTLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR 73:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 156   | 81.2        | 466    | 1 KFHU7  | coagulation factor  |
| 2          | 122   | 63.5        | 443    | 2 I46932 | coagulation factor  |
| 3          | 114   | 59.4        | 407    | 1 KFB07  | coagulation factor  |
| 4          | 97    | 50.5        | 461    | 1 JX0210 | protein C (activat  |
| 5          | 95    | 49.5        | 461    | 1 S18994 | protein C (activat  |
| 6          | 94    | 49.0        | 488    | 1 EXHU   | coagulation factor  |
| 7          | 94    | 49.0        | 492    | 1 EXBO   | coagulation factor  |
| 8          | 92    | 47.9        | 622    | 1 THHU   | thrombin (EC 3.4.2  |
| 9          | 88    | 45.8        | 456    | 1 KXBO   | protein C (activat  |
| 10         | 88    | 45.8        | 482    | 1 EXRT   | coagulation factor  |
| 11         | 88    | 45.8        | 617    | 2 S10511 | thrombin (EC 3.4.2  |
| 12         | 88    | 45.8        | 618    | 2 A35827 | thrombin (EC 3.4.2  |
| 13         | 84    | 43.8        | 475    | 1 EXCH   | coagulation factor  |
| 14         | 80    | 41.7        | 461    | 1 KXHU   | protein C (activat  |
| 15         | 78    | 40.6        | 416    | 1 KFB0   | coagulation factor  |
| 16         | 75    | 39.1        | 461    | 1 KFHU   | coagulation factor  |
| 17         | 72    | 37.5        | 625    | 1 TBBO   | thrombin (EC 3.4.2  |
| 18         | 70    | 36.5        | 452    | 1 A30351 | coagulation factor  |
| 19         | 70    | 36.5        | 459    | 2 U00419 | coagulation factor  |
| 20         | 62    | 32.3        | 642    | 2 S53433 | plasma protein S p  |
| 21         | 58    | 30.2        | 396    | 1 KXBOZ  | plasma protein Z -  |
| 22         | 58    | 30.2        | 675    | 1 KXBOS  | plasma protein S p  |
| 23         | 57    | 29.7        | 642    | 2 S53434 | plasma protein S p  |
| 24         | 57    | 29.7        | 646    | 2 KXKUS  | plasma protein S p  |
| 25         | 56    | 29.2        | 646    | 2 S38819 | plasma protein S -  |
| 26         | 55.5  | 28.9        | 576    | 2 G96763 | probable MAP kinase |
| 27         | 55    | 28.6        | 575    | 1 KXRTS  | plasma protein S p  |
| 28         | 53    | 27.6        | 422    | 1 KKHUZ  | plasma protein Z p  |
| 29         | 49.5  | 25.8        | 594    | 2 D64859 | probable MAP kinase |

|    |      |      |      |          |                     |
|----|------|------|------|----------|---------------------|
| 30 | 49.5 | 25.8 | 603  | 2 C96575 | probable MAP kinase |
| 31 | 48   | 25.0 | 673  | 2 A48089 | growth arrest-spec  |
| 32 | 48   | 25.0 | 673  | 1 KXMS   | plasma protein S p  |
| 33 | 46   | 24.0 | 674  | 2 I55476 | growth potentialin  |
| 34 | 46   | 24.0 | 678  | 2 B48089 | growth arrest-spec  |
| 35 | 45.5 | 23.7 | 83   | 2 T17839 | hypothetical prote  |
| 36 | 45   | 23.4 | 271  | 2 S66691 | probable membrane   |
| 37 | 45   | 23.4 | 879  | 2 S55864 | hypothetical prote  |
| 38 | 45   | 23.4 | 907  | 2 T15792 | hypothetical prote  |
| 39 | 45   | 23.4 | 1404 | 2 T06663 | DNA (cytosine-5')-  |
| 40 | 44.5 | 23.2 | 119  | 2 S28011 | outs protein - Ery  |
| 41 | 44.5 | 23.2 | 306  | 2 T49068 | protein kinase STY  |
| 42 | 44   | 22.9 | 1512 | 2 G85090 | hypothetical prote  |
| 43 | 43.5 | 22.7 | 639  | 2 C42049 | lismanolysin (EC    |
| 44 | 43   | 22.4 | 394  | 1 S30286 | tetracycline resis  |
| 45 | 43   | 22.4 | 440  | 2 C70198 | conserved hypothet  |

## ALIGNMENTS

### RESULT 1

KFHU7  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text\_change 08-Dec-2000  
C:Accession: A28332; A23819; A31166; B31186; S63524  
R/O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend  
A:Reference number: A28332; MUID:87260948; PMID:3037537  
A:Accession: A28332  
A:Molecule type: DNA  
A:Residues: 1-466 <OHA>  
A:Cross-references: GB:U02933; NID:G180333; PIDN:AAA51983.1; PID:G180334  
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A:Title: Characterization of a cDNA coding for human factor VII.  
A:Reference number: A23819; MUID:86205965; PMID:3486420  
A:Accession: A23819  
A:Molecule type: mRNA  
A:Residues: 1-466 <HAG>  
A:Cross-references: GB:M12323; NID:G182799; PIDN:AAA8040.1; PID:G182801  
R:Thim, L.; Bioern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.  
Biochemistry 27, 7785-7793, 1988  
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f  
A:Reference number: A90539; MUID:89088153; PMID:3264725  
A:Accession: A31186  
A:Molecule type: Protein  
A:Residues: 61-212 <THI>  
A:Accession: B31186  
A:Molecule type: Protein  
A:Residues: 213-466 <TH2>  
R:Bioern, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Peder  
J. Biol. Chem. 266, 11051-11057, 1991  
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a  
A:Reference number: A40529; MUID:91250411; PMID:1904059  
A:Contents: annotation; carbohydrate binding sites  
R:Persson, B.; Petersen, L.C.  
Eur. J. Biochem. 234, 293-300, 1995  
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox  
A:Reference number: S63524; MUID:96096752; PMID:8529655  
A:Accession: S63524  
A:Molecule type: Protein  
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>  
C:Genetics:  
A:Gene: GDB:F7  
A:Cross-references: GDB:119897; OMIM:227500  
A:Map position: 19q34-19q34  
A:Insertions: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
coagulation factor IX in the presence of calcium and tissue factor





F:212-445/Domain: trypsin homology <TRY>  
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
F:214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 50.5%; Score 97; DB 1; Length 461;  
Best Local Similarity 45.5%; Pred. No. 7.9e-09;  
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRDGLXKXCKXQCFXAFIFKDAKRTKLFWISY 44  
Db 42 ANSFLEMRPGSLREKCEMEICDFEAOEIFQNVEDTLAFWIKY 85

RESULT 5  
S18994  
protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
C:Accession: S18994; S24312  
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
Submitted to the EMBL Data Library, February 1992  
A:Description: The cDNA cloning and mRNA expression of rat protein C.  
A:Reference number: S18994

A:Accession: S18994  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <OKR>  
A:Cross-references: EMBL:X64336; NID:G56962; PIDD:CAA5617.1; PID:G56963  
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
Biochim. Biophys. Acta 1131, 329-332, 1992  
A:Title: The cDNA cloning and mRNA expression of rat protein C.  
A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <OKR>  
A:Cross-references: EMBL:X64336; NID:G56962; PIDD:CAA5617.1; PID:G56963  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:27-85/Domain: Gla domain homology <GLA>  
F:33-42/Domain: propeptide #status predicted <PRO>  
F:43-461/Product: protein C #status predicted <PRC>  
F:91-130/Domain: EGF homology <EG1>  
F:139-174/Domain: EGF homology <EG2>  
F:213-445/Domain: trypsin homology <TRY>  
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat  
F:215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 49.5%; Score 95; DB 1; Length 461;  
Best Local Similarity 45.5%; Pred. No. 1.8e-08;  
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRDGLXKXCKXQCFXAFIFKDAKRTKLFWISY 44  
Db 42 ANSFLEMRPGSLREKCEMEICDFEAOEIFQNVEDTLAFWIKY 85

RESULT 6  
EXHU  
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N:Alternate names: Stuart factor  
C:Species: Homo sapiens (man)  
C:Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
C:Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00  
R:Levtun, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
Biochemistry 25, 5098-5102, 1986

A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization is

A:Reference number: A24478; MUID:87026600; PMID:3768336  
A:Accession: A24478  
A:Molecule type: DNA  
A:Residues: 1-488 <LEV>  
A:Cross-references: GB:I29433; GB:ML4227; NID:G459809; PIDD:AAA52764.1; PID:G182831  
R:Messier, T.L.; Pittman, D.D.; Long, G.L.; Kautman, R.J.; Church, W.R.  
Gene 99, 291-294, 1991

A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag  
A:Reference number: J00917; MUID:91216473; PMID:1902434  
A:Accession: J00917

A:Molecule type: mRNA  
A:Residues: 1-488 <MBS>  
A:Cross-references: GB:M57285; NID:G182389; PIDD:AAA52421.1; PID:G182390  
R:Miao, C.H.; Levtun, S.P.; Chung, D.W.; Davie, E.W.  
J. Biol. Chem. 267, 7395-7401, 1992

A:Title: Liver-specific expression of the gene coding for human factor X, a blood coagul  
A:Reference number: A42485; MUID:92218390; PMID:1333796  
A:Accession: A42485

A:Molecule type: DNA  
A:Residues: 1-15 <MIA>  
A:Experimental source: liver  
A>Note: sequence extracted from NCHI backbone (NCBIN:93780, NCBI:93787)  
R:Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
Gene 41, 311-314, 1986

A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
A:Reference number: A25853; MUID:86221713; PMID:3011603  
A:Accession: A25853

A:Molecule type: mRNA  
A:Residues: 19-284, 'E', 289-488 <KAU>  
A:Cross-references: GB:M2613; NID:G180335; PIDD:AAA51984.1; PID:G180336  
R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulat  
A:Reference number: A22208; MUID:85216545; PMID:2582420  
A:Accession: A22208

A:Molecule type: mRNA  
A:Residues: 13-441, 'S', 443-488 <FUN>  
A:Cross-references: GB:K03194; NID:G182840; PIDD:AAA52490.1; PID:G182841  
R:Levtun, S.P.; Chung, D.W.; Kissel, W.; Kurachi, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A:Title: Characterization of a cDNA coding for human factor X.  
A:Reference number: A21284; MUID:84222026; PMID:6587384  
A:Accession: A21284

A:Molecule type: mRNA  
A:Residues: 13-284, 'E', 289-488 <LE2>  
A:Cross-references: GB:K01886  
R:McMullen, B.A.; Fujikawa, K.; Kissel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss

Biochemistry 22, 2875-2884, 1983  
A:Title: Complete amino acid sequence of the light chain of human blood coagulation fact  
A:Reference number: A20362; MUID:85257207; PMID:6871167  
A:Accession: A20362

A:Molecule type: protein  
A:Residues: 41-179 <MCM>  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993

A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39415

A:Molecule type: protein  
A:Residues: 183-234 <INO>  
A>Note: glycosylation sites  
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.C.; Hamsabhusanam, K.; Lyman, G.  
Gene 84, 517-519, 1989

A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
A:Reference number: I54051; MUID:90128299; PMID:2612918  
A:Accession: I54051

A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-references: GB:M33297; NID:G183860; PIDD:AAA52636.1; PID:G553330

R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla

J. Mol. Biol. 232, 947-966, 1993  
 A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A49458; PMID:93360277; PMID:8355279  
 A:Comment: annotation; X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-C  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 C:Gene: GDB:F10  
 A:Cross-References: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A>Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: signal sequence #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-234/Domain: activation peptide #status experimental <APT>  
 F:235-468/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:235-468/Domain: trypsin homology <TRY>  
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-184,241-246,261-277,390-404,415-443/  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:119,211/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:221-231/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:234-235/Cleavage site: Arg-1le (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 49.0%; Score 94; DB 1; Length 488;  
 Best Local Similarity 38.6%; Pred. No. 2,8e-08;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGSIXRXCXXXQSFXXAFXFKAXXPKLFWIY 44  
 Db 41 ANSFLMKKXHLERECMETCYEPAREVFEVSDKTNERNKY 84

RESULT 7  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #ext change 16-Jul-1999  
 C:Accession: A22867; A14997; A12030; S39414; A00925  
 R:Func, M.R.; Campbell, R.M.; Macgillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A:Reference number: A22867; PMID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FUN>  
 A:Cross-References: GDB:X00673; NID:9192; PIDN:CA55286.1; PID:9193  
 R:Entfeld, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; PMID:80130563; PMID:6766735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, N', 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A:Reference number: A20274; PMID:83308613; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Titani, K.; Fujikawa, K.; Entfeld, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; PMID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-297,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T  
 R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A:Reference number: A34412; PMID:89380326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PEP>  
 A>Note: beta-hydroxyaspartic acid site  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A:Reference number: S39414; PMID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196,199-209,216-233 <INO>  
 A>Note: carboxylate binding sites  
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D  
 Biochemistry 11, 4899-4903, 1972  
 A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
 A:Reference number: A12453; PMID:73053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Titani, K.; Davie, E.M.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to  
 A:Reference number: A13504; PMID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic  
 A:Reference number: A38024; PMID:84185716; PMID:6546930  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; PMID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding  
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C:Comment: The two chains are formed from a single-chain precursor by the excision of tw  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o  
 activation.  
 C:Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with sero  
 C:Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin  
 C:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: signal sequence #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <APT>  
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F:234-461/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #s  
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-184/Disulfide bonds: #status p  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:200/Binding site: sulfate (Thr) (covalent) (partial) #status experimental  
 F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-1le (coagulation factor IXa, coagulation factor VIIa) #stat



A:Contents: annotation; activation; calcium binding  
 R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.  
 J. Biol. Chem. 258, 5554-5560, 1983  
 A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin  
 A:Reference number: A37542; MUID:83213514; PMID:6406503  
 A:Contents: annotation; activation; calcium binding  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine protease that re  
 s.  
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 bin, which cleaves a tetradepetide from the amino end of the heavy chain; this react  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str  
 cognition of the thrombin-thrombomodulin complex.  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:24-83/Domain: Gla domain homology <Gla>  
 F:30-39/Domain: propeptide #status predicted <PRO>  
 F:40-194/Product: protein C light chain #status experimental <LCH>  
 F:98-128/Domain: EGF homology <EG1>  
 F:137-172/Domain: EGF homology <EG2>  
 F:197-456/Product: protein C heavy chain #status experimental <HCH>  
 F:197-210/Domain: activation peptide #status experimental <APT>  
 F:21-440/Domain: trypsin homology <TRY>  
 F:45-46-53-55-58-59-62-64-65-68-74/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:110-128-137-148-144-157-159-162-180-181-237-253-368-382-393-421/Disulfide bonds: #stat  
 F:136-289-397/Binding site: carbonylate (Asn) (covalent) #status predicted  
 F:252-298-397/Active site: His, Asp, Ser #status predicted  
 F:366/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 45.8%; Score 88; DB 1; Length 456;  
 Best Local Similarity 40.9%; Pred. No. 2-9e-07;  
 Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRDGLXRXCKXQCSFXXAFIFKDAKRTKLFWSY 44  
 Db 40 ANSFLEELRPGNVERCESEVCEFEAREIFONTEDTMAFWSPY 83

RESULT 10  
 EXRT  
 coagulation factor Xa (EC 3.4.21.6) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000  
 C:Accession: S49075; J04670; PS0191; PS0190; 162745  
 R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 Thromb. Res. 80, 63-73, 1995  
 A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra  
 A:Reference number: A58498; MUID:96093366; PMID:8578539  
 A:Accession: S49075  
 A:Molecule type: mRNA  
 A:Residues: 1-482 <STA>  
 A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
 A:Note: submitted to the EMBL Data Library, June 1994  
 A:Note: neither the complete nucleic acid sequence nor the complete translation are show  
 R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 Gene 169, 269-273, 1996  
 A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
 A:Reference number: J04670; MUID:96194815; PMID:8647460  
 A:Accession: J04670  
 A:Molecule type: mRNA  
 A:Residues: 1-482 <STA>  
 A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
 A:Experimental source: Cos-1 cell  
 R:Enyoji, K.; Miyazaki, H.  
 J. Biochem. 109, 890-898, 1991  
 A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
 A:Reference number: PS0190; MUID:92041742; PMID:1118949  
 A:Accession: PS0191  
 A:Molecule type: protein  
 A:Residues: 41-58, 'X', 60-65 <ENU>  
 A:Accession: PS0190

A:Molecule type: protein  
 A:Residues: 183-166, 'X', 188-207 <ENU>  
 R:Murakawa, M.; Okamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of t  
 A:Reference number: 146196; MUID:94222160; PMID:8168596  
 A:Accession: 162745  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 295-383, 'G', 385-455 <MUR>  
 A:Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:183-231/Domain: activation peptide #status predicted <APT>  
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F:232-460/Domain: trypsin homology <TRY>  
 F:46-47-54-56-59-60-65-66-69-72-79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:57-62-90-101-95-110-112-121-129-140-136-149-151-164-172-340-238-243-259-275-388-402-41  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:187/Binding site: carbonylate (Asn) (covalent) #status experimental  
 F:208/Binding site: carbonylate (Thr) (covalent) #status predicted  
 F:218/Binding site: carbonylate (Asn) (covalent) #status predicted  
 F:231-232/Cleavage site: Arg-His (coagulation factor IXa, coagulation factor VIIa) #stat  
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 45.8%; Score 88; DB 1; Length 482;  
 Best Local Similarity 38.6%; Pred. No. 3.1e-07;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRDGLXRXCKXQCSFXXAFIFKDAKRTKLFWSY 44  
 Db 41 ANSFPEIKKGNLRECEVEICSFEEARVFEEDNKTTFPMKY 84

RESULT 11  
 S10511  
 thrombin (EC 3.4.21.5) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-May-1993 #sequence revision 07-May-1993 #text\_change 03-May-2002  
 C:Accession: S10511; A60576; B42696  
 R:Dhanich, M.; Monard, D.  
 Nucleic Acids Res. 18, 4251, 1990  
 A:Title: cDNA sequence of rat prothrombin.  
 A:Reference number: S10511; MUID:90332426; PMID:2377469  
 A:Accession: S10511  
 A:Molecule type: mRNA  
 A:Residues: 1-617 <Dih>  
 A:Cross-references: EMBL:X52835; NID:g56969; PIDN:CAA37017.1; PID:g56970  
 R:Henrikson, K.P.; Jazin, E.B.; Greenwood, J.A.; Dickerman, H.W.  
 Endocrinology 126, 167-175, 1990  
 A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.  
 A:Reference number: A60576; MUID:90091942; PMID:2293980  
 A:Accession: A60576  
 A:Molecule type: protein  
 A:Residues: 44-58 <HEN>  
 A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute  
 R:Bantfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: B42696  
 A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 363-617, 'E' <BAN>  
 A:Cross-references: GB:M81397  
 C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology  
 C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hyd  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-43/Domain: propeptide #status predicted <PRO>  
 F:28-88/Domain: Gla domain homology <GLA>  
 F:44-617/Product: prothrombin #status experimental <PMAT>  
 F:109-187/Domain: kringe homology <KR1>  
 F:215-292/Domain: kringe homology <KR2>  
 F:360-609/Domain: trypsin homology <TRY>  
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #status  
 F:61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5  
 F:402,458,564/Active site: His, Asp, Ser #status predicted

Query Match 45.8%; Score 86; DB 2; Length 617;  
 Best Local Similarity 39.5%; Pred. No. 3.9e-07;  
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 2 NAFLXLRDGLXRXCKXKXCFXKXAFIFKDXARTKLFWISY 44  
 Db 46 SGFLERKGNLERECVBEQCSYEAFALSPDQTDVFMAY 88

## RESULT 12

thrombin (EC 3.4.21.5) precursor - mouse  
 A:Residues: 1-618 <DEG>  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Cross-references: GB:K52308; NID:g53813; PIDN:CAA36548.1; PID:g53814  
 A:Experimental source: strain C57BL/6  
 A:Note: the data were obtained from females resulting from the cross of M. domesticus an  
 R:Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of the cDNA coding for mouse prothrombin and localization of t  
 A:Reference number: A35827; MUID:91025551; PMID:2222810  
 A:Accession: A35827

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-618 <DEG>  
 A:Cross-references: GB:K52308; NID:g53813; PIDN:CAA36548.1; PID:g53814  
 A:Experimental source: strain C57BL/6  
 A:Note: the data were obtained from females resulting from the cross of M. domesticus an  
 R:Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of the cDNA coding for mouse prothrombin and localization and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: A42696  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 384-618, 'E' <BAN>  
 A:Cross-references: GB:M81394  
 C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology  
 C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hyd  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-43/Domain: propeptide #status predicted <PRO>  
 F:28-88/Domain: Gla domain homology <GLA>  
 F:44-618/Product: prothrombin B #status predicted <MAT>  
 F:109-187/Domain: kringe homology <KR1>  
 F:215-293/Domain: kringe homology <KR2>  
 F:361-610/Domain: trypsin homology <TRY>  
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #status  
 F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5  
 F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match 45.8%; Score 86; DB 2; Length 618;  
 Best Local Similarity 39.5%; Pred. No. 3.9e-07;  
 Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

OY 2 NAFLXLRDGLXRXCKXKXCFXKXAFIFKDXARTKLFWISY 44  
 Db 46 SGFLERKGNLERECVBEQCSYEAFALSPDQTDVFMAY 88

## RESULT 13

EXCH  
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken  
 N:Alternate names: virus-activating proteinase  
 C:Species: Gallus gallus (chicken)  
 C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: S15838; S20380; S20381  
 R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Nag  
 FEBS Lett. 283, 281-285, 1991  
 A:Title: Primary structure of the virus activating proteinase from chick embryo. Its ident  
 A:Reference number: S15838; MUID:91257322; PMID:2044767  
 A:Accession: S15838  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-475 <SUZ>  
 A:Cross-references: DDBJ:DD0844; NID:9222869; PIDN:BA00724.1; PID:9222870  
 FEBS Lett. 296, 274-278, 1992  
 A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib  
 A:Reference number: S20380; MUID:92164779; PMID:1537403  
 A:Accession: S20380  
 A:Molecule type: protein  
 A:Residues: 41-55 <GO2>  
 A:Accession: S20381  
 A:Molecule type: protein  
 A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-185/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-167/Domain: EGF homology <EG2>  
 F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:186-240/Domain: activation peptide #status predicted <APT>  
 F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F:241-468/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #st  
 F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:136-207,228,285/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 43.8%; Score 84; DB 1; Length 475;  
 Best Local Similarity 36.4%; Pred. No. 1.5e-06;  
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXLRDGLXRXCKXKXCFXKXAFIFKDXARTKLFWISY 44  
 Db 41 ANSFLERKGNLERECVBEQCSYEAFALSPDQTDVFMAY 84

## RESULT 14

KXHU  
 protein C (activated) (EC 3.4.21.69) precursor - human  
 N:Alternate names: autoprothrombin IIA; plasma protein C  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
 C:Accession: A22331; A25426; A21781; A23789; A00927  
 R:Forster, D.C.; Yoshitake, S.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
 A:Title: The nucleotide sequence of the gene for human protein C.  
 A:Reference number: A22331; MUID:85270390; PMID:2991887  
 A:Accession: A22331  
 A:Molecule type: DNA  
 A:Residues: 1-461 <POS1>  
 A:Cross-references: GB:M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334  
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A:Title: Evolution and organization of the human protein C gene.

A:Reference number: A25426; MUID:86120978; PMID:3511471  
 A:Accession: A25426  
 A:Molecule type: DNA  
 A:Residues: 1-445; 'L', 446-461 <PLU>  
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
 R:Poster, D.; Davie, E.W.; S.A. 81, 4766-4770, 1984  
 Proc. Natl. Acad. Sci. U.S.A.  
 A:Title: Characterization of a cDNA coding for human protein C.  
 A:Reference number: A21781; MUID:84272714; PMID:6589623  
 A:Accession: A21781  
 A:Molecule type: mRNA  
 A:Residues: 'Q', 107-461 <FOG2>  
 A:Cross-references: GB:K02059; NID:g190322; PIDN:AAA60164.1; PID:g190323  
 R:Beckmann, R.J.; Schmidt, R.J.; Sautter, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
 Nucleic Acids Res. 13, 5233-5247, 1985  
 A:Title: The structure and evolution of a 461 amino acid human protein C precursor and 1  
 A:Reference number: A23789; MUID:85269639; PMID:2991859  
 A:Accession: A23789  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <BEC>  
 A:Cross-references: GB:X02750; NID:935689; PIDN:CAA6528.1; PID:g763120  
 R:Miller, J.P.; Brose Jr., G.J.  
 J. Biol. Chem. 265, 11397-11404, 1990  
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m  
 A:Reference number: A44605; MUID:90293094; PMID:1694179  
 A:Contents: annotation; carbohydrate binding sites; activation peptide  
 A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
 R:Harrie, R.J.; Ling, V.T.; Spellman, M.W.  
 J. Biol. Chem. 267, 5102-5107, 1992  
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of facto  
 A:Reference number: A44606; MUID:92184750; PMID:1544894  
 A:Contents: annotation; beta-hydroxyaspartic acid  
 A:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
 lation of factor Va is strongly enhanced by complexing with protein S. Protein C also f  
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
 C:Genetics:  
 A:Gene: GDB:PROC  
 A:Cross-references: GDB:120317; OMIM:176860  
 A:Map position: 2q13-2q21  
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:127-86/Domain: Gla domain homology <GLA>  
 F:133-42/Domain: propeptide #status predicted <PRO>  
 F:43-197/Product: protein C light chain #status predicted <LCH>  
 F:92-131/Domain: EGF homology <EG1>  
 F:140-175/Domain: EGF homology <EG2>  
 F:200-461/Product: protein C heavy chain #status predicted <HCH>  
 F:200-211/Domain: activation peptide #status experimental <APT>  
 F:212-445/Domain: trypsin homology <TRY>  
 F:48-49, 56, 58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
 F:59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/D  
 F:106-111/Disulfide bonds: #status predicted  
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent  
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:119, 290, 355/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
 F:253, 299, 402/Active site: His, Asp, Ser #status predicted  
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 41.7%; Score 80; DB 1; Length 461;  
 Best Local Similarity 43.9%; Pred No. 7.3e-06;  
 Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLXLRDGSIXKXKXQCSFXXAFIXFDAXRTKLFW 41  
 DB 43 ANSFLERHSHSLERCEIEICDFEAKXEIFQVNDTLAFW 83

RESULT 15  
 KFBO

coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
 N:Alternate names: Christmas factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text\_change 16-Jul-1999  
 C:Accession: A14757; #20274; I45891; A00923  
 R:Katayama, K.; Ericsson, L.H.; Entfeld, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Tili  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
 A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac  
 A:Reference number: A14757; MUID:80056619; PMID:291916  
 A:Accession: A14757  
 A:Molecule type: protein  
 A:Residues: 1-63; 'T', 65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co-  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Accession: B20274  
 A:Molecule type: protein  
 A:Residues: 59-63; 'X', 65-69 <MCN>  
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
 Nature 299, 178-180, 1982  
 A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.  
 A:Reference number: 145891; MUID:82272386; PMID:6287289  
 A:Accession: 145891  
 A:Status: translated from GB/EMBL/DBJ  
 A:Title: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 52-139 <CHO>  
 A:Cross-references: GB:J00007; NID:g163053; PIDN:AAA30520.1; PID:g163054  
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, T.  
 J. Biochem. 104, 867-868, 1988  
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag  
 A:Reference number: A44556; MUID:89213999; PMID:3149637  
 A:Contents: annotation  
 A:Note: structure and location of a carbohydrate covalently bound to Ser  
 C:Comment: Factor IX is activated by factor XIIa, which excises the activation peptide pr  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
 A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:1-45/Domain: Gla domain homology (fragment) <GLA>  
 F:51-82/Domain: EGF homology <EG1>  
 F:88-124/Domain: EGF homology <EG2>  
 F:147-181/Domain: activation peptide #status experimental <APT>  
 F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:182-409/Domain: trypsin homology <TRY>  
 F:7, 8, 15, 17, 20, 21, 26, 27, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #sta  
 F:18-23, 51-62, 56-71, 73-82, 88-99, 95-109, 111-124, 132-290, 207-223, 337-351, 362-390/Disulfide  
 F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F:54/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:158, 166, 173, 261/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:222, 270, 366/Active site: His, Asp, Ser #status predicted

Query Match 40.6%; Score 78; DB 1; Length 416;  
 Best Local Similarity 41.2%; Pred No. 1.5e-05;  
 Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSIXKXKXQCSFXXAFIXFDAXRTKLFWSY 44  
 DB 12 GNLERCKEKCSFEARVFNTEKTETFEWQY 45

Search completed: March 19, 2003, 15:00:52  
 Job time: 30.125 secs

GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:30 ; Search time 5.5625 Seconds  
(without alignments)  
328.082 Million cell updates/sec

Title: 10ASP28PHE  
Perfect score: 192  
Sequence: 1 ANAFLLXRLRDSLRXCKXX.....XXAFXIFKDXRTLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 156   | 81.2        | 466    | 1  | FA7_HUMAN          |
| 2          | 122   | 63.5        | 444    | 1  | FA7_RABIT          |
| 3          | 114   | 59.4        | 407    | 1  | FA7_BOVIN          |
| 4          | 111   | 57.8        | 446    | 1  | FA7_MOUSE          |
| 5          | 100   | 52.1        | 490    | 1  | FA10_MOUSE         |
| 6          | 98    | 51.0        | 459    | 1  | PRTC_RABIT         |
| 7          | 97    | 50.5        | 461    | 1  | PRTC_PIG           |
| 8          | 95    | 49.5        | 461    | 1  | PRTC_MOUSE         |
| 9          | 94    | 49.0        | 488    | 1  | PRTC_RAT           |
| 10         | 94    | 49.0        | 492    | 1  | FA10_HUMAN         |
| 11         | 92    | 47.9        | 218    | 1  | FA10_BOVIN         |
| 12         | 92    | 47.9        | 622    | 1  | TMG1_HUMAN         |
| 13         | 88    | 45.8        | 456    | 1  | THRB_HUMAN         |
| 14         | 88    | 45.8        | 617    | 1  | THRB_BOVIN         |
| 15         | 88    | 45.8        | 618    | 1  | THRB_RAT           |
| 16         | 84    | 43.8        | 231    | 1  | THRB_MOUSE         |
| 17         | 84    | 43.8        | 475    | 1  | TMG3_HUMAN         |
| 18         | 81    | 42.2        | 458    | 1  | FA10_CHICK         |
| 19         | 80    | 41.7        | 461    | 1  | PRTC_RABIT         |
| 20         | 78    | 40.6        | 416    | 1  | PRTC_HUMAN         |
| 21         | 76    | 39.6        | 376    | 1  | FA9_BOVIN          |
| 22         | 75    | 39.1        | 461    | 1  | FA10_TROCA         |
| 23         | 73    | 38.0        | 202    | 1  | FA9_HUMAN          |
| 24         | 72    | 37.5        | 625    | 1  | TMG2_HUMAN         |
| 25         | 70    | 36.5        | 452    | 1  | THRB_BOVIN         |
| 26         | 70    | 36.5        | 459    | 1  | FA9_CANFA          |
| 27         | 66.5  | 34.6        | 226    | 1  | FA9_MOUSE          |
| 28         | 58    | 30.2        | 396    | 1  | TMG4_HUMAN         |
| 29         | 58    | 30.2        | 375    | 1  | Q9BZD6_homo_sapien |
| 30         | 57    | 29.7        | 649    | 1  | P07744_bos_taurus  |
| 31         | 57    | 29.7        | 649    | 1  | P07224_bos_taurus  |
| 32         | 56    | 29.2        | 646    | 1  | Q28520_macaca_mula |
| 33         | 55    | 28.6        | 675    | 1  | P07225_homo_sapien |

|    |      |      |     |   |            |
|----|------|------|-----|---|------------|
| 34 | 53   | 27.6 | 400 | 1 | PRTZ_HUMAN |
| 35 | 48   | 25.0 | 675 | 1 | PRTS_MOUSE |
| 36 | 45   | 23.4 | 271 | 1 | MD12_YEAST |
| 37 | 45   | 23.4 | 879 | 1 | YN65_YEAST |
| 38 | 44.5 | 23.2 | 133 | 1 | OUT5_ERWCH |
| 39 | 43   | 22.4 | 394 | 1 | TCR4_SALOR |
| 40 | 43   | 22.4 | 440 | 1 | Y788_BORBU |
| 41 | 42.5 | 22.1 | 356 | 1 | MURB_BUCAL |
| 42 | 41   | 21.4 | 263 | 1 | PIEA_STRMU |
| 43 | 41   | 21.4 | 393 | 1 | DPS5_PINSY |
| 44 | 41   | 21.4 | 616 | 1 | JEN1_YEAST |
| 45 | 40   | 20.8 | 343 | 1 | HMD_METVO  |

## ALIGNMENTS

RESULT 1  
ID FA7\_HUMAN STANDARD; PRT; 466 AA.  
AC P08709; 014339;  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).  
GN F7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86205965; PubMed=3486420;  
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K., Davie E.W.;  
RA "Characterization of a cDNA coding for human factor VII";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87260948; PubMed=3037537;  
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;  
RT "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.  
RX Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth B.J., Yi Q., Nickerson D.A.;  
RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RP [4]  
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=89088153; PubMed=3264725;  
RA Thim L., Bjorn S., Christensen M., Nicolaissen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;  
RT "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells.";  
RL Biochemistry 27:7785-7793(1988).  
RN [5]  
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
RX MEDLINE=91250411; PubMed=1904059;  
RA Bjorn S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komlyana Y., Pedersen A.H., Kistiel W.;  
RT "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine.";  
RL J. Biol. Chem. 266:11051-11057(1991).  
RP [6]  
RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
RX MEDLINE=90062160; PubMed=2511201;



RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [7]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175541; PubMed=8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RL Nature 380:41-46(1996).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPTI mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gispert G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Andersen J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93732811; PubMed=8364544;  
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 RT (151His and 333Ser) in the human coagulation factor VII gene.";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamiya O., Kemball-Cook G., Marin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Frangneil D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RX MEDLINE=94264305; PubMed=8204879;  
 RA Chating S., Clarke B., Stridiana S., Chiu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohira M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";  
 RL Thromb. Haemost. 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr159Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS W-283, K-325, V-358, Q-364, E-402 AND Q-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,  
 RA Zalcov R., Seligsohn U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN [21]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerri C., Gaidies R., Aguilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).  
 RN [22]  
 RP -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIa, FACTOR IXa, OR  
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-111le bond in factor X to  
 CC form factor Xa.  
 CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are  
 CC produced by alternative splicing.  
 CC -I- TISSUE SPECIFICITY: PLASMA.  
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.  
 CC -I- PHARMACEUTICAL: Available under the names Niasase or Novoseven  
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in



Query Match 81.2%; Score 156; DB 1; Length 466;  
Best Local Similarity 72.7%; Pred. No. 1,2e-19;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANAFLEXXLRDGLRCKXCKXQCSFXAXFIPKDXARTLFWISY 44  
DB 61 ANAFLEELRPGSLERCKEBCQSFPEARFIPKDXARTLFWISY 104

RESULT 2  
FA7\_RABIT STANDARD; PRT; 444 AA.  
AC P98139: P79224;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
DE F7.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=93150306; Pubmed=8383365;  
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."  
RT Thromb. Res. Suppl. 69:231-238 (1993).  
RL [2]  
RN REVISION TO 395.  
RC TISSUE=Liver;  
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;  
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XIa, FACTOR XIIa, FACTOR IXa, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: PLASMA.  
CC -1- PTM: THE VITAMIN K-DEPENDENT ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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CC -----  
CC EMBL: U77477; AAB37326.1; -.  
CC HSSP: P08709; 1FAK.  
CC MEROPS: S01.215; -.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.

DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00089; trypsin\_1.  
DR Pfam: PF00594; gla\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00179; EGF\_CA\_1.  
DR SMART: SM00001; EGF-like\_1.  
DR SMART: SM00069; GLA\_1.  
DR SMART: SM00020; TRY\_ SPC\_1.  
DR PROSITE: PS00010; ASX\_HYDROXYL\_1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS0186; EGF\_2; 1.  
DR PROSITE: PS01187; EGF\_CA\_1.  
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.  
DR PROSITE: PSS0240; TRYPSIN\_DOM\_1.  
DR PROSITE: PS00134; TRYPSIN\_HIS\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER\_1.  
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.  
KW EGF-like domain; Repeat; Signal; Hydroxylation.  
FT SIGNAL 1 21  
FT PROPEP 22 39  
FT CHAIN 40 191  
FT CHAIN 192 444  
FT DOMAIN 45 74  
FT DOMAIN 85 121  
FT DOMAIN 126 167  
FT DOMAIN 192 444  
FT SITE 191 192  
FT ACT\_SITE 232 232  
FT ACT\_SITE 281 281  
FT ACT\_SITE 383 383  
FT BINDING 377 377  
FT DISULFID 56 61  
FT DISULFID 89 100  
FT DISULFID 94 109  
FT DISULFID 111 120  
FT DISULFID 130 141  
FT DISULFID 137 151  
FT DISULFID 153 166  
FT DISULFID 174 301  
FT DISULFID 198 203  
FT DISULFID 217 233  
FT DISULFID 349 368  
FT DISULFID 379 407  
FT MOD\_RES 45 45  
FT MOD\_RES 46 46  
FT MOD\_RES 53 53  
FT MOD\_RES 55 55  
FT MOD\_RES 58 58  
FT MOD\_RES 59 59  
FT MOD\_RES 64 64  
FT MOD\_RES 65 65  
FT MOD\_RES 68 68  
FT MOD\_RES 74 74  
FT MOD\_RES 102 102  
FT CARBOHYD 211 211  
FT CARBOHYD 242 242  
FT CARBOHYD 306 306  
SQ SEQUENCE 444 AA; 49011 MM; 0481ABC4FE542786 CRC64;

Query Match 63.5%; Score 122; DB 1; Length 444;  
Best Local Similarity 54.5%; Pred. No. 1e-13;  
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

OY 1 ANAFLEXXLRDGLRCKXCKXQCSFXAXFIPKDXARTLFWISY 44  
DB 40 ANAFLEELRPGSLERCKEBCQSFPEARFIPKDXARTLFWISY 83

RESULT 3

FA7 BOVIN STANDARD; PRT; 407 AA.  
 ID FA7 BOVIN PRT; 407 AA.  
 AC P22457;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
 GN F7.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RX MEDLINE=89008362; PubMed=3049594;  
 RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;  
 RT "Bovine factor VII. Its purification and complete amino acid sequence."  
 RT J. Biol. Chem. 263:14868-14877(1988).  
 RN [2]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
 RX MEDLINE=8921399; PubMed=3149637;  
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T., Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX."  
 RT J. Biochem. 104:867-868(1988).  
 RN [3]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
 RX MEDLINE=9134709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."  
 RT Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [4]  
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR XA AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 DR PIR; A31979; A31979.  
 DR HSP; P08709; 1BF9.  
 DR MEROPS; S01.215; -.  
 DR Interpro; IPR000152; Asx\_hydroxyl.  
 DR Interpro; IPR001314; Chymotrypsin.  
 DR Interpro; IPR000561; EGF-like.  
 DR Interpro; IPR000742; EGF\_2.  
 DR Interpro; IPR001881; EGF\_Ca.  
 DR Interpro; IPR001438; EGF\_II.  
 DR Interpro; IPR002383; GLA\_blood.  
 DR Interpro; IPR001254; Ser\_protease\_Try.  
 DR Interpro; IPR000294; Vitk\_dep\_GLA.  
 DR Pfam; PF00008; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00072; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGF\_BLOOD.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_like; 1.

DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GUO\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase: Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.  
 KW EGF-like domain; Repeat.  
 FT CHAIN 153 407  
 FT DOMAIN 6 35  
 FT DOMAIN 46 82  
 FT DOMAIN 87 128  
 FT DOMAIN 153 407  
 FT SITE 152 153  
 FT ACT\_SITE 193 193  
 FT ACT\_SITE 242 242  
 FT ACT\_SITE 344 344  
 FT BINDING 338 338  
 FT DISULFID 17 22  
 FT DISULFID 50 61  
 FT DISULFID 55 70  
 FT DISULFID 72 81  
 FT DISULFID 91 102  
 FT DISULFID 98 112  
 FT DISULFID 114 127  
 FT DISULFID 135 262  
 FT DISULFID 159 164  
 FT DISULFID 178 194  
 FT DISULFID 310 329  
 FT DISULFID 340 368  
 FT MOD\_RES 6 6  
 FT MOD\_RES 7 7  
 FT MOD\_RES 14 14  
 FT MOD\_RES 16 16  
 FT MOD\_RES 19 19  
 FT MOD\_RES 20 20  
 FT MOD\_RES 25 25  
 FT MOD\_RES 26 26  
 FT MOD\_RES 29 29  
 FT MOD\_RES 35 35  
 FT MOD\_RES 52 52  
 FT CARBOHYD 145 145  
 FT CARBOHYD 203 203  
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;  
 Query Match 59.4%; Score 114; DB 1; Length 407;  
 Best Local Similarity 50.0%; Pred. No. 2,4e-12;  
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;  
 Oy 1 ANAFKXLRDGLRXXCKXCCFFXAFXIFDAXTKLFWISY 44  
 Db 1 ANGFLELLPGLSLRRCRELCSFEAHETFRNEERTRPWFWSY 44  
 RESULT 4  
 ID FA7 MOUSE STANDARD; PRT; 446 AA.  
 AC P70375;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
 GN F7 OR CF7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97127167; Pubmed=8972017;  
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine blood  
 coagulation factor VII gene";  
 RL Thromb. Haemost. 76:957-964(1996).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR  
 THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 CC EMBL; U66079; AAC3796.1; -.  
 DR HSSP; P08709; IBF9.  
 DR MEROPS; S01.215; -.  
 DR MGD; MGI.109325; F7.  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; Ytk\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA.1.  
 DR SMART; SM00001; EGF\_like.1.  
 DR SMART; SM00069; GLA.1.  
 DR SMART; SM00020; TYP\_SPC.1.  
 DR PROSITE; PS00010; ASK\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS01187; EGF\_CA.1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PSS0240; TRYPSIN\_DOM.1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS.1.  
 DR PROSITE; PS00133; TRYPSIN\_SER.1.  
 KM Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KM EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 193  
 FT CHAIN 194 446  
 FT DOMAIN 47 76  
 FT DOMAIN 87 123  
 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 128 169 EGF-LIKE 2.  
 FT DOMAIN 194 446 SERINE PROTEASE.  
 FT SITE 193 194 CLEAVAGE (BY FACTOR Xa, FACTOR XIa, OR  
 FT ACT\_SITE 234 234 FACTOR IXa, OR THROMBIN) (BY SIMILARITY).  
 FT ACT\_SITE 283 283 BY SIMILARITY.  
 FT ACT\_SITE 385 385 BY SIMILARITY.  
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 96 111 BY SIMILARITY.  
 FT DISULFID 113 122 BY SIMILARITY.  
 FT DISULFID 132 143 BY SIMILARITY.  
 FT DISULFID 139 153 BY SIMILARITY.  
 FT DISULFID 155 168 BY SIMILARITY.  
 FT DISULFID 176 303 BY SIMILARITY.  
 FT DISULFID 200 205 BY SIMILARITY.  
 FT DISULFID 219 235 BY SIMILARITY.  
 FT DISULFID 351 370 BY SIMILARITY.  
 FT DISULFID 381 409 BY SIMILARITY.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45C8C96E CRC64;  
 -----  
 Query Match 57.8%; Score 111; DB 1; Length 446;  
 Best Local Similarity 54.5%; Pred. No. 8, 7e-12;  
 Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;  
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 Oy 1 ANAFLXXLRDQSLKRXCKXOCXFXAFYFKDAXRTKLPFISY 44  
 Db 42 ANSLLEELPGLSEKNEECSPFEAREIFKSPERTKQFWIVY 85  
 -----  
 RESULT 5  
 FA10\_RABBIT STANDARD; PRT; 490 AA.  
 AC 019045;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97256311; Pubmed=9101642;  
 RA Penduthi U.R., Anderson K.D., James H.L.;  
 RT "Characterization of a full-length cDNA for rabbit factor X";  
 RL Thromb. Res. 85:503-514(1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 Arg-|-Ile bonds in prothrombin to form thrombin  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM (BY SIMILARITY).  
 CC -1- PM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)  
 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC DR EMBL; AF003200; AAB62542.1; -.  
 CC DR HSSP; P00742; IHCG.  
 CC DR MEROPS; S01\_216; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF-2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR PROSITE; PS00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
 FT PROPEP 21 40  
 FT CHAIN 41 180  
 FT CHAIN 184 490  
 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT CHAIN 86 122  
 FT DOMAIN 125 165  
 FT DOMAIN 233 490  
 FT MOD\_RES 46 46  
 FT MOD\_RES 47 47  
 FT MOD\_RES 54 54  
 FT MOD\_RES 56 56  
 FT MOD\_RES 59 59  
 FT MOD\_RES 60 60  
 FT MOD\_RES 65 65  
 FT MOD\_RES 66 66

FT MOD\_RES 69 69 SIMILARITY).  
 FT MOD\_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT MOD\_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT MOD\_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT MOD\_RES 103 103 SIMILARITY).  
 FT ACT\_SITE 274 274 HYDROXYLATION (BY SIMILARITY).  
 FT ACT\_SITE 320 320 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 417 417 CHARGE RELAY SYSTEM.  
 FT DISULFID 90 101 BY SIMILARITY.  
 FT DISULFID 95 110 BY SIMILARITY.  
 FT DISULFID 112 121 BY SIMILARITY.  
 FT DISULFID 129 140 BY SIMILARITY.  
 FT DISULFID 136 149 BY SIMILARITY.  
 FT DISULFID 151 164 BY SIMILARITY.  
 FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 239 244 BY SIMILARITY.  
 FT DISULFID 259 275 BY SIMILARITY.  
 FT DISULFID 388 402 BY SIMILARITY.  
 FT DISULFID 413 441 BY SIMILARITY.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;  
 Query Match 52.1%; Score 100; DB 1; Length 490;  
 Best Local Similarity 40.9%; Pred. No. 8.1e-10;  
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;  
 Oy 1 ANAFLLXLRDGLXRXCKXQCFYXAFYIFDXARXKLFMISY 44  
 Db 41 ANSFLEELKKNLEHRCMENGCSYEALVEFDRKTNFEMNKY 84  
 RESULT 6  
 PRTC\_PIG STANDARD; PRT; 459 AA.  
 AC 09GLP2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 ON NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=21129814; PubMed=11229814;  
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,  
 RA Kim H.K.W.;  
 RT "Poreine factor V. cDNA cloning, gene mapping, three-dimensional  
 RT protein modelling of membrane binding sites and comparative anatomy of  
 RT domains.";  
 RL Cell. Mol. Life Sci. 58:148-159 (2001).  
 CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that  
 CC regulates blood coagulation by inactivating factors Va and VIIa  
 CC in the presence of calcium ions and phospholipids.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved  
 CC into a light chain and a heavy chain held together by a disulfide  
 CC bond. The enzyme is then activated by thrombin, which cleaves a  
 CC tetradecapeptide from the amino end of the heavy chain; this  
 CC reaction, which occurs at the surface of endothelial cells, is

strongly promoted by thrombomodulin.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu  
 CC residues allows the modified protein to bind calcium  
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to  
 CC another site, beyond the Gla domain. This Gla-independent binding  
 CC site is necessary for the recognition of the  
 CC thrombin-thrombomodulin complex.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF191307; AAC28380.1; -.  
 CC HSSP: P04070; 1PCU.  
 CC MEROPS: S01.218; -.  
 DR InterPro: IPR000152; Aex\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR002383; Gla\_blood.  
 DR InterPro: IPR001254; Set\_protease\_Try.  
 DR InterPro: IPR00294; VitK\_dep\_Gla.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin\_1.  
 DR Pfam: PF00594; gla; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00181; EGF\_2.  
 DR SMART: SM00001; EGF-like; 2.  
 DR SMART: SM00069; Gla; 1.  
 DR SMART: SM00020; Tryp\_Spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF Ca; 1.  
 DR PROSITE: PS00011; GLV\_CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 41  
 FT CHAIN 42 459  
 FT CHAIN 42 196  
 FT CHAIN 199 459  
 FT CHAIN 199 213  
 FT SITE 213 214  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 214 459  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61

FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 255 255  
 FT ACT\_SITE 301 301  
 FT ACT\_SITE 400 400  
 FT ACT\_SITE 400 400  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 321  
 FT DISULFID 240 256  
 FT DISULFID 371 385  
 FT DISULFID 396 424  
 FT CARBOHYD 138 138  
 FT CARBOHYD 292 292  
 FT CARBOHYD 353 353  
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;  
 Query Match 51.0%; Score 98; DB 1; Length 459;  
 Best Local Similarity 45.5%; Pred. No. 1.7e-09;  
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 ANAFLLRLRDSGLRXCKXQCSFXXAFIFDARLTGLFWISY 44  
 Db 42 ANSFLELRPSLSRECKERTCFEAREIRFQNTENTWAFWSKY 85  
 ID PRTE\_MOUSE STANDARD; PRT; 461 AA.  
 AC P33587; O35498; (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=92316897; PubMed=1618739;  
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;  
 RT "Isolation and characterization of a mouse protein C cDNA."  
 RL J. Biochem. 111:491-495(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ;  
 RX MEDLINE=98152576; PubMed=9493582;  
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Nucleotide structure and characterization of the murine gene encoding  
 RT anticoagulant protein C."  
 RN Thromb. Haemost. 79:310-316(1998).  
 RN [3]  
 RP SEQUENCE OF 274-434 FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=94318474; PubMed=8043441;  
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;

RT "A comparative study of partial primary structures of the catalytic  
 region of mammalian protein C.";  
 RL Br. J. Haematol. 86:590-600(1994).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TERPESCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC EMBL; D10445; BAA01235.1; -  
 DR EMBL; AF034569; AAC33795.1; -  
 DR EMBL; DA3755; BAA07812.1; -  
 DR PIR; JX0210; JX0210.  
 DR HSSP; P04070; IPCU.  
 DR MEROPS; S01.218; -  
 DR MGD; MGI:97771; Proc.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser protease Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA\_  
 DR Pfam; PF00008; EGF\_2  
 DR Pfam; PF00089; trypsin\_1.  
 DR Pfam; PF00594; gla\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA\_1.  
 DR SMART; SM00001; EGF\_Like\_1.  
 DR SMART; SM00069; GLA\_1.  
 DR SMART; SM00020; TRYP\_SPC\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA\_1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION\_1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM\_1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER\_1.  
 KM Blood coagulation: Glycoprotein; Serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 FT SIGNL 1  
 FT PROPEP 34  
 FT CHAIN 42  
 FT CHAIN 199  
 FT PEPTIDE 199  
 FT SITE 212  
 FT SITE 213  
 FT DOMAIN 96

| FT | DOMAIN   | 135     | 175       | EGF-LIKE 2.                         |
|----|----------|---------|-----------|-------------------------------------|
| FT | DOMAIN   | 213     | 461       | SERINE PROTEASE.                    |
| FT | MOD_RES  | 47      | 47        | GAMMA-CARBOXYGLUTAMIC ACID          |
| FT | MOD_RES  | 48      | 48        | (BY SIMILARITY).                    |
| FT | MOD_RES  | 55      | 55        | GAMMA-CARBOXYGLUTAMIC ACID          |
| FT | MOD_RES  | 57      | 57        | (BY SIMILARITY).                    |
| FT | MOD_RES  | 60      | 60        | GAMMA-CARBOXYGLUTAMIC ACID          |
| FT | MOD_RES  | 61      | 61        | (BY SIMILARITY).                    |
| FT | MOD_RES  | 66      | 66        | GAMMA-CARBOXYGLUTAMIC ACID          |
| FT | MOD_RES  | 67      | 67        | (BY SIMILARITY).                    |
| FT | MOD_RES  | 70      | 70        | GAMMA-CARBOXYGLUTAMIC ACID          |
| FT | MOD_RES  | 112     | 112       | (BY SIMILARITY).                    |
| FT | ACT_SITE | 253     | 253       | HYDROXYLATION (BY SIMILARITY).      |
| FT | ACT_SITE | 299     | 299       | CHARGE RELAY SYSTEM.                |
| FT | ACT_SITE | 402     | 402       | CHARGE RELAY SYSTEM.                |
| FT | DISULFID | 58      | 63        | BY SIMILARITY.                      |
| FT | DISULFID | 91      | 110       | BY SIMILARITY.                      |
| FT | DISULFID | 100     | 105       | BY SIMILARITY.                      |
| FT | DISULFID | 104     | 119       | BY SIMILARITY.                      |
| FT | DISULFID | 121     | 130       | BY SIMILARITY.                      |
| FT | DISULFID | 139     | 150       | BY SIMILARITY.                      |
| FT | DISULFID | 146     | 159       | BY SIMILARITY.                      |
| FT | DISULFID | 161     | 174       | BY SIMILARITY.                      |
| FT | DISULFID | 182     | 319       | INTERCHAIN (BY SIMILARITY).         |
| FT | DISULFID | 238     | 254       | BY SIMILARITY.                      |
| FT | DISULFID | 373     | 387       | BY SIMILARITY.                      |
| FT | DISULFID | 398     | 426       | BY SIMILARITY.                      |
| FT | CARBOHYD | 214     | 214       | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 290     | 290       | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 355     | 355       | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CONFLICT | 328     | 328       | MISSING (IN REF. 2).                |
| FT | CONFLICT | 393     | 393       | N -> D (IN REF. 2).                 |
| FT | SEQUENCE | 461 AA; | 51945 MW; | 53FA0D858194D6E CRC64;              |

Query Match 50.5%; Score 97; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 2,6e-09;  
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDGLRXCXKXQCSFXKAFIPKDAKTXLFWISY 44  
 DB 42 ANSFLBMRPGLRRCMBEICDFEBAQELFQVEDTLAWIKY 85

RESULT 8  
 ID PRIC\_RAT STANDARD; PRT; 461 AA.  
 AC P31394;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autocryptochromin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=Miscar; TISSUE=Liver;  
 RX MEDLINE=92329550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C.";

RL Biochim. Biophys. Acta 1131:329-332(1992).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 DR EMBL: X64336; CAA5617.1; -.  
 DR PIR: S18994; S18994.  
 DR PIR: S24312; S24312.  
 DR HSP: P04070; 1PCU.  
 DR MEROPS: S01.218; -.  
 DR InterPro: IPR000152; Aax\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR Pfam: PF00594; gla; 1.  
 DR PRINTS: PRO0722; CHYMOTRYPSIN.  
 DR PRINTS: PRO0001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00001; EGF\_Like; 1.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; Tryp\_Spe; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Blood coagulation; glycoprotein; serine protease;  
 KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 32  
 FT PROPEP 33 41  
 FT CHAIN 42 196  
 FT CHAIN 199 461  
 FT PEPTIDE 199 212  
 FT SITE 212 213  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 213 461  
 FT MOD\_RES 47 47  
 (BY SIMILARITY).

FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 254 254  
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 FT ACT\_SITE 402 402  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
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 FT DISULFID 146 159  
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 FT DISULFID 182 320  
 FT DISULFID 239 255  
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 FT CARBOHYD 215 215  
 FT CARBOHYD 291 291  
 FT CARBOHYD 355 355  
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;  
 Query March 49.5%; Score 95; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 5.8e-09;  
 Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;  
 Qy 1 ANAFLLXLRDGLXKXCKXCCXCFXAFIFKDXARTLFWISY 44  
 Db 42 ANSFLEVRASGLERECMEHICDFEEAGEIFQNVEDTLAFWIKY 85  
 RESULT 9  
 FA10\_HUMAN STANDARD; PRT; 488 AA.  
 AC P00742; Q14340;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91216473; PubMed=1902434;  
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;  
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding  
 RL human coagulation factor X.";  
 RN Gene 99:291-294(1991).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026600; PubMed=3768336;  
 RA Leytus S.P., Foster D.C., Kutrach K., Davie E.W.;  
 RT "Gene for human factor X: a blood coagulation factor whose gene  
 organization is essentially identical with that of factor IX and  
 protein C.";  
 RT

RL Biochemistry 25:5098-5102(1986).  
 RN [3]  
 RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McCallilivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RN [4]  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA.";  
 RL Gene 41:311-314(1986).  
 RN [5]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884(1983).  
 RN [6]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [7]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [8]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612916;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.

CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, K03194; AAA52490.1; -;  
 CC EMBL, M57285; AAA52421.1; -;  
 CC EMBL, I29433; AAA52764.1; -;  
 CC EMBL, L00390; AAA52764.1; JOINED.  
 CC EMBL, L00391; AAA52764.1; JOINED.  
 CC EMBL, L00392; AAA52764.1; JOINED.  
 CC EMBL, L00393; AAA52764.1; JOINED.  
 CC EMBL, L00394; AAA52764.1; JOINED.  
 CC EMBL, L00395; AAA52764.1; JOINED.  
 CC EMBL, L00396; AAA52764.1; JOINED.  
 CC EMBL, M22613; AAA51984.1; -;  
 CC EMBL, K01886; AAA52486.1; -;  
 CC EMBL, M33297; AAA52636.1; -;  
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 CC PIR, A25853; A25853.  
 CC PIR, A24478; A24478.  
 CC PDB, IHCG; 08-MAY-95.  
 CC PDB, IFXK; 29-OCT-97.  
 CC PDB, IFXY; 17-JUN-98.  
 CC PDB, 1XKA; 23-MAR-99.  
 CC PDB, 1XKB; 23-MAR-99.  
 CC MEROPS, S01.216; -;  
 CC GlycoSuiteDB, P00742; -;  
 CC Genew; HGNC:3528; F10.  
 CC MIM; 227600; -;  
 CC InterPro; IPR000152; Asx\_hydroxyl.  
 CC InterPro; IPR001314; Chymotrypsin.  
 CC InterPro; IPR000561; EGF-like.  
 CC InterPro; IPR000742; EGF-2.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR002383; GLA\_blood.  
 CC InterPro; IPR001254; Ser\_protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00008; EGF; 2.  
 CC Pfam; PF00089; trypsin; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PRINTS; PR00001; GLABLOOD.  
 CC SMART; SM00179; EGF\_CA; 1.  
 CC SMART; SM00001; EGF\_like; 1.  
 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; TYP\_SPC; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 2.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC PROSITE; PS02040; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC GlycoProtein; Hydroxylase; Serine protease; Plasma; Blood coagulation;  
 CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 CC Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.  
 CC FT SIGNAL 1 31 POTENTIAL.  
 CC FT PROPEP 32 40  
 CC FT CHAIN 41 179 FACTOR X LIGHT CHAIN.  
 CC FT CHAIN 183 488 FACTOR X HEAVY CHAIN.  
 CC FT PROPEP 183 234 ACTIVATION PEPTIDE.



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FT CHAIN 235 488 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 165 EGF-LIKE 2.
FT DOMAIN 235 488 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 103 103 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 199 199 HYDROXYLATION.
FT CARBOHYD 211 211 O-LINKED (GALNAC. . .).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
FT CARBOHYD 231 231 /FTID=CAR_000012.
FT CARBOHYD 231 231 /FTID=CAR_000013.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 322 322 CHARGE RELAY SYSTEM.
FT ACT_SITE 419 419 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 CHARGE RELAY SYSTEM.
FT DISULFID 95 110
FT DISULFID 112 121
FT DISULFID 129 140

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Query Match 49.0%; Score 94; DB 1; Length 488;  
 Best Local Similarity 38.6%; Pred. No. 9.1e-09;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Oy 1 ANAFLLXLRDGLKXCKXQCSFYXAFIFKDAKRTKLFWISY 44
Db 41 ANSFLEMKKGLHRECMETCSYEAREVFEDSDKTFNFMKY 84

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RESULT 10
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DC 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DB Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGilivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Entfeld D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin

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RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492. CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Entfeld D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233. AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=7305314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjork I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sumernagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";

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RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sumnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,  
 RW Trethewell J.;  
 RT "The relative orientation of Ca2+ binding and EGF domains in coagulation  
 factor X is altered by Ca2+ binding to the first EGF domain. A  
 combined NMR-small angle X-ray scattering study.";  
 RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 -----  
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 CC EMBL; X00673; CAA25286.1; -.  
 DR PIR; A00925; EXBO.  
 DR PDB; IAPC; 31-JAN-94.  
 DR PDB; ICCF; 31-MAY-94.  
 DR PDB; 1MHE; 15-MAY-97.  
 DR PDB; 1MHF; 15-MAY-97.  
 DR MEROPS; S01.216; -.  
 DR GlycoSuiteDB; P00743; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA blood.  
 DR InterPro; IPR001254; Ser-protease\_Try.  
 DR InterPro; IPR000294; Vitr\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS0186; EGF\_2; 2.  
 DR PROSITE; PS0187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.

| FT | SIGNAL   | 1   | 23  | POTENTIAL.                               |
|----|----------|-----|-----|--|
| FT | PROPEP   | 24  | 40  | FACTOR X LIGHT CHAIN.                    |
| FT | CHAIN    | 41  | 180 | FACTOR X HEAVY CHAIN.                    |
| FT | CHAIN    | 183 | 492 | ACTIVATION PEPTIDE.                      |
| FT | PROPEP   | 183 | 233 | ACTIVATED FACTOR XA, HEAVY CHAIN.        |
| FT | CHAIN    | 234 | 492 | MAY BE REMOVED BUT IS NOT NECESSARY FOR  |
| FT | PROPEP   | 476 | 492 | ACTIVATION.                              |
| FT | DOMAIN   | 86  | 122 | EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN   | 125 | 165 | EGF-LIKE 2.                              |
| FT | DOMAIN   | 234 | 492 | SERINE PROTEASE.                         |
| FT | ACT SITE | 275 | 275 | CHARGE RELAY SYSTEM.                     |
| FT | ACT SITE | 321 | 321 | CHARGE RELAY SYSTEM.                     |
| FT | ACT SITE | 418 | 418 | CHARGE RELAY SYSTEM.                     |
| FT | MOD_RES  | 46  | 46  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 47  | 47  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 54  | 54  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 56  | 56  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 59  | 59  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 60  | 60  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 65  | 65  | GAMMA-CARBOXYGLUTAMIC ACID.              |
| FT | MOD_RES  | 66  | 66  | GAMMA-CARBOXYGLUTAMIC ACID.              |

Query Match 49.0%; Score 94; DB 1; Length 492;  
 Best Local Similarity 40.9%; Pred. No. 9.2e-09;  
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

DB 41 ANSFLEVKQGNLRECEBACSLFEARVFDABGTDFMSKY 84

RESULT 11  
 TMG1 HUMAN  
 ID 014658; STANDARD; PRT; 218 AA.  
 AC 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-  
 rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein  
 1).  
 OS Homo sapiens (Human).  
 GN PRG1 OR TMG1 OR PRG1.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97404347; PubMed=9256434;  
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;  
 RT "Primary structure and tissue distribution of two novel proline-rich  
 gamma-carboxyglutamic acid proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.  
 CC -1- PTM: Gla residues are produced after subsequent posttranslational  
 modifications of glutamic acid by a vitamin K-dependent gamma-  
 carboxylase.  
 -----  
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 -----  
 CC EMBL; AF009242; AAB67070.1; -.  
 DR HSSP; P00740; ICFH.  
 DR Genew; HGNC:9469; PRG1.  
 DR MIM; 604428; -.  
 DR InterPro; IPR002383; GLA blood.  
 DR InterPro; IPR000294; Vitr\_dep\_GLA.

DR Pfam; PF00594; glaf; 1.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SMO0069; GLA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 KW Gamma-carboxylutamic acid; Vitamin K; Transmembrane.  
 FT PROPEP 1 20  
 FT CHAIN 21 218  
 FT DOMAIN 21 83  
 FT TRANSMEM 84 106  
 FT DOMAIN 107 218  
 FT DOMAIN 24 61  
 FT DOMAIN 131 135  
 FT SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;  
 Query Match 47.9%; Score 92; DB 1; Length 218;  
 Best Local Similarity 38.6%; Pred. No. 9.2e-09;  
 Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;  
 OY 1 ANAFLLXLRDGLRXKXKXQCSFXXAFIFDAXRTKLFWTSY 44  
 DB 21 ANGFEERIGNIEKCEBFCFEERARBAFENNEKTFEWSY 64  
 RESULT 12  
 THRB\_HUMAN STANDARD; PRT; 622 AA.  
 AC P00734;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).  
 GN F2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88077877; PubMed=2825773;  
 RA Degen S.J.F., Davie E.W.;  
 RT "Nucleotide sequence of the gene for human prothrombin.";  
 RL Biochemistry 26:6165-6177(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT MET-165.  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Ozuna M., Poel C.L., Toth E.J., Yi O., Nickerson D.A.;  
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 8-622 FROM N.A.  
 RX MEDLINE=83231469; PubMed=6305407;  
 RA Degen S.J.F., McMillin R.T.A., Davie E.W.;  
 RT "Characterization of the complementary deoxyribonucleic acid and gene  
 coding for human prothrombin.";  
 RL Biochemistry 22:2087-2097(1983).  
 RN [4]  
 RP SEQUENCE OF 44-314.  
 RX MEDLINE=77193964; PubMed=266717;  
 RA Walz D.A., Hewett-Emmett D., Seegers W.H.;  
 RT "Amino acid sequence of human prothrombin fragments 1 and 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).  
 RN [5]  
 RP SEQUENCE OF 315-622.  
 RX MEDLINE=77207112; PubMed=8739923;  
 RA Butkowsky R.J., Blon J., Downing M.R., Mann K.G.;  
 RT "Primary structure of human prothrombin 2 and alpha-thrombin.";  
 RL J. Biol. Chem. 252:4942-4957(1977).  
 RN [6]  
 RP PROCESSING.  
 RX MEDLINE=87008532; PubMed=3759958;  
 RA Rabiet M.J., Blachin A., Furie B.C.;  
 RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin  
 activation in human plasma.";  
 RL J. Biol. Chem. 261:13210-13215(1986).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=90059942; PubMed=2583108;  
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;  
 RT "The refined 1.9 A crystal structure of human alpha-thrombin:  
 interaction with D-Phe-Pro-Arg chloromethylketone and significance of  
 the Tyr-Pro-Tyr insertion segment.";  
 RL EMBO J. 8:3467-3475(1989).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=90327074; PubMed=2374926;  
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,  
 RA Roitisch C., Fenton J.W. II;  
 RT "The structure of a complex of recombinant hirudin and human alpha-  
 thrombin.";  
 RL Science 249:277-280(1990).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=94350942; PubMed=8071320;  
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,  
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;  
 RT "Crystallographic structure of human gamma-thrombin.";  
 RL J. Biol. Chem. 269:22000-22006(1994).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=97357286; PubMed=9214615;  
 RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,  
 RA Esmion C.T., Stubbs M.T.;  
 RT "The thrombin E192Q-BPTI complex reveals gross structural  
 rearrangements: implications for the interaction with antithrombin  
 and thrombomodulin.";  
 RL EMBO J. 16:2977-2984(1997).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.  
 RX MEDLINE=99162521; PubMed=10051558;  
 RA Guinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;  
 RT "Unexpected crucial role of residue 225 in serine proteases.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).  
 RN [12]  
 RP VARIANT BARCELONA.  
 RX MEDLINE=87033739; PubMed=3771562;  
 RA Rabiet M.-J., Furie B.C., Furie B.;  
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine  
 for arginine at residue 273.";  
 RL J. Biol. Chem. 261:15045-15048(1986).  
 RN [13]  
 RP VARIANT FRANKFURT.  
 RX MEDLINE=95313001; PubMed=7792730;  
 RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharer I.;  
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by  
 substitution of Glu-466 by Ala.";  
 RL Thromb. Haemost. 73:203-209(1995).  
 RN [14]  
 RP VARIANTS HIMI-1 AND HIMI-2.  
 RX MEDLINE=93043342; PubMed=1421398;  
 RA Morishita E., Saito M., Kunabashiri I., Asakura H., Matsuda T.,  
 RA Yamaguchi K.;  
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional  
 prothrombin molecules (Met-337-->Thr and Arg-388-->His).";  
 RL Blood 80:2275-2280(1992).  
 RN [15]  
 RP VARIANT PADUA-1.  
 RX MEDLINE=95169989; PubMed=7865694;  
 RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;  
 RT "Prothrombin Padua I: incomplete activation due to an amino acid  
 substitution at a factor Xa cleavage site.";  
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).  
 RN [16]  
 RP VARIANT QUICK-1.  
 RX MEDLINE=89207504; PubMed=3242619;  
 RA Henriksen R.A., Mann K.G.;  
 RT "Identification of the primary structural defect in the dysfibrinogen  
 Quick-1.";







CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION  
CC OF PROTHROMBIN TO THROMBIN.  
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A  
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &  
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES  
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &  
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR  
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF  
CC THROMBIN.  
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL  
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION  
CC BY FACTOR XA.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.  
CC -----  
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CC or send an email to [license@ibt-sib.ch](mailto:license@ibt-sib.ch)).  
CC -----  
DR EMBL; X52308; CAA36548.1; -  
DR PIR; A35827; A35827.  
DR HSSP; P00734; 1B7X.  
DR MEROPS; S01.217; -.  
DR MGD; MGI:88380; F2.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR002383; GLA blood.  
DR InterPro; IPR000001; Kringle.  
DR InterPro; IPR003966; Prothrombin.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00051; Kringle; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR PRINTS; PR00018; KRINGLE.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR ProDom; PD000395; Kringle; 2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00130; KR; 2.  
DR SMART; SM00020; Tryp\_Spec; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 2.  
DR PROSITE; PS00070; KRINGLE\_2; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;  
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;  
KW Hydrolyase; Serine protease; Kringle; Signal.  
FT SIGNAL; 1 24  
FT PROPEP 25 43  
FT CHAIN 44 618  
FT PEPTIDE 44 200  
FT PEPTIDE 201 324  
FT CHAIN 325 360  
FT CHAIN 361 618  
FT DOMAIN 109 187  
FT DOMAIN 215 292  
FT DOMAIN 361 618  
FT SITE 200 201  
FT SITE 324 325  
FT SITE 360 361  
FT ACT\_SITE 403 403  
FT ACT\_SITE 459 459  
FT ACT\_SITE 565 565  
FT MOD\_RES 50 50  
FT MOD\_RES 51 51  
POTENTIAL.  
PROTHROMBIN.  
ACTIVATION PEPTIDE (FRAGMENT 1).  
ACTIVATION PEPTIDE (FRAGMENT 2).  
THROMBIN LIGHT CHAIN (A).  
THROMBIN HEAVY CHAIN (B).  
KRINGLE 1.  
KRINGLE 2.  
SERINE PROTEASE.  
CLEAVAGE (BY THROMBIN).  
CLEAVAGE (BY FACTOR XA).  
CLEAVAGE (BY FACTOR XA).  
CHARGE RELAY SYSTEM (BY SIMILARITY).  
CHARGE RELAY SYSTEM (BY SIMILARITY).  
CHARGE RELAY SYSTEM (BY SIMILARITY).  
CHARGE RELAY SYSTEM (BY SIMILARITY).  
GAMMA-CARBOXYGLUTAMIC ACID.  
GAMMA-CARBOXYGLUTAMIC ACID.

FT MOD\_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.  
FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
FT DISULFID 61 66 BY SIMILARITY.  
FT DISULFID 91 104 BY SIMILARITY.  
FT DISULFID 109 187 BY SIMILARITY.  
FT DISULFID 130 170 BY SIMILARITY.  
FT DISULFID 158 182 BY SIMILARITY.  
FT DISULFID 215 293 BY SIMILARITY.  
FT DISULFID 236 276 BY SIMILARITY.  
FT DISULFID 264 288 BY SIMILARITY.  
FT DISULFID 333 479 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 388 404 BY SIMILARITY.  
FT DISULFID 533 547 BY SIMILARITY.  
FT DISULFID 561 591 BY SIMILARITY.  
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).  
FT SEQUENCE 618 AA; 70268 MW; B89P719AFAFD601B0 CRC64;

Query Match 45.8%; Score 88; DB 1; Length 618;  
Best Local Similarity 39.5%; Pred. No. 1.3e-07;  
Matches 17; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NAFLLXLRDGSIXRXCKXQCSFFXAXFIFDAXRTKLFWISY 44  
Db 46 SGFLEELKNGNLERECVEQCSYEAEFALESPOOTDVFWMKY 88

Search completed: March 19, 2003, 14:52:51  
Job time : 6.625 secs

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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:32 ; Search time 46.1875 Seconds  
(without alignments)  
196.288 Million cell updates/sec

Title: 10ASP28PHE  
Perfect score: 192  
Sequence: 1 ANAFLLXRLRDSLRXCCKX.....XXAFIFXDAXRTLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 156   | 81.2        | 701    | 4 Q96PQ8  | Q96PQ8 homo sapien  |
| 2          | 111   | 57.8        | 446    | 11 Q61109 | Q61109 mus musculus |
| 3          | 97    | 50.5        | 460    | 11 Q91WN8 | Q91WN8 mus musculus |
| 4          | 92    | 47.9        | 100    | 4 Q15253  | Q15253 homo sapien  |
| 5          | 91    | 47.4        | 460    | 11 Q99PC6 | Q99PC6 mus musculus |
| 6          | 88    | 45.8        | 482    | 11 Q63207 | Q63207 ratu         |
| 7          | 87    | 45.3        | 456    | 6 Q9GMD9  | Q9GMD9 canis fami   |
| 8          | 86    | 44.8        | 469    | 6 Q9GMD9  | Q9GMD9 ornithorh    |
| 9          | 86    | 44.8        | 481    | 11 Q54740 | Q54740 mus musculu  |
| 10         | 86    | 44.8        | 481    | 11 Q99132 | Q99132 mus musculu  |
| 11         | 86    | 44.8        | 481    | 11 Q88947 | Q88947 mus musculu  |
| 12         | 86    | 44.8        | 481    | 11 Q95ME8 | Q95ME8 bos taurus   |
| 13         | 75    | 33.1        | 456    | 4 Q14316  | Q14316 homo sapien  |
| 14         | 75    | 33.1        | 461    | 6 Q95ND7  | Q95ND7 pan troglod  |
| 15         | 75    | 33.1        | 461    | 6 Q95ND6  | Q95ND6 pan troglod  |
| 16         | 73    | 38.0        | 179    | 4 Q8TRAS3 | Q8TRAS3 homo sapien |

|    |      |      |     |           |                     |
|----|------|------|-----|-----------|---------------------|
| 17 | 73   | 38.0 | 198 | 11 Q8R182 | Q8R182 mus musculus |
| 18 | 71   | 37.0 | 138 | 6 Q28994  | Q28994 sus scrofa   |
| 19 | 70   | 36.5 | 108 | 3 Q9PTW7  | Q9PTW7 struthio ca  |
| 20 | 67   | 34.9 | 433 | 13 Q90YK1 | Q90YK1 brachydanio  |
| 21 | 67   | 34.9 | 607 | 13 Q91001 | Q91001 gallus gall  |
| 22 | 62   | 32.3 | 98  | 13 P82807 | P82807 notechis sc  |
| 23 | 62   | 32.3 | 648 | 6 Q29094  | Q29094 sus scrofa   |
| 24 | 59   | 30.7 | 399 | 11 Q9COW3 | Q9COW3 mus musculus |
| 25 | 57   | 29.7 | 650 | 4 Q9NSD0  | Q9NSD0 homo sapien  |
| 26 | 57   | 29.7 | 650 | 4 Q16519  | Q16519 homo sapien  |
| 27 | 55.5 | 28.9 | 431 | 10 Q94EY5 | Q94EY5 arabidopsis  |
| 28 | 55.5 | 28.9 | 492 | 10 Q9SMU7 | Q9SMU7 cicer ariet  |
| 29 | 55.5 | 28.9 | 543 | 10 Q9MB23 | Q9MB23 arabidopsis  |
| 30 | 55.5 | 28.9 | 576 | 10 Q9CV34 | Q9CV34 arabidopsis  |
| 31 | 55.5 | 28.9 | 589 | 10 Q9LMS2 | Q9LMS2 arabidopsis  |
| 32 | 54.5 | 28.4 | 196 | 10 Q04284 | Q04284 selaginella  |
| 33 | 53.5 | 27.9 | 459 | 10 Q9SE22 | Q9SE22 oryza sativ  |
| 34 | 53   | 27.6 | 25  | 11 Q9QVH6 | Q9QVH6 ratu         |
| 35 | 52.5 | 27.3 | 506 | 10 Q9SEPO | Q9SEPO oryza sativ  |
| 36 | 52.5 | 27.3 | 506 | 10 Q9SE23 | Q9SE23 oryza sativ  |
| 37 | 52.5 | 27.3 | 542 | 5 Q8T613  | Q8T613 halocynthia  |
| 38 | 52.5 | 27.3 | 567 | 10 Q8M4J2 | Q8M4J2 arabidopsis  |
| 39 | 51.5 | 26.8 | 510 | 10 Q9MB22 | Q9MB22 arabidopsis  |
| 40 | 51.5 | 26.8 | 619 | 10 Q9LV37 | Q9LV37 arabidopsis  |
| 41 | 49.5 | 25.8 | 588 | 10 Q9LM33 | Q9LM33 arabidopsis  |
| 42 | 49.5 | 25.8 | 603 | 10 Q9LP67 | Q9LP67 arabidopsis  |
| 43 | 48.5 | 25.8 | 606 | 10 Q9SJC9 | Q9SJC9 arabidopsis  |
| 44 | 48.5 | 25.8 | 651 | 10 Q8S218 | Q8S218 oryza sativ  |
| 45 | 48.5 | 25.3 | 575 | 10 Q94E17 | Q94E17 oryza sativ  |

## ALIGNMENTS

RESULT 1  
Q96PQ8 PRELIMINARY: PRT; 701 AA.  
ID Q96PQ8  
AC Q96PQ8: 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Factor VII active site mutant immunocongulate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034;  
RA Hu Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
RT cells for immunotherapy in mouse models of prostatic cancer.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
DR EMBL: AF272774; AAK58686.1; -.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF 2.  
DR InterPro: IPR001881; EGF-Ca.  
DR InterPro: IPR003066; IG\_MHC.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; gla; 1.  
DR Pfam: PF00047; Ig; 2.  
DR Pfam: PF00089; trypsin; 1.  
DR SMART: SMO0181; EGF\_2.  
DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE: PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE: PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KM Hydrolase; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 81.2%; Score 156; DB 4; Length 701;  
Best Local Similarity 72.7%; Pred. No. 1.6e-20;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRXXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 61 ANAFLELRPGSLERCKEQCSFEERARLIFKHRTKLFWISY 104

## RESULT 2

061109 PRELIMINARY; PRT; 446 AA.  
AC 061109;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Coagulation factor VII.  
GN F7 OR FVII.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA MEDLINE=96276538; PubMed=8701412;

RA Idueggle E., Rosen E., Geng J.P., Carmeliet P., Collen D.,

RA Castellino F.J.;

RT "Characterization of a cDNA encoding murine coagulation factor VII.";

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY.

DR EMBL; U44795; AAC52570.1; -.

DR HSSP; P08709; 1FAK.

DR MEROPS; S01.215; -.

DR MGD; MGI:109325; F7.

DR InterPro; IPR002086; Aldehyde\_dehydr.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR002383; GLA\_blood.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR Pfam; PR00008; EGF\_2.

DR Pfam; PR00594; Glu\_1.

DR Pfam; PR00089; trypsin\_1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF\_CA\_1.

DR SMART; SM00001; EGF\_like\_1.

DR SMART; SM00069; GLA\_1.

DR SMART; SM00020; Tryp\_Spc\_1.

DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00025; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS01187; EGF\_CA\_1.

DR PROSITE; PS00011; GLUTCARBOXYLATION; 1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;

KW Serine protease.

SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 57.8%; Score 111; DB 11; Length 446;

Best Local Similarity 54.5%; Pred. No. 2.9e-12;  
Matches 24; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRXXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 42 ANSLEELRPGSLERCKEQCSFEERARLIFKSPEHTKQFWIVY 85

## RESULT 3

091WN8 PRELIMINARY; PRT; 460 AA.

AC 091WN8;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to protein C.

GN PROC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Strauberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC01896; AAH1896.1; -.

DR MGD; MGI:97771; Proc.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VltK\_dep\_GLA.

DR Pfam; PR00008; EGF\_2.

DR Pfam; PR00594; Glu\_1.

DR Pfam; PR00089; trypsin\_1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS00186; EGF\_2; UNKNOWN\_2.

DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.

DR PROSITE; PS00011; GLUTCARBOXYLATION; UNKNOWN\_1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.

KM Hydrolase; Serine protease.

SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 50.5%; Score 97; DB 11; Length 460;  
Best Local Similarity 45.5%; Pred. No. 1.3e-09;  
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRXXCKXQCSFXXAFIFKDXARTKLFWISY 44  
Db 42 ANSLEELRPGSLERCKEQCSFEERARLIFKQVEDTLAFWIKY 85

RESULT 4  
015253 PRELIMINARY; PRT; 100 AA.  
AC 015253;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Thrombin precursor (Fragment).

GN F2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=87182874; PubMed=3471151;

RA MacGillivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;

"Recombinant genetic approaches to functional mapping of thrombin."  
RL Ann. N.Y. Acad. Sci. 485:73-79(1986).  
DR EMBL; M33031; AAA60220.1; -.  
DR HSSP; P00735; 2PRL.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00069; GLA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
KW Signal.  
FT SIGNAL 1 43 POTENTIAL.  
FT CHAIN 44 >100 POTENTIAL.  
FT NON\_TER 100 100  
SQ SEQUENCE 100 AA; 11302 MW; FDOE5D0174E1F6FE CRC64;  
Query Match 47.9%; Score 92; DB 4; Length 100;  
Best Local Similarity 38.6%; Pred. No. 2.3e-09;  
Matches 17; Conservative 6; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRDGLRXKXCKXOCSEFXKAFIFPDAXRTKLFWISY 44  
Db 44 ANFLEVRKGNLRECVETCSYEAFALSSSTATDVFWMKY 87  
RESULT 5  
Q99PC6 PRELIMINARY; PRT; 460 AA.  
AC Q99PC6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Anticoagulant protein C.  
GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL;  
RA Korf I.;  
RT "Complete sequence of UC72A01."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; AF318182; AAK07918.1; -.  
DR HSSP; P04070; 1PCU.  
DR MEROPS; S01.218; -.  
DR MGD; MGI:97771; Proc.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR Ca InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00001; EGF\_like; 2.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; Asx\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease.  
SQ SEQUENCE 460 AA; 51784 MW; 0293BC259D3ED16 CRC64;  
Query Match 47.4%; Score 91; DB 11; Length 460;  
Best Local Similarity 43.2%; Pred. No. 1.8e-08;  
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRDGLRXKXCKXOCSEFXKAFIFPDAXRTKLFWISY 44  
Db 42 ANFLEVRKGNLRECVETCSYEAFALSSSTATDVFWMKY 85  
RESULT 6  
Q63207 PRELIMINARY; PRT; 482 AA.  
AC Q63207;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Factor X.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE=96093366; PubMed=8578539;  
RA Statton C., Ross R.P., Hutson S., Wallin R.;  
RT "Evidence for competition between vitamin K-dependent clotting factors  
RT for intracellular processing by the vitamin K-dependent gamma-  
RT carboxylase".  
RL Thromb. Res. 80:63-73(1995).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; X79807; CAA56202.1; -.  
DR HSSP; P00742; 1XKA.  
DR MEROPS; S01.216; -.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_like; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; Asx\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease.  
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;  
Query Match 45.8%; Score 88; DB 11; Length 482;  
Best Local Similarity 38.6%; Pred. No. 6.9e-08;  
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKQCSFXAEXIFKQAKRTKLFWISY 44  
Db 41 ANSFEEIKKGNLERECVEEICSFEEAREVEFDNEKTEFFWNKY 84

## RESULT 7

ID Q9TTR0 PRELIMINARY; PRT; 456 AA.  
AC Q9TTR0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Protein C precursor.  
GN PROC.  
OC Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,  
RA Brenig B.;  
RT "Molecular characterization and chromosomal assignment of the canine  
RT protein C gene";  
RL Mamm. Genome 10:135-139 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99371952; PubMed=10443005;  
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;  
RT "Analysis of canine protein C gene polymorphisms";  
RL Anim. Genet. 30:237-238 (1999).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL: AJ001979; CA05126.1; -.  
DR HSSP: P04070; 1PCU.  
DR MEROPS: S01.218; -.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; gla\_1.  
DR Pfam: PF00089; trypsin\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00069; GLA\_1.  
DR SMART: SM00020; TRYP\_SPC\_1.  
DR PROSITE: PS00010; ASX\_HYDROXYL\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_Ca\_1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;  
KW Hydroxylation; Repeat; Serine protease; Signal.  
FT SIGNAL 1 42 POTENTIAL.  
FT CHAIN 43 192 PROTEIN C LIGHT CHAIN.  
FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.  
FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.  
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

## Query Match

Best local Similarity 45.3%; Score 87; DB 6; Length 456;  
Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKQCSFXAEXIFKQAKRTKLFWISY 44

Db 43 ANSFEEIRAGSLERECMEICDFEAKELFQNVDDTLAWSKY 86

## RESULT 8

ID Q9GMD9 PRELIMINARY; PRT; 469 AA.  
AC Q9GMD9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Coagulation factor X.  
OS Ornithorhynchus anatinus (Duckbill platypus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.  
OX NCBI\_TaxID=9258;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21015017; PubMed=1132153;  
RA Poorafshar M., Aveskog M., Munday B., Helman L.;  
RT "Identification and structural analysis of four serine proteases in a  
RT monotreme, the platypus, Ornithorhynchus anatinus";  
RL Immunogenetics 52:19-28 (2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL: AF275654; AAG00453.1; -.  
DR HSSP: P00742; 1XKB.  
DR MEROPS: S01.216; -.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF\_2.  
DR Pfam: PF00594; gla\_1.  
DR Pfam: PF00089; trypsin\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00179; EGF\_Ca\_1.  
DR SMART: SM00001; EGF\_like\_2.  
DR SMART: SM00069; GLA\_1.  
DR SMART: SM00020; TRYP\_SPC\_1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_Ca\_1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

## Query Match

Best local Similarity 44.8%; Score 86; DB 6; Length 469;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLRCKXKQCSFXAEXIFKQAKRTKLFWISY 44  
Db 41 ANSFEEIKKGNLERECNEETCSYEAREVEFDXTNEFWNIY 84

## RESULT 9

ID Q54740 PRELIMINARY; PRT; 481 AA.  
AC Q54740;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Coagulation factor X precursor (EC 3.4.21.6).

```
GN F10 OR FA10.
OS Mus musculus (Mouse).
OG Plasmid pluscript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Konnermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; IXXA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 1.
DR SMART; SM00179; EGF_like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Plasmid;
KM Repeat; Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5EF9D97AE CRC64;

Query Match 44.8%; Score 86; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 1.7e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAPLXLRLDGSILRXKCKXQCSFXAXFIPDXARTKLFWSY 44
Db 41 ANSFPEEFKGNLBRRCMEICSYEVRBIFEDDEKTYXWTKY 84

RESULT 10
O99132 PRELIMINARY; PRT; 481 AA.
AC O99132;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coagulation factor X.
GN F10
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; BC003877; AA03877.1; -.
DR HSSP; P00742; IXXA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vltk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00001; EGF_CA; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Calcium-binding; EGF-like domain; Glycoprotein; Hydrolyase; Repeat;
KM Serine protease.
SQ SEQUENCE 481 AA; 54004 MW; BD88B96C9A0B7E7F CRC64;

Query Match 44.8%; Score 86; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 1.7e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 1 ANAPLXLRLDGSILRXKCKXQCSFXAXFIPDXARTKLFWSY 44
Db 41 ANSFPEEFKGNLBRRCMEICSYEVRBIFEDDEKTYXWTKY 84

RESULT 11
O88947 PRELIMINARY; PRT; 481 AA.
AC O88947;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coagulation factor X precursor.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX STRAIN=C57BL/6 X CBA; PubMed=9684791;
RX MEDLINE=98347933; PubMed=9684791;
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,
RA Castellino F.J., Rosen E.D.;
RT "Cloning and characterization of a cDNA encoding murine coagulation
RT factor X.";
RL Thromb. Haemost. 80:87-91(1998).
RN [2]
RP SEQUENCE FROM N.A.
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RC STRAIN=1295J;
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
RT "Cloning and Characterization of the Murine Factor X Gene.";
RT Thromb Haemost. 0:0-0(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AF087644; AAC36345.1; -.
DR EMBL; AF211347; AAC22980.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MG1.103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00001; EGF_1like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease; Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EFPD271E CRC64;

Query Match 44.8%; Score 86; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 1.7e-07;
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLLXLRDQSLKRXKXQCSFXAXFIFKDAKRTKLFWISY 44
DB 41 ANSFEEFKKGNLERECMEECISYEVEEIFEDEKTKYWTXY 84

RESULT 12
ID Q95ME8 PRELIMINARY; PRT; 49 AA.
AC Q95ME8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coagulation factor IX (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizlata M.N., Amara E.J.;
RT "Partial sequence of bovine F9 coding gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394598; AAK7555.1; -.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

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FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6023 MW; DISCEDE9CCBA4A14 CRC64;

Query Match 40.6%; Score 78; DB 6; Length 49;
Best Local Similarity 41.2%; Pred. No. 4.6e-07;
Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 11 GSLKRXKXQCSFXAXFIFKDAKRTKLFWISY 44
DB 15 GNLRECKEKCKCSFEAREVFENTKTEFMWQY 48

RESULT 13
ID Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (plasma THROMBOPLASTIC component, Christmas
DE disease, HAEMOPHILIA B) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RX MEDLINE=88327116; PubMed=3416069;
RA Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076 (1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; 1CFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF_1-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; GLA_blood.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0010; EGF_BLOOD.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

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Query Match 39.1%; Score 75; DB 4; Length 456;  
Best Local Similarity 41.2%; Pred. No. 1.9e-05;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLRXCKXKXQCSFXKXFIKDAKRTKLFWISY 44  
Db 53 GNLERECMEKCSFEARREVENTERTEFWKQY 86

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DT 01-DEC-2001 (TRENBLrel. 19, last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, last annotation update)  
DE Coagulation factor XI.  
GN P9.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
OX NCBI\_Taxid=9598;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=504;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and  
RT chimpanzees.";  
RL Genes Genet. Syst. 0:0-0(2001).  
DR EMBL; AB062470; BAB58885.1; JOINED.  
DR EMBL; AB062458; BAB58885.1; JOINED.  
DR EMBL; AB062460; BAB58885.1; JOINED.  
DR EMBL; AB062462; BAB58885.1; JOINED.  
DR EMBL; AB062464; BAB58885.1; JOINED.  
DR EMBL; AB062466; BAB58885.1; JOINED.  
DR EMBL; AB062468; BAB58885.1; JOINED.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
DR PROSITE; PS00011; GUU\_CARBOXYLATION; UNKNOWN\_1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 39.1%; Score 75; DB 6; Length 461;  
Best Local Similarity 41.2%; Pred. No. 1.9e-05;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLRXCKXKXQCSFXKXFIKDAKRTKLFWISY 44  
Db 58 GNLERECMEKCSFEARREVENTERTEFWKQY 91

## RESULT 15

Q95ND6 PRELIMINARY; PRT; 461 AA.  
AC Q95ND6;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, last annotation update)

DE Coagulation factor XI.

GN P9.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

OX NCBI\_Taxid=9598;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=505;

RA Satta Y.;

RT "Comparison of DNA and protein polymorphisms between humans and

RT chimpanzees.";

RL Genes Genet. Syst. 0:0-0(2001).

DR EMBL; AB062471; BAB58886.1; JOINED.

DR EMBL; AB062459; BAB58886.1; JOINED.

DR EMBL; AB062461; BAB58886.1; JOINED.

DR EMBL; AB062463; BAB58886.1; JOINED.

DR EMBL; AB062465; BAB58886.1; JOINED.

DR EMBL; AB062467; BAB58886.1; JOINED.

DR EMBL; AB062469; BAB58886.1; JOINED.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR InterPro; IPR000294; VltK\_dep\_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.

DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.

DR PROSITE; PS00011; GUU\_CARBOXYLATION; UNKNOWN\_1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; UNKNOWN\_1.

KW Hydrolase; Serine protease.

SQ SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF65B5 CRC64;

Query Match 39.1%; Score 75; DB 6; Length 461;  
Best Local Similarity 41.2%; Pred. No. 1.9e-05;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLRXCKXKXQCSFXKXFIKDAKRTKLFWISY 44  
Db 58 GNLERECMEKCSFEARREVENTERTEFWKQY 91

Search completed: March 19, 2003, 15:13:33  
Job time : 47.3125 secs

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GenCore version 5.1.4.p5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:34 ; Search time 9.75 Seconds  
(without alignments)  
132.780 Million cell updates/sec

Title: 10ASP28PHE  
Perfect score: 192  
Sequence: 1 ANAFLLXLRDGLRCKXCKX.....XAXFIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTCUTS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 165   | 85.9        | 44     | 3     | US-08-955-636-28 Sequence 28, Appli |
| 2          | 163   | 84.9        | 44     | 3     | US-08-955-636-27 Sequence 27, Appli |
| 3          | 159   | 82.8        | 44     | 3     | US-08-955-636-26 Sequence 26, Appli |
| 4          | 156   | 81.2        | 44     | 3     | US-08-955-636-3 Sequence 3, Appli   |
| 5          | 156   | 81.2        | 406    | 1     | US-08-293-778-24 Sequence 24, Appli |
| 6          | 156   | 81.2        | 406    | 1     | US-08-295-411-5 Sequence 5, Appli   |
| 7          | 156   | 81.2        | 406    | 2     | US-08-955-471-5 Sequence 5, Appli   |
| 8          | 156   | 81.2        | 406    | 5     | PCT-US92-10242-5 Sequence 5, Appli  |
| 9          | 156   | 81.2        | 444    | 1     | US-08-475-845-2 Sequence 2, Appli   |
| 10         | 156   | 81.2        | 444    | 2     | US-08-327-690-2 Sequence 2, Appli   |
| 11         | 156   | 81.2        | 444    | 2     | US-08-660-289-2 Sequence 2, Appli   |
| 12         | 156   | 81.2        | 444    | 2     | US-08-537-807-2 Sequence 2, Appli   |
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| 17         | 156   | 81.2        | 444    | 5     | PCT-US94-05779-2 Sequence 2, Appli  |
| 18         | 156   | 81.2        | 466    | 1     | US-07-882-202A-4 Sequence 4, Appli  |
| 19         | 156   | 81.2        | 466    | 1     | US-08-021-615A-4 Sequence 4, Appli  |
| 20         | 156   | 81.2        | 466    | 1     | US-08-321-777-4 Sequence 4, Appli   |
| 21         | 156   | 81.2        | 466    | 4     | US-09-009-217-14 Sequence 14, Appli |
| 22         | 156   | 81.2        | 466    | 4     | US-09-009-656-14 Sequence 14, Appli |
| 23         | 156   | 81.2        | 466    | 5     | PCT-US93-04493-4 Sequence 4, Appli  |
| 24         | 153   | 79.7        | 44     | 3     | US-08-955-636-30 Sequence 30, Appli |
| 25         | 150   | 78.1        | 44     | 3     | US-08-955-636-29 Sequence 29, Appli |
| 26         | 141   | 73.4        | 41     | 1     | US-08-229-280-4 Sequence 4, Appli   |
| 27         | 122   | 63.5        | 44     | 3     | US-08-955-636-4 Sequence 4, Appli   |

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| 28 | 103 | 53.6 | 139 | 1 | US-08-330-978-2  | Sequence 2, Appli  |
| 29 | 103 | 53.6 | 139 | 1 | US-08-474-042-2  | Sequence 2, Appli  |
| 30 | 103 | 53.6 | 139 | 1 | US-08-484-558-2  | Sequence 2, Appli  |
| 31 | 103 | 53.6 | 139 | 1 | US-08-774-592-2  | Sequence 2, Appli  |
| 32 | 103 | 53.6 | 437 | 1 | US-08-487-037-2  | Sequence 2, Appli  |
| 33 | 103 | 53.6 | 437 | 1 | US-08-487-037-3  | Sequence 3, Appli  |
| 34 | 103 | 53.6 | 488 | 1 | US-08-487-037-1  | Sequence 1, Appli  |
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| 36 | 94  | 49.0 | 44  | 3 | US-08-955-636-25 | Sequence 25, Appli |
| 37 | 94  | 49.0 | 44  | 3 | US-08-955-636-35 | Sequence 35, Appli |
| 38 | 94  | 49.0 | 448 | 2 | US-08-295-411-3  | Sequence 3, Appli  |
| 39 | 94  | 49.0 | 448 | 2 | US-08-955-471-3  | Sequence 3, Appli  |
| 40 | 94  | 49.0 | 448 | 5 | PCT-US92-10068-1 | Sequence 1, Appli  |
| 41 | 94  | 49.0 | 448 | 5 | PCT-US92-10242-3 | Sequence 3, Appli  |
| 42 | 94  | 49.0 | 487 | 1 | US-08-469-486-53 | Sequence 53, Appli |
| 43 | 94  | 49.0 | 487 | 2 | US-08-469-658-53 | Sequence 53, Appli |
| 44 | 94  | 49.0 | 492 | 2 | US-08-469-486-2  | Sequence 2, Appli  |
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ALIGNMENTS

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RESULT 1
US-08-955-636-28
; Sequence 28, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-28

Query Match      85.9%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.2e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ANAFLLXLRDGLRCKXCKXCFXAXFIFKDXRTKLFWISY 44
Db 1 ANAFLLXLRDGLRCKXCKXCFXAXFIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neisestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-27

Query Match 84.9%; Score 163; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 2.5e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRDGSIXRXCXXQCSFXXAFIIFKDAKRTKLFWISY 44  
DB 1 ANAFLXXLRDGSIXRXCXXQCSFXXARXIFKDAKRTKLFWISY 44

## RESULT 3

US-08-955-636-26  
Sequence 26, Application US/08955636A  
Patent No. 6017862  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 44  
TYPE: PRF  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-26

Query Match 82.8%; Score 159; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 1.2e-19;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRDGSIXRXCXXQCSFXXAFIIFKDAKRTKLFWISY 44  
DB 1 ANAFLXXLRDGSIXRXCXXQCSFXXARXIFKDAKRTKLFWISY 44

## RESULT 4

US-08-955-636-3  
Sequence 3, Application US/08955636A  
Patent No. 6017862  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 44  
TYPE: PRF  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-3

Query Match 81.2%; Score 156; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 3.7e-19;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANAFLXXLRDGSIXRXCXXQCSFXXAFIIFKDAKRTKLFWISY 44  
DB 1 ANAFLXXLRDGSIXRXCXXQCSFXXARXIFKDAKRTKLFWISY 44

## RESULT 5

US-08-293-778-24  
Sequence 24, Application US/08293778  
Patent No. 5580560  
GENERAL INFORMATION:  
APPLICANT: Nicolaesen, Elise M.  
APPLICANT: Bjorn, Soren E.  
APPLICANT: Wiberg, Finn C.  
APPLICANT: Woodbury, Richard  
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,778  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,509  
FILING DATE:  
APPLICATION NUMBER: DK 3235/87  
FILING DATE: 25-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/434,149  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtib, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129,224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

## Query Match

81.2%; Score 156; DB 1; Length 406;  
Best Local Similarity 72.7%; Pred. No. 3.9e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLXXLRDGSIXRXCXXQCSFXXAFIIFKDAKRTKLFWISY 44  
DB 1 ANAFLXXLRDGSIXRXCXXQCSFXXARXIFKDAKRTKLFWISY 44

## RESULT 6

US-08-295-411-5

```
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5
;
Query Match 81.2%; Score 156; DB 1; Length 406;
Best Local Similarity 72.7%; Pred. No. 3.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRDGLXRXCKXQCSFXXAFIFDAXRTKLFWISY 44
Db 1 ANAFLLELRPGSLERCKEBCQSFEEAREIFDARTKLFWISY 44
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RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
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; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5
;
Query Match 81.2%; Score 156; DB 2; Length 406;
Best Local Similarity 72.7%; Pred. No. 3.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRDGLXRXCKXQCSFXXAFIFDAXRTKLFWISY 44
Db 1 ANAFLLELRPGSLERCKEBCQSFEEAREIFDARTKLFWISY 44
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RESULT 8
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
```

```

: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/10242
: FILING DATE: 19921118
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,989
: FILING DATE: 18-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SCRO472P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 406 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..152
: OTHER INFORMATION: /note="Factor VII Light Chain"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 153..406
: OTHER INFORMATION: /note="Factor VII Heavy Chain"
: PCT-US92-10242-5

Query Match 81.2%; Score 156; DB 5; Length 406;
Best Local Similarity 72.7%; Pred. No. 3.9e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLRXCKXQCSFXXAFKIFKDAKRTKLFWISY 44
Db 1 ANAFLLELRPGSLERCKEQQCSFEAREIFKDAERTKLFWISY 44

RESULT 9
US-08-475-845-2
: Sequence 2, Application US/08475845
: Patent No. 5788965
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stewart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/475,845
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920
: FILING DATE: 28-FEB-1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 13952-8-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-475-845-2

Query Match 81.2%; Score 156; DB 1; Length 444;
Best Local Similarity 72.7%; Pred. No. 4.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLRXCKXQCSFXXAFKIFKDAKRTKLFWISY 44
Db 39 ANAFLLELRPGSLERCKEQQCSFEAREIFKDAERTKLFWISY 82

RESULT 10
US-08-327-690-2
: Sequence 2, Application US/08327690
: Patent No. 5817788
: GENERAL INFORMATION:
: APPLICANT: Berkner, Kathleen L.
: APPLICANT: Petersen, Lars C.
: APPLICANT: Hart, Charles E.
: APPLICANT: Hedner, Ulla
: APPLICANT: Bregengaard, Claus
: TITLE OF INVENTION: Modified Factor VII
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Stewart Street Tower
: CITY: San Francisco
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/327,690
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/065,725
: FILING DATE: 21-MAY-1993
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/662,920

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FILING DATE: 28-FEB-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-327-690-2

Query Match 81.2%; Score 156; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXKXCKXQCSFYXAFIFDAXRTKLFWISY 44  
Db 39 ANAFLELRPGSLRECKEBCQSFPEARIFDAXRTKLFWISY 82

RESULT 11  
US-08-660-289-2  
Sequence 2, Application US/08660289  
Patent No. 5833982  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,289  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,845  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-660-289-2

Query Match 81.2%; Score 156; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXKXCKXQCSFYXAFIFDAXRTKLFWISY 44  
Db 39 ANAFLELRPGSLRECKEBCQSFPEARIFDAXRTKLFWISY 82

RESULT 12  
US-08-537-807-2  
Sequence 2, Application US/08537807  
Patent No. 5861374  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,807  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05779  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 08/065,725  
FILING DATE: 21-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 81.2%; Score 156; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRDGLXKXCKXQCSFYXAFIFDAXRTKLFWISY 44  
Db 39 ANAFLELRPGSLRECKEBCQSFPEARIFDAXRTKLFWISY 82

RESULT 13  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5997864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.

APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 81.2%; Score 156; DB 2; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLDGSLXRCXKXQCSFXXAFIFKDAERTKLFWISY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEERAREIFKDAERTKLFWISY 82

RESULT 14  
US-08-464-233-2  
Sequence 2, Application US/08464233  
Patent No. 6039944  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,233  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-233-2

Query Match 81.2%; Score 156; DB 3; Length 444;  
Best Local Similarity 72.7%; Pred. No. 4.3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFLLXLDGSLXRCXKXQCSFXXAFIFKDAERTKLFWISY 44  
DB 39 ANAFLELRPGSLERCKEQCSFEERAREIFKDAERTKLFWISY 82

RESULT 15  
US-09-189-607-2  
Sequence 2, Application US/09189607  
Patent No. 6168789  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,607  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/660,289  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-189-607-2

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Query Match      81.2%; Score 156; DB 4; Length 444;
Best Local Similarity 72.7%; Pred. No. 4.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY      1 ANAFLLXLRDGLXRXCKXXQCSFXXAPXIFKDAARTKLFWISY 44
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      39 ANAFLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 82

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Search completed: March 19, 2003, 15:16:15  
 Job time : 9.75 secs

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GenCore version 5.1.4 p5 4578  
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## OM protein - protein search, using sw model

Run on: March 20, 2003, 13:27:42 ; Search time 8.375 Seconds

(without alignments)  
280.876 Million cell updates/sec

Title: 10ASP28PNE

Perfect score: 1 ANAFLLXLRDGLRSLXKCKXX.....XAXFIFKDXRTLFWMISY 44

Sequence: 1 ANAFLLXLRDGLRSLXKCKXX.....XAXFIFKDXRTLFWMISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 22153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 22153

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCRT\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 156   | 81.2        | 406    | 9  | US-10-109-498-1    |
| 2          | 92    | 47.9        | 419    | 9  | US-10-182-263-6    |
| 3          | 91    | 47.4        | 419    | 9  | US-10-182-263-3    |
| 4          | 91    | 47.4        | 419    | 9  | US-10-182-263-4    |
| 5          | 91    | 47.4        | 419    | 9  | US-10-182-263-5    |
| 6          | 80    | 41.7        | 419    | 9  | US-10-182-263-1    |
| 7          | 80    | 41.7        | 419    | 9  | US-09-978-917A-4   |
| 8          | 80    | 41.7        | 461    | 9  | US-10-182-263-2    |
| 9          | 80    | 41.7        | 461    | 9  | US-09-978-917A-2   |
| 10         | 75    | 39.1        | 415    | 10 | US-09-118-748-2    |
| 11         | 75    | 39.1        | 461    | 9  | US-10-132-829-5    |
| 12         | 75    | 39.1        | 461    | 10 | US-09-884-901-3    |
| 13         | 66.5  | 34.6        | 96     | 9  | US-09-759-130B-313 |
| 14         | 66.5  | 34.6        | 209    | 9  | US-09-759-130B-310 |
| 15         | 66.5  | 34.6        | 226    | 9  | US-09-759-130B-310 |
| 16         | 51.5  | 26.8        | 95     | 9  | US-09-759-130B-356 |
| 17         | 51.5  | 26.8        | 208    | 9  | US-09-759-130B-355 |
| 18         | 51.5  | 26.8        | 225    | 9  | US-09-759-130B-353 |
| 19         | 44.5  | 23.2        | 729    | 9  | US-10-145-396-11   |

|    |      |      |      |    |                     |                    |
|----|------|------|------|----|---------------------|--------------------|
| 20 | 44   | 22.9 | 273  | 9  | US-09-764-668-968   | Sequence 968, App  |
| 21 | 43.5 | 22.7 | 347  | 10 | US-09-780-053-4     | Sequence 4, Appli  |
| 22 | 43.5 | 22.7 | 730  | 9  | US-10-145-396-12    | Sequence 12, Appli |
| 23 | 43.5 | 22.7 | 730  | 10 | US-09-780-053-2     | Sequence 2, Appli  |
| 24 | 42   | 21.9 | 1266 | 9  | US-09-931-969A-2    | Sequence 2, Appli  |
| 25 | 42   | 21.9 | 1266 | 9  | US-10-079-699-2     | Sequence 2, Appli  |
| 26 | 42   | 21.9 | 1266 | 10 | US-09-757-781-63    | Sequence 63, Appli |
| 27 | 42   | 21.9 | 1356 | 10 | US-09-757-781-2     | Sequence 2, Appli  |
| 28 | 40   | 20.8 | 240  | 9  | US-09-782-504-4     | Sequence 4, Appli  |
| 29 | 40   | 20.8 | 447  | 10 | US-09-815-242-13490 | Sequence 13490, A  |
| 30 | 40   | 20.8 | 447  | 10 | US-09-815-242-13612 | Sequence 13612, A  |
| 31 | 40   | 20.8 | 447  | 10 | US-09-735-564-2     | Sequence 2, Appli  |
| 32 | 39   | 20.3 | 88   | 10 | US-09-811-284-194   | Sequence 194, App  |
| 33 | 39   | 20.3 | 115  | 9  | US-09-883-152-21    | Sequence 21, Appli |
| 34 | 39   | 20.3 | 115  | 9  | US-09-986-480-192   | Sequence 192, App  |
| 35 | 39   | 20.3 | 130  | 9  | US-09-986-480-145   | Sequence 135, App  |
| 36 | 39   | 20.3 | 254  | 9  | US-10-104-019-21    | Sequence 21, Appli |
| 37 | 39   | 20.3 | 744  | 10 | US-09-862-179A-1    | Sequence 1, Appli  |
| 38 | 39   | 20.3 | 873  | 9  | US-10-200-154-2     | Sequence 2, Appli  |
| 39 | 39   | 20.3 | 873  | 10 | US-09-954-043-2     | Sequence 2, Appli  |
| 40 | 39   | 20.3 | 1337 | 10 | US-09-757-781-62    | Sequence 62, Appli |
| 41 | 38.5 | 20.1 | 111  | 10 | US-09-899-896-7     | Sequence 7, Appli  |
| 42 | 38   | 19.8 | 47   | 10 | US-09-739-254-109   | Sequence 109, App  |
| 43 | 38   | 19.8 | 47   | 10 | US-09-904-615-109   | Sequence 109, App  |
| 44 | 38   | 19.8 | 176  | 9  | US-10-078-770-106   | Sequence 106, App  |
| 45 | 38   | 19.8 | 333  | 9  | US-09-738-626-5683  | Sequence 5683, Ap  |

## ALIGNMENTS

RESULT 1  
US-10-109-498-1  
Sequence 1, Application US/10109498  
Publication No. US20030044908A1  
GENERAL INFORMATION:  
APPLICANT: Persson, Egon  
TITLE OF INVENTION: Coagulation Factor VII Derivatives  
FILE REFERENCE: 6286,200-US  
CURRENT APPLICATION NUMBER: US/10/109,498  
CURRENT FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: 60/281,261  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: PA 2001 00477  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 406  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(406)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-109-498-1  
Query Match 81.2%; Score 156; DB 9; Length 406;  
Best Local Similarity 95.5%; Pred. No. 6.4e-20;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Cy 1 ANAFLLXLRDGLRSLXKCKXXCFFXAXFIFKDXRTLFWMISY 44  
Db 1 ANAFLLXLRDGLRSLXKCKXXCFFXAXFIFKDXRTLFWMISY 44  
RESULT 2  
US-10-182-263-6  
Sequence 6, Application US/10182263  
Publication No. US2003002354A1  
GENERAL INFORMATION:  
APPLICANT: Gerlitz, Bruce E  
APPLICANT: Jones, Bryan E

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; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6

Query Match          47.4%; Score 91; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.8e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRDGSIXRCKXXQCSFXXAFXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLEKRCIEICDFEAKKEIFEDVDDTLAFW 41

RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          47.4%; Score 91; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.8e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRDGSIXRCKXXQCSFXXAFXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLEKRCIEICDFEAKKEIFEDVDDTLAFW 41

RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
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; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          47.4%; Score 91; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.8e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRDGSIXRCKXXQCSFXXAFXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLEKRCIEICDFEAKKEIFEDVDDTLAFW 41

RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          47.4%; Score 91; DB 9; Length 419;
Best Local Similarity 48.8%; Pred. No. 2.8e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRDGSIXRCKXXQCSFXXAFXIFKDAKRTKLFW 41
Db 1 ANSFLELRHGSLEKRCIEICDFEAKKEIFEDVDDTLAFW 41

RESULT 6
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Geriltz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-182-263-1

Query Match 41.7%; Score 80; DB 9; Length 419;  
Best Local Similarity 43.9%; Pred. No. 2.6e-06;  
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLRXCKXKQCFXAXFIFDAXRTKLFW 41  
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQVNDTLAFW 41

RESULT 7

US-09-978-917A-4  
Sequence 4, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219u8310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978,917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-917A-4

Query Match 41.7%; Score 80; DB 9; Length 419;  
Best Local Similarity 43.9%; Pred. No. 2.6e-06;  
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLRXCKXKQCFXAXFIFDAXRTKLFW 41  
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQVNDTLAFW 41

RESULT 8

US-10-182-263-2  
Sequence 2, Application US/10182263  
Publication No. US20030022354A1

GENERAL INFORMATION:  
APPLICANT: Gerlitz, Bruce E  
APPLICANT: Jones, Bryan E  
APPLICANT: Ginnell, Brian W  
TITLE OF INVENTION: PROTEIN C DERIVATIVES  
FILE REFERENCE: X-13611  
CURRENT APPLICATION NUMBER: US/10/182,263  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: 60/181948  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: 60/189199  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-182-263-2

Query Match 41.7%; Score 80; DB 9; Length 461;  
Best Local Similarity 43.9%; Pred. No. 2.9e-06;  
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLRXCKXKQCFXAXFIFDAXRTKLFW 41  
Db 43 ANSFLELRHSSLERECIEICDFEAKEIFQVNDTLAFW 83

RESULT 9

US-09-978-917A-2  
Sequence 2, Application US/09978917A  
Publication No. US20030027299A1

GENERAL INFORMATION:  
APPLICANT: Maxygen Aps; Maxygen Holdings  
TITLE OF INVENTION: Protein C or activated protein C-like molecules  
FILE REFERENCE: 0219u8310 - protein C  
CURRENT APPLICATION NUMBER: US/09/978,917A  
CURRENT FILING DATE: 2001-10-17  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(42)  
FEATURE:  
NAME/KEY: CHAIN  
LOCATION: (43)...(461)  
US-09-978-917A-2

Query Match 41.7%; Score 80; DB 9; Length 461;  
Best Local Similarity 43.9%; Pred. No. 2.9e-06;  
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLXLRDGLRXCKXKQCFXAXFIFDAXRTKLFW 41  
Db 43 ANSFLELRHSSLERECIEICDFEAKEIFQVNDTLAFW 83

RESULT 10

US-09-118-748-2  
Sequence 2, Application US/09118748A  
Patent No. US20020031799A1

GENERAL INFORMATION:  
APPLICANT: Stafford, Darrel W.  
APPLICANT: Chang, Jinli  
TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting  
TITLE OF INVENTION: Activlyz  
FILE REFERENCE: 5470-183  
CURRENT APPLICATION NUMBER: US/09/118,748A  
CURRENT FILING DATE: 1998-07-17  
EARLIER APPLICATION NUMBER: 60/053,571  
EARLIER FILING DATE: 1997-07-21  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-118-748-2

Query Match 39.1%; Score 75; DB 10; Length 415;  
Best Local Similarity 41.2%; Pred. No. 2e-05;  
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 11 GSLRXCKXKQCFXAXFIFDAXRTKLFWISY 44  
Db 12 GNLERECMEKCSFEAREVFENTERTEFWKQY 45

RESULT 11

US-10-132-829-5  
Sequence 5, Application US/10132829  
Publication No. US20030044982A1

GENERAL INFORMATION:  
APPLICANT: Chien, Kenneth R  
APPLICANT: Hoshijima, Masahiko  
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII  
FILE REFERENCE: 6627-P41170

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; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-132-829-5

Query Match          39.1%; Score 75; DB 9; Length 461;
Best Local Similarity 41.2%; Pred. No. 2.3e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLRXCKXXQCSFXXAFIFKDXRTKLFWISY 44
DB 58 GNLRECMERKCSFEEAREVFEINTERTEFWKQY 91

RESULT 12
US-09-884-901-3
; Sequence 3, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOFW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homosapien
US-09-884-901-3

Query Match          39.1%; Score 75; DB 10; Length 461;
Best Local Similarity 41.2%; Pred. No. 2.3e-05;
Matches 14; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 11 GSLRXCKXXQCSFXXAFIFKDXRTKLFWISY 44
DB 58 GNLRECMERKCSFEEAREVFEINTERTEFWKQY 91

RESULT 13
US-09-759-130B-313
; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiser, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match          34.6%; Score 66.5; DB 9; Length 96;
Best Local Similarity 36.4%; Pred. No. 0.00014;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY 2 NAF-LXXLRDGLRXCKXXQCSFXXAFIFKDXRTKLFWISY 44
DB 36 NRPDLFTPGNLRECMERKCSFEEAREVFEINTERTEFWKQY 79

RESULT 14
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Frazer, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiser, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 96
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-759-130B-312
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-130B-312

Query Match      34.6%; Score 66.5; DB 9; Length 209;
Best Local Similarity 36.4%; Pred. No. 0.00032;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRDGLXRCXKXCSFXAXFIPDAXRTKLFWISY 44
Db      36 NRPDLFTPGNLERECNBEICNYEAREIFVDEDKTIAFWQY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
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; ORGANISM: Homo sapiens
; US-09-759-130B-310

Query Match      34.6%; Score 66.5; DB 9; Length 226;
Best Local Similarity 36.4%; Pred. No. 0.00035;
Matches 16; Conservative 4; Mismatches 23; Indels 1; Gaps 1;

QY      2 NAF-LXXLRDGLXRCXKXCSFXAXFIPDAXRTKLFWISY 44
Db      53 NRPDLFTPGNLERECNBEICNYEAREIFVDEDKTIAFWQY 96

Search completed: March 20, 2003, 13:30:13
Job time : 9.375 secs
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GenCore version 5.1.4.P5 4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:26 ; Search time 31.375 Seconds  
(without alignments)  
186.869 Million cell updates/sec

Title: 10GLN28GLU  
Perfect score: 190  
Sequence: 1 ANAFLLXLRGSLRXCKX.....XXAEXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
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2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 162   | 85.3        | 44     | AAV18310  | Modified GLA domain |
| 2          | 161   | 84.7        | 44     | AAV18302  | Modified GLA domain |
| 3          | 160   | 84.2        | 44     | AAV18311  | Modified GLA domain |
| 4          | 159   | 83.7        | 44     | AAV18305  | Human factor VII G  |
| 5          | 159   | 83.7        | 44     | AAV18395  | Human factor VII G  |
| 6          | 159   | 83.7        | 401    | AAV184870 | Mutant blood coagu  |
| 7          | 159   | 83.7        | 401    | AAV184871 | Mutant blood coagu  |
| 8          | 159   | 83.7        | 406    | AAV185764 | Factor VII (VII)    |
| 9          | 159   | 83.7        | 406    | AAV14509  | Modified blood coa  |
| 10         | 159   | 83.7        | 406    | AAV14510  | Modified blood coa  |

|    |     |      |     |          |                    |
|----|-----|------|-----|----------|--------------------|
| 11 | 159 | 83.7 | 406 | AAU77745 | Human factor VIIA  |
| 12 | 159 | 83.7 | 406 | AAV52171 | Human FVII SEQ ID  |
| 13 | 159 | 83.7 | 406 | AAV52172 | Mammalian expresse |
| 14 | 159 | 83.7 | 406 | AAV52181 | Human FVII mutant  |
| 15 | 159 | 83.7 | 406 | AAV52182 | Human FVII mutant  |
| 16 | 159 | 83.7 | 406 | AAV52183 | Human FVII mutant  |
| 17 | 159 | 83.7 | 406 | AAV52184 | Human FVII mutant  |
| 18 | 159 | 83.7 | 406 | AAV52185 | Human FVII mutant  |
| 19 | 159 | 83.7 | 406 | AAV52186 | Human FVII mutant  |
| 20 | 159 | 83.7 | 406 | AAV52187 | Human FVII mutant  |
| 21 | 159 | 83.7 | 406 | AAV52188 | Wild-type human b1 |
| 22 | 159 | 83.7 | 406 | AAV52189 | Mutant blood coagu |
| 23 | 159 | 83.7 | 406 | AAV52190 | Mutant blood coagu |
| 24 | 159 | 83.7 | 406 | AAV52191 | Mutant blood coagu |
| 25 | 159 | 83.7 | 406 | AAV52192 | Mutant blood coagu |
| 26 | 159 | 83.7 | 406 | AAV52193 | Human coagulation  |
| 27 | 159 | 83.7 | 406 | AAV52194 | Human coagulation  |
| 28 | 159 | 83.7 | 406 | AAV52195 | Human coagulation  |
| 29 | 159 | 83.7 | 406 | AAV52196 | Human coagulation  |
| 30 | 159 | 83.7 | 406 | AAV52197 | Human coagulation  |
| 31 | 159 | 83.7 | 406 | AAV52198 | Human coagulation  |
| 32 | 159 | 83.7 | 406 | AAV52199 | Human coagulation  |
| 33 | 159 | 83.7 | 406 | AAV52200 | Human coagulation  |
| 34 | 159 | 83.7 | 406 | AAV52201 | Human coagulation  |
| 35 | 159 | 83.7 | 406 | AAV52202 | Human coagulation  |
| 36 | 159 | 83.7 | 406 | AAV52203 | Human coagulation  |
| 37 | 159 | 83.7 | 406 | AAV52204 | Human coagulation  |
| 38 | 159 | 83.7 | 406 | AAV52205 | Human coagulation  |
| 39 | 159 | 83.7 | 406 | AAV52206 | Human coagulation  |
| 40 | 159 | 83.7 | 406 | AAV52207 | Human coagulation  |
| 41 | 159 | 83.7 | 406 | AAV52208 | Human coagulation  |
| 42 | 159 | 83.7 | 406 | AAV52209 | Human coagulation  |
| 43 | 159 | 83.7 | 406 | AAV52210 | Human coagulation  |
| 44 | 159 | 83.7 | 406 | AAV52211 | Human coagulation  |
| 45 | 159 | 83.7 | 406 | AAV52212 | Human coagulation  |

#### ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| AAV18310 | AAV18310 standard; peptide; 44 AA.                                  |
| AC       | AAV18310;   |
| XX       |   |
| DT       | 17-AUG-1999 (first entry)   |
| XX       |   |
| DE       | Modified GLA domain of vitamin K-dependent protein.                 |
| XX       |   |
| KW       | GLA domain; mutain; vitamin K-dependent protein; clotting disorder; |
| KW       | therapy.  |
| XX       |   |
| OS       | Homo sapiens.   |
| OS       | Synthetic.  |
| XX       |   |
| FH       | Key   |
| FT       | Misc-difference 1..44   |
| FT       | Location/Qualifiers   |
| FT       | /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"          |
| XX       |   |
| PN       | MO9920767-A1.   |
| XX       |   |
| PD       | 29-APR-1999.  |
| XX       |   |
| PF       | 20-OCT-1998; 98MO-US22152.  |
| XX       |   |
| PR       | 23-OCT-1997; 97US-0955636.  |
| XX       |   |
| PA       | (MINU ) UNIV MINNESOTA.   |
| XX       |   |
| PI       | Neisestuen Gl;  |
| XX       |   |

DR WPI; 1999-288309/24.  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
  
Query Match 85.3%; Score 162; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 4.2e-20;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ANAFLXXLRGSLXRCCKXXQCSFXXAEXIFPDAXRTKLFWISY 44  
DB 1 ANAFLXXLRGSLXRCCKXXQCSFXXAEXIFPDAXRTKLFWISY 44  
|||||  
  
RESULT 2  
AA18302  
ID AAY18302 standard; peptide; 44 AA.  
XX  
AC AAY18302;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KW therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
FT  
FT  
FT  
FT  
FN W09920767-A1.  
PN  
XX  
XX 29-APR-1999.  
PD  
XX  
XX 20-OCT-1998; 98WO-US22152.  
PF  
XX  
XX 23-OCT-1997; 97US-0955636.  
PR  
XX  
XX (MINU ) UNIV MINNESOTA.  
PA  
XX  
XX Nelsestuen GL;  
PI  
XX  
XX WPI; 1999-288309/24.  
DR  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Claim 11; Page 81; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
XX  
SQ Sequence 44 AA;  
  
Query Match 84.7%; Score 161; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 6.1e-20;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ANAFLXXLRGSLXRCCKXXQCSFXXAEXIFPDAXRTKLFWISY 44  
DB 1 ANAFLXXLRGSLXRCCKXXQCSFXXAEXIFPDAXRTKLFWISY 44  
|||||  
  
RESULT 3  
AA18311  
ID AAY18311 standard; peptide; 44 AA.  
XX  
AC AAY18311;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KW therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  
FT acid"  
FT  
FT  
FT  
FN W09920767-A1.  
PN  
XX  
XX 29-APR-1999.  
PD  
XX  
XX 20-OCT-1998; 98WO-US22152.  
PF  
XX  
XX 23-OCT-1997; 97US-0955636.  
PR  
XX  
XX (MINU ) UNIV MINNESOTA.  
PA  
XX  
XX Nelsestuen GL;  
PI  
XX  
XX WPI; 1999-288309/24.  
DR  
XX  
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
PT acid domain, useful for treating clotting disorders  
XX  
XX  
PS Disclosure; Page 80; 86pp; English.  
XX  
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
  
Query Match 84.2%; Score 160; DB 20; Length 44;  
Best Local Similarity 95.5%; Pred. No. 9.1e-20;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ANAFLXXLRGSLXRCCKXXQCSFXXAEXIFPDAXRTKLFWISY 44  
DB 1 ANAFLXXLRGSLXRCCKXXQCSFXXAEXIFPDAXRTKLFWISY 44  
|||||



|  |  |
|--|--|
| RESULT 4   |  |
| AAI18305   |  |
| ID AAI18305 standard; peptide; 44 AA.  |  |
| XX   |  |
| AC AAI18305;   |  |
| XX   |  |
| DT 17-AUG-1999 (first entry)   |  |
| XX   |  |
| DE Human factor VII GLA domain.  |  |
| XX   |  |
| KM GLA domain; vitamin K-dependent protein; clotting disorder;   |  |
| KW therapy.  |  |
| XX   |  |
| OS Homo sapiens.   |  |
| XX   |  |
| FH Key Location/Qualifiers   |  |
| FT Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic  |  |
| FT FT acid"  |  |
| XX   |  |
| PN W09920767-A1.   |  |
| XX   |  |
| PD 29-APR-1999.  |  |
| XX   |  |
| PF 20-OCT-1998; 98WO-US22152.  |  |
| XX   |  |
| PR 23-OCT-1997; 97US-0955636.  |  |
| XX   |  |
| PA (MINU ) UNIV MINNESOTA.   |  |
| XX   |  |
| PI NetSeestuen GL;   |  |
| DR WPI; 1999-288309/24.  |  |
| XX   |  |
| PT vitamin K-dependent polypeptide with modified gamma-carboxyglutamic   |  |
| PT acid domain, useful for treating clotting disorders   |  |
| XX   |  |
| PS Disclosure; Page 15; 86pp; English.   |  |
| XX   |  |
| This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein. |  |
| CC CC  |  |
| CC   |  |
| CC   |  |
| CC   |  |
| Sequence 44 AA:  |  |
| Query Match 83.7%; Score 159; DB 20; Length 44;  |  |
| Best Local Similarity 95.5%; Pred. No. 1.3e-19;  |  |
| Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  |  |
| OY 1 ANAFLLXRLRGSLRXCKKXQCSFXXXAEKIFDAXRTKLFWISY 44<br>     <br>1 ANAFLLXRLRPGSLRXCKKXQCSFXXXAEKIFDAXRTKLFWISY 44  |  |
| DB 1 ANAFLLXRLRPGSLRXCKKXQCSFXXXAEKIFDAXRTKLFWISY 44   |  |
| RESULT 5   |  |
| AAB36395   |  |
| ID AAB36395 standard; peptide; 44 AA.  |  |
| XX   |  |
| AC AAB36395;   |  |
| XX   |  |
| DT 27-FEB-2001 (first entry)   |  |
| XX   |  |
| DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO.3.   |  |
| XX   |  |
| KM Vitamin K-dependent protein; factor VII; protein C; GLA domain;   |  |
| KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;<br>factor X; prothrombin; enhanced membrane binding affinity;   |  |

```

KW      clot formation; thrombolytic; haemostatic; bleeding disorder;
KM      Thrombosis; clotting disorder; haemophilia A; haemophilia B;
KM      liver disease.
XX
OS      Homo sapiens.
XX
PN      WO2006753-A2.
XX
PD      09-NOV-2000.
XX
PF      28-APR-2000; 2000WO-US11416.
XX
PR      29-APR-1999; 99US-0302239.
XX
PA      (MINN ) UNIV MINNESOTA.
XX
PI      Nelsstuen GL;
XX
DR      WPI; 2001-007226/01.
XX
PT      Novel vitamin K-dependent polypeptide useful for treating clotting
PT      disorders such as thrombosis and hemophilia, comprises modified
PT      gamma-carboxy glutamic acid domain that enhances membrane binding
PT      affinity -
XX
PS      Disclosure; Page 12; 81pp; English.
XX
CC      The present invention describes a vitamin K-dependent polypeptide (I)
CC      comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC      at least one amino acid substitution, that enhances membrane binding
CC      affinity and the activity of the polypeptide relative to a corresponding
CC      native vitamin K-dependent polypeptide and inhibits clot formation.
CC      (I) can have thrombolytic and haemostatic activities, and can be used
CC      as an inhibitor of clot formation. (I) is useful for decreasing clot
CC      formation in a mammal, a factor VII or factor IX containing a modified
CC      GLA domain is useful for increasing clot formation and for treating a
CC      bleeding disorder, including thrombosis and clotting disorders such as
CC      haemophilia A, haemophilia B and liver disease. The present sequence
CC      represents a wild type human factor VII GLA domain sequence, given in
CC      the exemplification of the present invention.
XX
SQ      Sequence    44 AA;

Query Match          83.7%; Score 159; DB 22; Length 44;
Best Local Similarity 95.5%; Pred. No. 1,3e-19;
Matches   42; Conservative   0; Mismatches   2; Indels   0; Gaps   0,

QY      1 ANAFLLXLRQGSILKRXCKXQCSPFXAXEIFDANRTLTFWISY 44
        |||
        |||
DB      1 ANAFLLXLRPGSLKRXCKXQCSPFXAXEIFDANRTLTFWISY 44
        |||
        |||

RESULT 6
AAB84870 ID AAB84870 standard; Protein; 401 AA.
AAB84870;
AC      AAB84870;
DE      Mutant blood coagulant factor VII (FVII-31).
DT      31-JUL-2001 (first entry)
DX      Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW      mutant; mutlein.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
Key      Location/Qualifiers
FT      Misc-difference 311..317
       /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
       -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
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PN JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
XX Claim 14; Page 20-21; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 83.7%; Score 159; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGSIXRCKXKQCSFYXAEKIFDAXRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANAFLEELRPGSLERCKEQCSFEAREIFDAXRTKLFWISY 44

RESULT 7
AAB84871
ID AAB84871 standard; Protein; 401 AA.
XX
XX AAB84871;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-39).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutuin.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 235..239 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
XX Asp-Arg-Lys-Thr-Leu"
XX Misc-difference 311..317 /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX /note= "Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX 24-AUG-1999; 99JP-0237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
XX N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia -
XX
```

```
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients.
XX
XX Sequence 401 AA;
SQ
Query Match 83.7%; Score 159; DB 22; Length 401;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGSIXRCKXKQCSFYXAEKIFDAXRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ANAFLEELRPGSLERCKEQCSFEAREIFDAXRTKLFWISY 44

RESULT 8
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX
XX AAR35764;
XX
XX 24-SEP-1993 (first entry)
XX
XX Factor VII (VII).
XX
XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX Factor VII; CF; chymotrypsinogen; SP; serine protease; binding;
XX exosite; catalytic activity.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Region 1..152
XX FT /note= "Factor VII light chain"
XX FT 153..406
XX FT /note= "Factor VII heavy chain"
XX FT 374..388
XX FT /note= "exosite 1"
XX FT 290..310
XX FT /note= "exosite 2"
XX FT 290..310
XX FT /note= "pref. PC polypeptide; claim 2, page 136"
XX FT 374..388
XX FT /note= "pref. PC polypeptide; claim 2, page 136"
XX FT 289..304
XX FT /note= "pref. PC polypeptide; claim 4, page 137"
XX FT 290..304
XX FT /note= "pref. PC polypeptide; claim 4, page 137"
XX FT 245..266
XX FT /note= "claim 9, page 138-139 describes an antibody
XX that reacts with Factor VII; fragments
XX 289-304, 290-304, 290-310, 374-388 and
XX 400-414 but not with fragment 245-266"
XX
XX WO9309804-A.
XX
XX 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US10242.
XX
XX 18-NOV-1991; 91US-0793989.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Griffin JH, Mesters RM;
XX
XX WPI; 1993-182244/22.
XX
XX Serine protease derived-polypeptide(s) and anti-peptide
XX
```



CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser. The modified proteins are useful for treating CC bleeding disorders such as thrombocytopenia and von Willebrand's CC disease. They are also suitable for addition to plasma substitutes. CC The present sequence is a specific example of a modified factor VII CC protein.

SQ Sequence 406 AA;

Query Match 83.7%; Score 159; DB 18; Length 406;  
Best Local Similarity 72.7%; Pred. No. 1,3e-18;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGSILRXCKXXQCSFXXAEXIFKDXRRTKLFWISY 44  
Db 1 ANAFLEELRPGSLERCKEQCSFEARERFKDAERTKLFWISY 44

RESULT 10

AAW14510  
ID AAW14510 standard; protein; 406 AA.

XX AAW14510;

DT 14-MAY-1997 (first entry)

XX Modified blood coagulation Factor VII (R315S).

KM Blood coagulation; factor 7; mutein; mutation; modification;  
KM thrombocytopenia; von Willebrand's disease; plasma substitute.

OS Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Disulfide-bond /note= "proteolytic site"

FT Disulfide-bond 50..61

FT Disulfide-bond 55..70

FT Modified-site 63

FT /label= OTHER

FT /note= "beta-hydroxy-aspartic acid"

FT Disulfide-bond 72..81

FT Disulfide-bond 91..102

FT Disulfide-bond 98..112

FT Disulfide-bond 114..127

FT Disulfide-bond 135..162

FT Disulfide-bond 143..144

FT Cleavage-site /note= "proteolytic site"

FT Modified-site 145

FT Disulfide-bond /note= "glycosylation site"

FT Disulfide-bond 159..164

FT Disulfide-bond 178..194

FT Active-site 193

FT Active-site 242

FT Active-site 344

FT Cleavage-site 290..291

FT Disulfide-bond /note= "proteolytic site"

FT Disulfide-bond 310..329

FT Cleavage-site 315..316

FT Misc-difference 315

FT /note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"

FT Modified-site 322

FT Disulfide-bond /note= "glycosylation site"

FT Cleavage-site 340..368

FT Cleavage-site 341..342

FT Cleavage-site /note= "proteolytic site"

FT Cleavage-site 392..393

FT Cleavage-site /note= "proteolytic site"

FT Cleavage-site 396..397

FT Cleavage-site /note= "proteolytic site"

FT Cleavage-site 402..403

FT Cleavage-site /note= "proteolytic site"

PN USS580560-A.

XX 03-DEC-1996.

XX 13-NOV-1989; 89US-0434149.

XX 09-AUG-1993; 93US-0104509.

XX 13-NOV-1989; 89US-0434149.

XX 12-JUN-1992; 92US-0896248.

XX 22-AUG-1994; 94US-0293778.

XX (NOVO ) NOVO-NORDISK AS.

XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;

XX WPI; 1997-033523/03.

XX Mutated human factor VII or VIIa proteins - with amino acid

XX substitutions to improve proteolytic stability

XX Example 4; Page -; 28pp; English.

XX Modified human factor VII or VIIa proteins are stabilised against

XX proteolytic cleavage by substitution of one of the residues Lys32,

XX Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and

XX Lys341 by an amino acid that provides a proteolytically more stable

XX peptide bond, provided that Lys32 is replaced by Gln, Glu, His,

XX Gly, Thr, Ala or Ser. The modified proteins are useful for treating

XX bleeding disorders such as thrombocytopenia and von Willebrand's

XX disease. They are also suitable for addition to plasma substitutes.

XX The present sequence is a specific example of a modified factor VII

XX protein.

```
XX SQ Sequence 406 AA;
Query Match 83.7%; Score 159; DB 18; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFILXLRQSLRXKCKXOCSPFXAXEIPKDAKRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLELRPGSLRECKEBCSFPEAREIFKDAKRTKLFWISY 44

RESULT 11
AAU77745
ID AAU77745 standard; protein; 406 AA.
XX
AC AAU77745;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human factor VIIa active site mutant.
XX
KW Factor VIIa; human; shock heat treatment; protein stability;
KM protein manufacture; protein conformation; mutant; mutein.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Active-site 193
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 344
FT /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344
FT /label= Gly, Met, Thr
FT /note= "Preferably Ala. Wild type Ser"
XX
XX MO200177141-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-DK00234.
XX
XX 06-APR-2000; 2000DK-0000573.
XX
XX 17-APR-2000; 2000US-197650P.
XX
XX (NOVO ) NOVO NORDISK AS.
XX
XX Matchless F;
XX
XX WPI; 2001-657162/75.
XX
XX Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX PT involves a shock heat treatment -
XX
XX Disclosure; Page -; 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
XX shock heat treatment of the polypeptide. The method is useful in a
XX pharmaceutical composition, in the industrial or large scale method of
XX manufacturing a polypeptide, also as a unit operation during preparation,
XX purification, recovery and/or formulation of polypeptides. The shock heat
XX treatment improves the protein stability without substantial loss of
XX biological activity. The method can be applied to change polypeptide
XX conformation in a very fast and non-invasive manner. The polypeptide
XX formed is stable. The method is also useful for decreasing the
XX association of the polypeptide. This sequence represents a modified
XX human factor VIIa protein, mutated at the catalytic site, described
XX in the invention.
XX Note: This sequence does not appear in the specification but has
XX been obtained using information given in the invention.
```

```
XX SQ Sequence 406 AA;
Query Match 83.7%; Score 159; DB 22; Length 406;
Best Local Similarity 72.7%; Pred. No. 1.3e-18;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANAFILXLRQSLRXKCKXOCSPFXAXEIPKDAKRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ANAFLELRPGSLRECKEBCSFPEAREIFKDAKRTKLFWISY 44

RESULT 12
AAM52171
ID AAM52171 standard; Protein; 406 AA.
XX
AC AAM52171;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human FVII SEQ ID NO 1.
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KM myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH Misc-difference 6
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 7
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 14
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 16
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 19
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 20
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 25
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 26
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 29
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Misc-difference 35
XX FT /label= Glu, OTHER
XX FT /note= "OTHER = gamma carboxylutamic acid"
XX FT Modified-site 52
XX FT /note= "O-glycosylated"
XX FT Modified-site 60
XX FT /note= "O-glycosylated"
XX FT Modified-site 145
XX FT /note= "N-glycosylated"
XX FT Cleavage-site 152..153
XX FT /note= "proteolytic cleavage site converting FVII zymogen
XX to an activated form, comprising two chains
XX linked by a single disulphide bridge"
XX FT Modified-site 322
XX FT /note= "N-glycosylated"
XX
XX MO200158935-A2.
```

XX 16-AUG-2001.  
PD  
XX  
XX 12-FEB-2001; 2001WO-DK00094.  
PF  
XX 11-FEB-2000; 2000DK-0000218.  
PR  
XX 18-OCT-2000; 2000DK-0001558.  
XX  
XX (MAXY-) MAXYGEN APS.  
XX  
PI Andersen KV, Pedersen AH, Bornaes C;  
XX  
XX WPI; 2001-581807/65.  
DR  
XX N-PSDB; AA199982.  
XX  
XX New conjugate, useful for treating Factor VIIa related diseases or  
PT disorders such as haemophilia, liver disease, myocardial infarction and  
PT deep-vein thrombosis, comprises non-polypeptide group covalently  
PT attached to polypeptide group -  
XX  
XX Claim 1; Page 81-83; 89pp; English.  
XX  
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiatic, hepatotropic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.  
XX  
XX Sequence 406 AA;  
SQ  
XX  
XX Query Match 83.7%; Score 159; DB 22; Length 406;  
XX Best Local Similarity 95.5%; Pred. No. 1.3e-18;  
XX Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ANAFLLXXLRGSLXRXCKXQCSFXAXEIXFDAXRTKLFWISY 44  
DB 1 ANAFLLXXLRGSLXRXCKXQCSFXAXEIXFDAXRTKLFWISY 44  
RESULT 13  
AAM52172  
ID AAM52172 standard; Protein; 406 AA.  
XX  
XX AAM52172;  
AC  
XX  
XX 07-FEB-2002 (first entry)  
DT  
XX  
XX Mammalian expressed human FVII SEQ ID NO 3.  
DE  
XX  
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
KW cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;  
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 52  
FT /note= "O-glycosylated" 60  
FT Modified-site 60  
FT /note= "O-glycosylated" 145  
FT Modified-site 145  
FT /note= "N-glycosylated" 152..153  
FT Cleavage-site 152..153

FT /note= "proteolytic cleavage site converting FVII zymogen  
FT to an activated form, comprising two chains  
FT linked by a single disulphide bridge"  
FT Modified-site 322  
FT /note= "N-glycosylated"  
XX  
XX WO200158935-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 12-FEB-2001; 2001WO-DK00094.  
XX  
XX 11-FEB-2000; 2000DK-0000218.  
PR  
XX 18-OCT-2000; 2000DK-0001558.  
XX  
XX (MAXY-) MAXYGEN APS.  
XX  
PI Andersen KV, Pedersen AH, Bornaes C;  
XX  
XX WPI; 2001-581807/65.  
DR  
XX N-PSDB; AA199983.  
XX  
XX New conjugate, useful for treating Factor VIIa related diseases or  
PT disorders such as haemophilia, liver disease, myocardial infarction and  
PT deep-vein thrombosis, comprises non-polypeptide group covalently  
PT attached to polypeptide group -  
XX  
XX Disclosure; Page 85-86; 89pp; English.  
XX  
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)  
CC polypeptide conjugates, comprising at least one non-polypeptide group  
CC covalently attached to a polypeptide, where the amino acid sequence of  
CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at  
CC least one amino acid residue containing an attachment group for the  
CC non-polypeptide group has been introduced or removed. The FVIIa  
CC conjugates have haemostatic, thrombolytic, cardiatic, hepatotropic and  
CC cerebroprotective activity and are useful for treating FVIIa/TF-related  
CC diseases or disorders such as haemophilia, liver disease, myocardial  
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates  
CC have increased functional in vivo half life and/or increased plasma half  
CC life, increased bioavailability and/or reduced sensitivity to proteolytic  
CC degradation. Consequently medical treatment using the conjugates has a  
CC number of advantages over currently available such as longer duration  
CC between injections.  
XX  
XX Sequence 406 AA;  
SQ  
XX  
XX Query Match 83.7%; Score 159; DB 22; Length 406;  
XX Best Local Similarity 72.7%; Pred. No. 1.3e-18;  
XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 1 ANAFLELRPSLRECKECCSFEEAREIFDAERTKLFWISY 44  
DB 1 ANAFLELRPSLRECKECCSFEEAREIFDAERTKLFWISY 44  
RESULT 14  
AAM52181  
ID AAM52181 standard; Protein; 406 AA.  
XX  
XX AAM52181;  
AC  
XX  
XX 07-FEB-2002 (first entry)  
DT  
XX  
XX Human FVII mutant T106N.  
DE  
XX  
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
KW cardiatic; hepatotropic; cerebroprotective; haemophilia; liver disease;  
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.

```

XX Key Location/Qualifiers
FH Misc-difference 6 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 35 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Modified-site 52 /label= Glu, OTHER
FT /note= "O-glycosylated"
FT
FT Modified-site 60 /note= "O-glycosylated"
FT
FT Misc-difference 106 /note= "O-glycosylated"
FT
FT Modified-site 145 /note= "Wild-type Thr substituted by Asn"
FT /note= "N-glycosylated"
FT
FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
FT to an activated form, comprising two chains
FT linked by a single disulphide bridge"
FT
FT Modified-site 322 /note= "N-glycosylated"
FT
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001, 2001WO-DK00094.
XX
XX 11-FEB-2000, 2000DK-0000218.
XX
XX 18-OCT-2000, 2000DK-0001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI, 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as haemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently
XX attached to polypeptide group -
XX
XX Example 3, Page -, 89pp, English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at

```

```

CC least one amino acid residue containing an attachment group for the
CC non-polypeptide group has been introduced or removed. The FVIIa
CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a human FVII mutant,
CC having an addition in vivo glycosylation site and tested for its
CC amidolytic activity.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC (AAM52171).
XX
XX Sequence 406 AA;
SQ
Query Match 83.7%; Score 159; DB 22; Length 406;
Best Local Similarity 95.5%; Pred. No. 1,3e-18;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ANAFLLXLRQGLRXCKXXQCSFXXAEXIPKDXRTKLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXQCSFXXARXIPKDXRTKLFWISY 44
RESULT 15
AAM52182
ID AAM52182 standard; Protein; 406 AA.
XX
XX AAM52182;
AC
XX 07-FEB-2002 (first entry)
DT
XX
XX Human FVII mutant K143N/N145T.
DE
XX
XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KW muteln.
XX
XX Homo sapiens.
OS
XX Synthetic.
FH Key Location/Qualifiers
FT /label= Glu, OTHER
FT Misc-difference 6 /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 7 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 14 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 16 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 19 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 20 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 25 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 26 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"
FT
FT Misc-difference 29 /label= Glu, OTHER
FT /note= "OTHER = gamma carboxyglutamic acid"

```





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## OM protein - protein search, using sw model

Run on: March 19, 2003, 14:42:31 ; Search time 29.0625 Seconds  
(without alignments)  
145.545 Million cell updates/sec

Title: 10Gln28Glu  
Perfect score: 190  
Sequence: 1 ANAFLLXLRQSLXKXCKXX.....XXAEXIFKAXRTLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR 73: \*  
2: pir1: \*  
3: pir2: \*  
4: pir3: \*  
5: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 159   | 83.7        | 466    | 1 KFHU7  | coagulation factor  |
| 2          | 125   | 65.8        | 443    | 2 I46932 | coagulation factor  |
| 3          | 115   | 60.5        | 407    | 1 KFB07  | coagulation factor  |
| 4          | 102   | 53.7        | 461    | 1 JX0210 | protein C (activat  |
| 5          | 102   | 53.7        | 492    | 1 EXBO   | coagulation factor  |
| 6          | 101   | 53.2        | 461    | 1 S18994 | protein C (activat  |
| 7          | 99    | 52.1        | 488    | 1 EXHU   | coagulation factor  |
| 8          | 93    | 48.9        | 482    | 1 EXKT   | coagulation factor  |
| 9          | 92    | 48.4        | 456    | 1 EXCH   | coagulation factor  |
| 10         | 91    | 47.9        | 475    | 1 KXBO   | protein C (activat  |
| 11         | 85    | 44.7        | 461    | 1 KXHU   | protein C (activat  |
| 12         | 85    | 44.7        | 622    | 1 KTHU   | thrombin (EC 3.4.2  |
| 13         | 83    | 43.7        | 461    | 1 KFHU   | coagulation factor  |
| 14         | 82    | 43.2        | 416    | 1 KFB0   | coagulation factor  |
| 15         | 81    | 42.6        | 617    | 2 S10511 | thrombin (EC 3.4.2  |
| 16         | 81    | 42.6        | 618    | 2 A35827 | thrombin (EC 3.4.2  |
| 17         | 74    | 38.9        | 452    | 1 A30351 | coagulation factor  |
| 18         | 74    | 38.9        | 459    | 2 J00419 | coagulation factor  |
| 19         | 70    | 36.8        | 642    | 2 S53433 | plasma protein S p  |
| 20         | 65    | 34.2        | 625    | 1 TBBO   | thrombin (EC 3.4.2  |
| 21         | 65    | 34.2        | 642    | 2 S53434 | plasma protein S p  |
| 22         | 65    | 34.2        | 676    | 1 KKHUS  | plasma protein S p  |
| 23         | 63    | 33.2        | 675    | 1 KXBOS  | plasma protein S p  |
| 24         | 61    | 32.1        | 396    | 1 KXBOZ  | plasma protein S p  |
| 25         | 61    | 32.1        | 646    | 2 S38819 | plasma protein S -  |
| 26         | 60    | 31.6        | 676    | 1 KXKTS  | plasma protein S p  |
| 27         | 58.5  | 30.8        | 575    | 2 G96763 | probable MAP kinase |
| 28         | 56    | 29.5        | 422    | 1 KKHUZ  | plasma protein Z p  |
| 29         | 56    | 29.5        | 673    | 2 A48089 | growth arrest-spec  |

|    |      |      |     |          |                     |
|----|------|------|-----|----------|---------------------|
| 30 | 54   | 28.4 | 674 | 2 I55476 | growth potentiating |
| 31 | 54   | 28.4 | 678 | 2 B48089 | growth arrest-spec  |
| 32 | 53   | 27.9 | 675 | 1 KXMS   | plasma protein S p  |
| 33 | 52.5 | 27.6 | 594 | 2 D84859 | probable MAP kinase |
| 34 | 52.5 | 27.6 | 603 | 2 C96575 | probable MAP kinase |
| 35 | 49   | 25.8 | 211 | 2 D36936 | uncharacterized lo  |
| 36 | 45.5 | 23.9 | 161 | 2 F82637 | conserved hypotet   |
| 37 | 45.5 | 23.9 | 455 | 2 C83494 | probable 2-isoprop  |
| 38 | 45   | 23.7 | 879 | 2 S55864 | hypothetical prote  |
| 39 | 44   | 23.2 | 413 | 1 VHVNH  | nucleoprotein - in  |
| 40 | 43.5 | 22.9 | 322 | 2 T20272 | hypothetical prote  |
| 41 | 42.5 | 22.4 | 319 | 2 T15137 | hypothetical prote  |
| 42 | 42.5 | 22.4 | 410 | 2 T25574 | hypothetical prote  |
| 43 | 42.5 | 22.4 | 907 | 2 T15792 | hypothetical prote  |
| 44 | 42   | 22.1 | 255 | 2 J50054 | hypothetical 26.6K  |
| 45 | 42   | 22.1 | 396 | 2 H97500 | hypothetical prote  |

## ALIGNMENTS

RESULT 1  
KFH07  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text\_change 08-Dec-2000  
C:Accession: A28322; A23819; J31186; B31186; S63524  
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend  
A:Reference number: A28322; MUID:87260948; PMID:3037537  
A:Accession: A28322  
A:Molecule type: DNA  
A:Residues: 1-466 <OH>  
A:Cross-references: GB:J02933; NID:G180333; PIDN:AAA51983.1; PID:G180334  
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A:Title: Characterization of a cDNA coding for human factor VII.  
A:Reference number: A23819; MUID:86205965; PMID:3486420  
A:Accession: A23819  
A:Molecule type: mRNA  
A:Residues: 1-466 <HAG>  
A:Cross-references: GB:M13232; NID:G182799; PIDN:AA8040.1; PID:G182801  
R:Thm, L.; Bioern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A...  
Biochemistry 27, 7785-7793, 1988  
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f  
A:Reference number: A90539; MUID:89086153; PMID:3264725  
A:Accession: A31186  
A:Molecule type: Protein  
A:Residues: 61-212 <THI>  
A:Accession: B31186  
A:Molecule type: Protein  
A:Residues: 213-466 <TH2>  
R:Bioern, S.; Foster, D.C.; Thm, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen, A...  
J. Biol. Chem. 266, 11051-11057, 1991  
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a  
A:Reference number: A40529; MUID:91250411; PMID:1904059  
A:Contents: annotation; carbohydrate binding sites  
R:Persson, B.; Petersen, L.C.  
Eur. J. Biochem. 234, 293-300, 1995  
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox  
A:Reference number: S63524; MUID:96096752; PMID:8525655  
A:Accession: S63524  
A:Molecule type: Protein  
A:Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>  
C:Genetics:  
A:Gene: GDB:F7  
A:Cross-references: GDB:119897; OMIM:227500  
A:Map position: 13q34-13q34  
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-60/Domain: propeptide #status predicted <PRO>  
F:45-104/Domain: Gla domain homology <Gla>  
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F:110-141/Domain: EGF homology <EG1>  
F:151-187/Domain: EGF homology <EG2>  
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:213-447/Domain: trypsin homology <TRY>  
F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,  
F:112,120/Binding site: carboxylate (Ser) (covalent) #status experimental  
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
F:205,383/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:212-213/Cleavage site: Arg-1le (coagulation factor XIIIa) #status experimental  
F:253,302,404/Active site: His, Asp, Ser #status predicted  
F:350-351/Cleavage site: Arg-Gly (coagulation factor XIa) #status predicted

## Query Match

Best Local Similarity 83.7%; Score 159; DB 1; Length 466;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQSLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
Db 61 ANAFLEELRPGSLERCKECCSFEEARIEFKDAERTKLFWISY 104

## RESULT 2

146932 coagulation factor VII - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #ext\_change 12-Feb-1999

C:Accession: I46932

A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII

A:Reference number: I46932; PMID:93190306; PMID:8383365

A:Accession: I46932

A:Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: mRNA

A:Residues: 1-443 <BRO>

A:Cross-references: GB:S56300; NID:9266294; PID:9266295

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

F:24-83/Domain: Gla domain homology <Gla>

F:89-120/Domain: EGF homology <EG2>

F:130-166/Domain: EGF homology <EG2>

F:192-425/Domain: trypsin homology <TRY>

## Query Match

Best Local Similarity 65.8%; Score 125; DB 2; Length 443;  
Matches 24; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQSLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
Db 40 ANAFLEELRPGSLERCKECCSFEEARIEFKDAERTKLFWISY 83

## RESULT 3

KFB07

coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #ext\_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TAK>

R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:83308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCW>

A>Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Haase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A4456; PMID:89213999; PMID:1149637

A:Accession: A4456

A:Contents: annotation

A>Note: structure and location of covalently bound carboxylate

A:Function:

C:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F:1-132/Product: coagulation factor VIIa light chain #status experimental <MA1>

F:50-81/Domain: EGF homology <EG1>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:52/Binding site: carboxylate (Ser) (covalent) #status experimental

F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment

F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-1le (coagulation factor XIIIa) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor XIa) #status experimental

Query Match 60.5%; Score 115; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 7.4e-12;

Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQSLRXCKXQCSFXXAEXIFKDAKRTKLFWISY 44  
Db 1 ANGFLEELRPGSLERCKECCSFEEARIEFKDAERTKLFWISY 44

## RESULT 4

JX0210 protein C (activated) (EC 3.4.21.69) precursor - mouse

N:Alternate names: vitamin K-dependent serine proteinase

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #ext\_change 16-Jun-2000

C:Accession: JX0210

R:Takeya, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.

J. Biochem. 111, 491-495, 1992

A:Title: Isolation and characterization of a mouse protein C cDNA.

A:Reference number: JX0210; PMID:92316897; PMID:1618739

A:Accession: JX0210

A:Molecule type: mRNA

A:Residues: 1-461 <TAD>

A:Cross-references: GB:D10445; NID:9220385; PID:BA01235.1; PID:9220386

A:Experimental source: liver

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re

B.

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F:1-33/Domain: signal sequence #status predicted <SIG>

F:37-85/Domain: Gla domain homology <Gla>

F:94-91/Domain: propeptide #status predicted <PRO>

F:42-196,199-461/Product: protein C #status predicted <PC>

F:91-130/Domain: light chain #status predicted <PCL>

F:139-174/Domain: EGF homology <EG2>

F:199-461/Domain: heavy chain #status predicted <PCH>

F:199-211/Domain: activation peptide #status predicted <ACT>

F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>



A:Title: The cDNA cloning and mRNA expression of rat protein C.  
A:Reference number: S24312; MUID:92329550; PMID:1621650  
A:Accession: S24312  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <OKA2>  
A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA5617.1; PID:G56963  
C:Keywords: beta-hydroxyaspartic acid, glycoprotein, hydrolase, serine proteinase  
E:1-32/Domain: signal sequence #status predicted <SIG>  
E:127-85/Domain: Gla domain homology <Gla>  
E:133-42/Domain: propeptide #status predicted <PRO>  
F:1-461/Product: protein C #status predicted <PRC>  
F:91-130/Domain: EGF homology <EG1>  
F:139-174/Domain: EGF homology <EG2>  
F:213-445/Domain: trypsin homology <TRY>  
F:477-48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted  
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:121-130,139-150,146-159,161-174,182-220,239-255,373-387,398-426/Disulfide bonds: #status predicted  
F:225,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:255,300,402/Active site: His, Asp, Ser #status predicted

Query Match 53.2%; Score 101; DB 1; Length 461;  
Best Local Similarity 45.5%; Pred. No. 2.2e-09;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAPLXLROGSLRXCKKXKOCSEFXKAEKIFKDAKRTKLFWSTY 44  
Db 42 ANSFLEVRAQSLERECMEIEICDFEBADEIFQNVEDTLAFTWKY 85

RESULT 7

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N:Alternate names: Stuart factor  
C:Species: Homo sapiens (man)  
C:Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 08-Dec-2000  
C:Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00187  
R:Levy, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
Biochemistry 25, 5098-5102, 1986  
A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization is conserved in man  
A:Reference number: A24478; MUID:87026600; PMID:3768336  
A:Accession: A24478  
A:Molecule type: DNA  
A:Residues: 1-488 <LE5>  
A:Cross-references: GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831  
R:Meisler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.  
Gene 99, 291-294, 1991  
A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X  
A:Reference number: J00917; MUID:91216473; PMID:1902434  
A:Accession: J00917  
A:Molecule type: mRNA  
A:Residues: 1-488 <ME5>  
A:Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390  
R:Miao, C.H.; Levy, S.P.; Chung, D.W.; Davie, E.W.  
J. Biol. Chem. 267, 7395-7401, 1992  
A:Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor  
A:Reference number: A42485; MUID:92218390; PMID:1313796  
A:Accession: A42485  
A:Molecule type: DNA  
A:Residues: 1-15 <MIA>  
A:Experimental source: liver  
A:Note: Sequence extracted from NCBI backbone (NCBIN:93780; NCBIPI:93787)  
R:Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
Gene 41, 311-314, 1986  
A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
A:Reference number: A25853; MUID:86221713; PMID:3011603  
A:Accession: A25853  
A:Molecule type: mRNA  
A:Residues: 19-284, 'E', 289-488 <KAU>  
A:Cross-references: GB:M2613; NID:g180335; PIDN:AAA51984.1; PID:g180336  
R:Fung, M.R.; Hay, C.; Macgillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.  
A:Reference number: A22208; MUID:85216545; PMID:2582420  
A:Accession: A22208  
A:Molecule type: mRNA  
A:Residues: 13-441, 'S', 443-488 <FUN>  
A:Cross-references: GB:K0199; NID:G182840; PIDN:AAA52490.1; PID:G182841  
R:Letys, S.P.; Chung, D.W.; Kistel, W.; Kurachi, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
A:Title: Characterization of a cDNA coding for human factor X.  
A:Reference number: A21284; MUID:84222026; PMID:6587384  
A:Accession: A21284  
A:Molecule type: mRNA  
A:Residues: 13-284, 'E', 289-488 <LE2>  
A:Cross-references: GB:K01865  
R:McNallen, B.A.; Fujikawa, K.; Kistel, W.; Saeagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss  
Biochemistry 22, 2875-2884, 1983  
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.  
A:Reference number: A20362; MUID:83257207; PMID:6871167  
A:Accession: A20362  
A:Molecule type: protein  
A:Residues: 41-179 <MCM>  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X.  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39415  
A:Molecule type: protein  
A:Residues: 183-234 <INO>  
A:Note: glycosylation sites  
A:Note: identification and characterization of beta-hydroxyaspartic acid  
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.U.; Hamsabhusanam, K.; Lyman, G.  
Gene 84, 517-519, 1989  
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.  
A:Reference number: 154051; MUID:90128299; PMID:2612918  
A:Accession: 154051  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-references: GB:M32297; NID:G183860; PIDN:AAA52636.1; PID:G553330  
R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinaky, A.; Park, C.H.; Bode, W.; Huber, R.; Blyas  
J. Mol. Biol. 232, 947-966, 1993  
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A:Reference number: A49458; MUID:93360277; PMID:8355279  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
C:Comment: The two chains held together by one disulfide bond are formed from a single-chain polypeptide.  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa (in the extrinsic pathway).  
A:Genetics: GDB:F10  
A:Cross-references: GDB:119890; OMIM:227600  
A:Map position: 13q34-13q34  
A:Introns: 24/1, 77/3, 86/1, 124/1, 150/3, 249/3, 289/1  
A:Note: deficiency of this factor causes Stuart disease  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V and calcium ions.  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic acid  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EGF>  
F:123-164/Domain: EGF homology <EG2>  
F:183-234/Product: coagulation factor X heavy chain #status experimental <HCH>  
F:235-488/Product: activation peptide #status experimental <APT>  
F:235-488/Domain: coagulation factor Xa heavy chain #status experimental <ACT>  
F:235-488/Domain: trypsin homology <TRY>  
F:46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxylglutamic acid (Glu) #status experimental  
F:57-62/Disulfide bonds: #status predicted  
F:90-102, 95-110, 112-121, 129-140, 136-149, 151-164, 172-342, 241-246, 261-277, 390-404, 415-443/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:103/Modified site: carbonyl-beta-hydroxyaspartic acid (Thr) (covalent) #status experimental  
F:199, 211/Binding site: carbohydrate (Aen) (covalent) #status experimental  
F:221, 231/Binding site: carbohydrate (Aen) (covalent) #status experimental

F/234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F/276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 52.1%; Score 99; DB 1; Length 488;  
Best Local Similarity 38.6%; Pred. No. 5,1e-09;  
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFPLXLRQSLRXKXCKXQCFXXAEXIFPDARXTKLFWISY 44  
DB 41 ANSFLEMKKGLHRECMETCSYEAREVFPDSOKTFENFKY 84

RESULT 8  
EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000  
C:Accession: S49075; J04670; P50191; P50190; I62745  
R:Stanton, C.; Rose, P.; Hutson, S.; Wallin, R.  
Thromb. Res. 80, 63-73, 1995  
A>Title: Evidence for competition between vitamin K-dependent clotting factors for intr  
A:Reference number: A58498; MUID:96093366; PMID:8578539  
A:Accession: S49075  
A:Molecule type: mRNA  
A:Residues: 1-482 <STAL>  
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAAS6202.1; PID:G506601  
A>Note: submitted to the EMBL Data Library, June 1994  
A>Note: neither the complete nucleic acid sequence nor the complete translation are show  
R:Stanton, C.; Rose, P.; Hutson, S.; Wallin, R.  
Gene 169, 269-273, 1996  
A>Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
A:Reference number: J04670; MUID:96194815; PMID:8647460  
A:Accession: J04670  
A:Molecule type: mRNA  
A:Residues: 1-482 <STI2>  
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAAS6202.1; PID:G506601  
A:Experimental source: Cos-1 cell  
R:Enjoji, K.; Miyazaki, K.; Kato, H.  
J. Biochem. 109, 890-898, 1991  
A>Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
A:Reference number: P50190; MUID:92041742; PMID:1718949  
A:Accession: P50191  
A:Molecule type: protein  
A:Residues: 41-58, 'X', 60-65 <ENJ1>  
A:Accession: P50190  
A:Molecule type: protein  
A:Residues: 183-186, 'X', 188-207 <ENJ2>  
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
Eur. J. Haematol. 52, 162-168, 1994  
A>Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
A:Reference number: I6196; MUID:94222160; PMID:8168596  
A:Accession: I62745  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 295-383, 'G', 385-455 <MUR>  
A:Cross-references: GB:D1215; NID:G415309; PIDN:BA04756.1; PID:G455396  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
F/1-23/Domain: signal sequence #status predicted <SIG>  
F/24-40/Domain: propeptide #status predicted <PRO>  
F/25-84/Domain: Gla domain homology <GLA>  
F/90-121/Domain: EGF homology <EG1>  
F/129-164/Domain: EGF homology <EG2>  
F/183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
F/183-231/Domain: activation peptide #status predicted <AP>  
F/232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
F/232-460/Domain: trypsin homology <TRY>  
F/46,47,54,56,65,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
F/57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41

F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F/187/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F/208/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F/218/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F/274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 48.9%; Score 93; DB 1; Length 482;  
Best Local Similarity 38.6%; Pred. No. 5.4e-08;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFPLXLRQSLRXKXCKXQCFXXAEXIFPDARXTKLFWISY 44  
DB 41 ANSFEEIKKGLHRECMETCSYEAREVFPDNEKTEFENFKY 84

RESULT 9  
EXCH

coagulation factor Xa (EC 3.4.21.6) precursor - chicken  
N:Alternate names: virus-activating proteinase  
C:Species: Gallus gallus (chicken)  
C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: S15838; S20380; S20381  
R:Suzuki, H.; Harada, A.; Hayaishi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na  
FEBS Lett. 283, 281-285, 1991  
A>Title: Primary structure of the virus activating protease from chick embryo. Its ident  
A:Reference number: S15838; MUID:91257322; PMID:2044767  
A:Accession: S15838  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-475 <STU>  
A:Cross-references: DDBJ:D00844; NID:G222869; PIDN:BA00724.1; PID:G222870  
R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.  
FEBS Lett. 296, 274-278, 1992  
A>Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib  
A:Reference number: S20380; MUID:92164779; PMID:1537403  
A:Accession: S20380  
A:Molecule type: protein  
A:Residues: 41-55 <GOT>  
A:Accession: S20381  
A:Molecule type: protein  
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
F/1-20/Domain: signal sequence #status predicted <SIG>  
F/21-40/Domain: propeptide #status predicted <PRO>  
F/25-84/Domain: Gla domain homology <GLA>  
F/41-185/Product: coagulation factor X light chain #status experimental <LCH>  
F/90-121/Domain: EGF homology <EG1>  
F/129-167/Domain: EGF homology <EG2>  
F/186-475/Product: coagulation factor X heavy chain #status predicted <HCH>  
F/186-245/Domain: activation peptide #status predicted <AP>  
F/241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
F/241-468/Domain: trypsin homology <TRY>  
F/46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s  
F/57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42  
F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F/196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 48.4%; Score 92; DB 1; Length 475;  
Best Local Similarity 38.6%; Pred. No. 8e-08;  
Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANAFPLXLRQSLRXKXCKXQCFXXAEXIFPDARXTKLFWISY 44  
DB 41 ANSFLEMKKGLHRECMETCSYEAREVFPDNEKTEFENFKY 84

RESULT 10

KXBO  
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)  
 N:Alternate names: autoprothrombin IIA; plasma protein C  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #ext\_change 16-Jul-1999  
 C:Accession: A26250; A18385; A18386; A00928  
 R:Long, G.L.; Balagaje, R.M.; Macgillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984  
 A>Title: Cloning and sequence of liver cDNA coding for bovine protein C.  
 A:Reference number: A26250; UID:85014826; PMID:6091100  
 A:Accession: A26250  
 A:Molecule type: mRNA  
 A:Residues: 1-456 <LON>  
 R:Fernlund, P.; Stenflo, J.  
 J. Biol. Chem. 257, 12170-12179, 1982  
 A>Title: Amino acid sequence of the light chain of bovine protein C.  
 A:Reference number: A18385; UID:83007325; PMID:6696876  
 A:Accession: A18385  
 A:Molecule type: protein  
 A:Residues: 40-194 <FER>  
 A>Note: 82-Lys was also found  
 R:Draakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983  
 A>Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.  
 A:Reference number: A19316; UID:83169769; PMID:6572939  
 A:Contents: annotation; revision to residue 110  
 R:Stenflo, J.; Fernlund, P.  
 J. Biol. Chem. 257, 12180-12190, 1982  
 A>Title: Amino acid sequence of the heavy chain of bovine protein C.  
 A:Reference number: A18386; UID:83007326; PMID:6696877  
 A:Accession: A18386  
 A:Molecule type: protein  
 A:Residues: 197-454, 'PV' <STE>  
 R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.  
 J. Biol. Chem. 258, 5548-5553, 1983  
 A>Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F  
 A:Reference number: A37541; UID:83213513; PMID:6504092  
 A:Contents: annotation; activation; calcium binding  
 R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.  
 J. Biol. Chem. 258, 5554-5560, 1983  
 A>Title: Structural changes required for activation of protein C are induced by Ca<sup>2+</sup> dir  
 A:Reference number: A37542; UID:83213514; PMID:6406503  
 A:Contents: annotation; activation; calcium binding  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
 s.  
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str  
 cognition of the thrombin-thrombomodulin complex.  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F:1-23/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:124-83/Domain: Gla domain homology <GLA>  
 F:30-39/Domain: propeptide #status predicted <PRO>  
 F:40-194/Product: protein C light chain #status experimental <LCH>  
 F:98-128/Domain: EGF homology <EGF>  
 F:137-172/Domain: EGF homology <EG2>  
 F:197-456/Product: protein C heavy chain #status experimental <HCH>  
 F:197-210/Domain: activation peptide #status experimental <APT>  
 F:211-440/Domain: trypsin homology <TRY>  
 F:45-46,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:119-128,137-148,144-157,159-172,180-338,237-253,368-382,393-421/Disulfide bonds: #stat  
 F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:252,298,397/Active site: His, Asp, Ser #status predicted  
 F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.9%; Score 91; DB 1; Length 456;  
 Best Local Similarity 40.9%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLXKCKXXQCSFXAEXIFKDXRTKTFWISY 44

DB 40 ANSFLELRPGNVERCSSEVCFEEAREPIFONTEDTMAFWSPY 83  
 RESULT 11  
 KXHU  
 protein C (activated) (EC 3.4.21.69) precursor - human  
 N:Alternate names: autoprothrombin IIA; plasma protein C  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #ext\_change 16-Jul-1999  
 C:Accession: A22331; A25426; A21781; A23789; A00927  
 R:Foster, D.C.; Yoshitake, S.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
 A>Title: The nucleotide sequence of the gene for human protein C.  
 A:Reference number: A22331; UID:85270390; PMID:2991887  
 A:Accession: A22331  
 A:Molecule type: DNA  
 A:Residues: 1-461 <FOS1>  
 A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334  
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
 A>Title: Evolution and organization of the human protein C gene.  
 A:Reference number: A25426; UID:86120978; PMID:3511471  
 A:Accession: A25426  
 A:Molecule type: DNA  
 A:Residues: 1-445, 'L', 446-461 <PLU>  
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
 R:Foster, D.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
 A>Title: Characterization of a cDNA coding for human protein C.  
 A:Reference number: A21781; UID:84272714; PMID:6589623  
 A:Accession: A21781  
 A:Molecule type: mRNA  
 A:Residues: 'Q', 107-461 <FOS2>  
 A:Cross-references: GB:X02750; NID:g190322; PIDN:AAA60164.1; PID:g190323  
 R:Seckmann, R.U.; Schmidt, R.U.; Satterre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
 Nucleic Acids Res. 13, 5233-5247, 1985  
 A>Title: The structure and evolution of a 461 amino acid human protein C precursor and i  
 A:Reference number: A23789; UID:85269639; PMID:2991859  
 A:Accession: A23789  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <BEC>  
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120  
 R:Mietlich, J.P.; Broze Jr., G.J.  
 J. Biol. Chem. 265, 11397-11404, 1990  
 A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m  
 A:Reference number: A44605; UID:90293094; PMID:1594179  
 A:Contents: annotation; carbohydrate binding sites; activation peptide  
 A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
 R:Harris, R.U.; Ling, V.T.; Speliman, M.W.  
 J. Biol. Chem. 267, 5102-5107, 1992  
 A>Title: O-linked fucose is present in the first external growth factor domain of facto  
 A:Reference number: A44606; UID:92184750; PMID:1544894  
 A:Contents: annotation; beta-hydroxyaspartic acid  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
 ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also f  
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
 C:Genetics:  
 A:Gene: GDB:PROC  
 A:Cross-references: GDB:120317; OMIM:176860  
 A:Map position: 2q31-2q32  
 A:Insertions: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:27-66/Domain: Gla domain homology <GLA>  
 F:33-42/Domain: propeptide #status predicted <PRO>  
 F:43-197/Product: protein C light chain #status experimental <LCH>  
 F:92-131/Domain: EGF homology <EG1>  
 F:140-175/Domain: EGF homology <EG2>  
 F:200-461/Product: protein C heavy chain #status predicted <HCH>  
 F:200-211/Domain: activation peptide #status experimental <APT>

F:212-445/Domain: trypsin homology <TRY>  
F:48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp  
F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D  
F:106-111/Disulfide bonds: #status predicted  
F:110/Binding site: carbohydrate (thr) (covalent) #status absent  
F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:133,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
F:253,299,402/Active site: His, Asp, Ser #status predicted  
F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 44.7%; Score 85; DB 1; Length 461;  
Best Local Similarity 43.9%; Pred. No. 1.2e-06;  
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRGGSLRXKXCCXOCFFXXAXEIPFDXRTKLFW 41  
Db 43 ANFLFEEVNRKGLRERCEVETCSIEAFDALESSTRTVDFWAKY 83

RESULT 12

thrombin (EC 3.4.21.5) precursor [validated] - human  
N/Alternate names: coagulation factor II  
N/Contains: prothrombin  
C/Species: Homo sapiens (man)  
C/Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000  
C/Accession: A29351, A00914, B00914; A37549; A37550; I51552  
R/Degen, S.J.F.; Davie, E.W.  
Biochemistry 26, 6165-6177, 1987  
A>Title: Nucleotide sequence of the gene for human prothrombin.  
A/Reference number: A29351; MUID:88077877; PMID:2825773  
A/Accession: A29351

A/Molecule type: DNA  
A/Residues: 1-622 <DEG>  
A/Cross-references: GB:M17262; GB:M33691; NID:G558069; PIDN:AA63054.1; PID:G339641  
R/Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.  
Biochemistry 22, 2087-2097, 1983  
A>Title: Characterization of the complementary deoxyribonucleic acid and gene coding for  
A/Reference number: A00914; MUID:83231469; PMID:6305407  
A/Accession: A00914

A/Molecule type: mRNA  
A/Residues: 8-163, 'N', 165-622 <DE2>  
A/Cross-references: GB:V00595; GB:U00307; NID:G37128; PIDN:CAA23842.1; PID:G1335344  
A/Accession: B00914

A/Molecule type: DNA  
A/Residues: 186-311 <DE3>  
R/Waltz, D.A.; Hewett-Emlert, D.; Seegers, W.H.  
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977  
A/Reference number: A37549; MUID:77193964; PMID:266717  
A/Accession: A37549

A/Molecule type: protein  
A/Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,  
R/Butkowsk, R.J.; Eilion, J.; Downing, M.R.; Mann, K.G.  
J. Biol. Chem. 252, 4942-4957, 1977  
A>Title: Primary structure of human prothrombin 2 and alpha-thrombin.  
A/Reference number: A37550; MUID:77207112; PMID:873923  
A/Accession: A37550

A/Molecule type: protein  
A/Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-  
R/Rabier, M.J.; Blashill, A.; Furie, B.; Furie, B.C.  
J. Biol. Chem. 261, 13210-13215, 1986  
A/Reference number: A37551; MUID:87008532; PMID:3759958  
A/Contents: annotation; activation cleavages  
R/MacGillivray, R.T.; Irwin, D.M.; Guineto, E.R.; Stone, J.C.  
Ann. N. Y. Acad. Sci. 485, 73-79, 1986  
A>Title: Recombinant genetic approaches to functional mapping of thrombin.  
A/Reference number: I51952; MUID:87182874; PMID:3471151  
A/Accession: I51952

A/Status: translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-2, 'R', 5-100 <RES>  
A/Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724

C/Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
C/Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds  
(a) can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain  
ter 314-Arg, are released in natural blood clotting.  
C/Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.  
C/Comment: The gamma-carboxyglutamate residues bind calcium ions, result from the carboxy  
ent interaction with the negatively charged phospholipid membrane surface.  
C/Comment: The prothrombin precursor is synthesized in the liver.  
C/Genetics:  
A/Gene: GDB:F2  
A/Cross-references: GDB:119894; OMIM:176930  
A/Map position: 11p11-11q12  
A/Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552  
C/Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology  
C/Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupl  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-43/Domain: propeptide #status predicted <PRO>  
F:28-87/Domain: Gla domain homology <GLA>  
F:44-622/Product: prothrombin #status experimental <MAT>  
F:108-186/Domain: activation peptide #status experimental <APT>  
F:213-291/Domain: kringe homology <KR1>  
F:328-363/Product: thrombin light chain #status experimental <LCH>  
F:364-622/Product: thrombin heavy chain #status experimental <HCH>  
F:364-613/Domain: trypsin homology <TRY>  
F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:60-65,90-103,108-166,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status  
F:121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:336-482,536-550,564-594/Disulfide bonds: #status predicted  
F:391-407/Disulfide bonds: #status experimental  
F:406,462/Active site: His, Asp #status predicted  
F:416/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:568/Active site: Ser #status experimental

Query Match 44.7%; Score 85; DB 1; Length 622;  
Best Local Similarity 36.4%; Pred. No. 1.7e-06;  
Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRGGSLRXKXCCXOCFFXXAXEIPFDXRTKLFWISY 44  
Db 44 ANFLFEEVNRKGLRERCEVETCSIEAFDALESSTRTVDFWAKY 87

RESULT 13

KFNU  
coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
N/Alternate names: antihemophilic factor B; Christmas factor  
C/Species: Homo sapiens (man)  
C/Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 15-Sep-2000  
C/Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20  
R/Yoshitake, S.; Schach, B.G.; Roeder, D.C.; Davie, E.W.; Kurachi, K.  
Biochemistry 24, 3736-3750, 1985  
A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).  
A/Reference number: A00922; MUID:8600558; PMID:2994716  
A/Accession: A00922

A/Molecule type: DNA  
A/Residues: 1-461 <YOS>  
A/Cross-references: GB:K02402; NID:G182612; PIDN:AB59620.1; PID:G182613  
R/Janson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro  
EMBO J. 3, 1053-1060, 1984  
A>Title: The gene structure of human anti-haemophilic factor IX.  
A/Reference number: A37570; MUID:84236100; PMID:6329734  
A/Accession: A37570

A/Molecule type: DNA  
A/Residues: 1-461 <ANS>  
A/Cross-references: GB:K02048  
R/Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
Blood 72, 1074-1076, 1988  
A>Title: The putative factor IX gene promoter in hemophilia B Leyden.  
A/Reference number: A30511; MUID:86327116; PMID:3416069  
A/Accession: A30511

A/Molecule type: DNA  
A/Residues: 8-24 <REI>



A.Cross-references: EMBL:X55008; NID:g311288; PIDN:CB830245.2; PID:g4469253  
 R.Koeberl, D.D.; Bottema, C.D.K.; Bueterde, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor  
 A.Reference number: A32989; NUID:89311752; PMID:2773937  
 A.Accession: A32989  
 A>Status: not compared with conceptual translation  
 A.Molecule type: DNA  
 A.Residues: 30-92 <KOE>  
 R.McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lunblad, R.L.; Roberts, H.R.; Graham, J.B.; S  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2647-2651, 1985  
 A>Title: Evidence for a prevalent dimorphism in the activation peptide of human coagul  
 A.Reference number: A22673; NUID:85190593; PMID:3857619  
 A.Accession: A22673  
 A.Molecule type: mRNA  
 A.Residues: 1-193, 'T', 195-461 <MCG>  
 A.Cross-references: GB:M1309; NID:g180552; PIDN:AA52023.1; PID:g180553  
 A>Note: The authors translated the codon ACA for residue 29 as Tyr  
 R.Jay, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Finkel, A.; Tolstosh  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A>Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba  
 A.Reference number: A21337; NUID:83220788; PMID:6687940  
 A.Accession: A21337  
 A.Molecule type: mRNA  
 A.Residues: 1-193, 'T', 195-461 <JAY>  
 A.Cross-references: GB:J00137; NID:g182610; PIDN:AA52763.1; PID:g182611  
 R.Jagdeewaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A>Title: Isolation and characterization of human factor IX cDNA: identification of Tag I  
 A.Reference number: A37546; NUID:84300526; PMID:6089357  
 A.Accession: A37546  
 A.Molecule type: mRNA  
 A.Residues: 38-193, 'T', 195-326 <JAG>  
 A.Cross-references: GB:M35672  
 R.Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
 A>Title: Isolation and characterization of a cDNA coding for human factor IX.  
 A.Reference number: A30623; NUID:83065193; PMID:65959130  
 A.Accession: A30623  
 A.Molecule type: mRNA  
 A.Residues: 1-13, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'N', 299-356, 'N',  
 A.Cross-references: GB:J00136; NID:g182608; PIDN:AA58726.1; PID:g182609  
 R.Tharakn, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
 Vox Sang. 58, 21-29, 1990  
 A>Title: Development of an immunofluorescence process for factor IX purification.  
 A.Reference number: A60486; NUID:90194857; PMID:2316207  
 A.Accession: A60486  
 A.Molecule type: protein  
 A.Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>  
 R.McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
 A.Reference number: A20274; NUID:83308813; PMID:6688526  
 A.Accession: A20274  
 A.Molecule type: protein  
 A.Residues: 105-109, 'X', 111-115 <MCM>  
 R.Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle  
 Eur. J. Biochem. 172, 565-572, 1988  
 A>Title: Characterization of two differently processed forms of human recombinant factor  
 A.Reference number: S02527; NUID:88166735; PMID:3280312  
 A.Accession: S02527  
 A.Molecule type: protein  
 A.Residues: 29-63 <BAL>  
 A>Note: processed forms expressed in recombinant system  
 R.Jallat, S.; Perrard, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,  
 EMBO J. 9, 3295-3301, 1990  
 A>Title: Characterization of recombinant human factor IX expressed in transgenic mice an  
 A.Reference number: S12058; NUID:91006024; PMID:2209546  
 A.Accession: S12058  
 A.Molecule type: mRNA; protein  
 A.Residues: 1-68 <JAL>  
 A>Note: processed forms expressed in recombinant system

R.Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campe  
 EMBO J. 9, 475-480, 1990  
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium  
 A.Reference number: S12377; NUID:90151623; PMID:2406129  
 A.Accession: S12377  
 A.Molecule type: protein  
 A.Residues: 92-130 <HAN>  
 A>Note: NMR detection of calcium binding by domain expressed in recombinant system  
 R.de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,  
 Thromb. Haemost. 70, 370-371, 1993  
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi  
 A.Reference number: I59612; NUID:94054330; PMID:8236150  
 A.Accession: I59612  
 A.Molecule type: DNA  
 A>Status: translated from GB/EMBL/DBJ  
 A.Residues: 444-461 <RES>  
 A.Cross-references: GB:S66752; NID:g439773; PIDN:AA82858.1; PID:g439774  
 R.Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.  
 Science 239, 491-494, 1988  
 A>Title: Genomic amplification with transcript sequencing.  
 A.Reference number: I59529; NUID:88127096; PMID:3340835  
 A.Accession: I59529  
 A>Status: translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 290-359 <RES>  
 A.Cross-references: GB:M19063; NID:g182622; PIDN:AA52456.1; PID:g182623  
 R.Gyawala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.; Iw  
 Biochemistry 33, 5167-5171, 1994  
 A>Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin  
 A.Reference number: A54255; NUID:9427047; PMID:8172892  
 A.Accession: A54255  
 A.Molecule type: protein  
 A.Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>  
 A>Note: the residues designated 'X' were determined to be threonine bound to carbohydrate  
 R.Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.  
 J. Clin. Invest. 61, 1528-1538, 1978  
 A>Title: Activation of human factor IX (Christmas factor).  
 A.Reference number: A18483; NUID:78194509; PMID:559613  
 A.Contents: annotation; activation; active site; carbohydrate binding  
 A.McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
 Am. Soc. Hematol. Abstr. 64(suppl.1), 262a, 1984  
 A.Reference number: A37563  
 A.Contents: annotation  
 A>Note: 194-Thr was also found  
 R.Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
 J. Biol. Chem. 259, 5698-5704, 1984  
 A>Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
 A.Reference number: A37543; NUID:84185715; PMID:6425296  
 A.Contents: annotation; calcium binding  
 R.Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
 J. Biol. Chem. 260, 2583, 1985  
 A.Reference number: A37544  
 A.Contents: annotation; calcium binding; correction  
 R.Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
 Cell 45, 343-348, 1986  
 A>Title: Defective propeptide processing of blood clotting factor IX caused by mutation  
 A.Reference number: A37545; NUID:86189947; PMID:3009023  
 A.Contents: annotation; signal sequence cleavage site  
 R.Suenho, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,  
 J. Biol. Chem. 264, 21257-21265, 1989  
 A>Title: Blood clotting factor IX (BIM) Nagoya: substitution of arginine 180 by tryptophan  
 A.Reference number: A30622; NUID:90078229; PMID:2592373  
 A.Contents: annotation; sequence of mutant BIM Nagoya  
 A.Note: carboxylation, glycosylation, and cleavage sites  
 R.Baron, M.; Norman, D.G.; Harvey, T.S.; Handford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee  
 submitted to the Brookhaven Protein Data Bank, November 1991  
 A.Reference number: A51252; PDB:1IXA  
 A.Contents: annotation; conformation by (1)H-NMR, residues 92-130  
 A>Note: recombinant form expressed in yeast  
 C.Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr  
 C.Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C.Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with sero  
 C.Genetics:



A:Gene: GDB:F9  
A:Cross-references: GDB:119900; OMIM:306900  
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A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
A:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of factor V  
A:Pathway: blood coagulation intrinsic pathway  
A:Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
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F:31-91/Domain: Gla domain homology <Gla>  
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F:97-128/Domain: BGF homology <EG1>  
F:134-170/Domain: BGF homology <EG2>  
F:192-226/Domain: activation peptide #status experimental <ACT>  
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F:227-454/Domain: trypsin homology <TRY>  
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F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D  
F:99/Binding site: carboxylate (Ser) (covalent) #status experimental  
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental  
F:203,213/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:205,215/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

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Db 57 QGNLRECKEKCSFPAEAREVFNERTETFEWKQY 91

RESULT 14  
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N:Alternate names: Christmas factor  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Nov-1980 #sequence revision 03-Aug-1994 #text\_change 16-Jul-1999  
C:Accession: A14757; B20274; I45891; A00923  
R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Th  
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa  
A:Reference number: A14757; MUID:80056619; PMID:291916  
A:Accession: A14757  
A:Molecule type: protein  
A:Residues: 1-63, 'T', 65-416 <KAT>  
R:McMullen, B.A.; Fujikawa, K.; Kistel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
A:Reference number: A20274; MUID:83308813; PMID:668526  
A:Accession: B20274  
A:Molecule type: protein  
A:Residues: 59-63, 'X', 65-69 <MCW>  
R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
Nature 299, 178-180, 1982  
A:Title: Molecular cloning of the gene for human anti-naemophilic factor IX.  
A:Reference number: I45891; MUID:82272386; PMID:6287289  
A:Accession: I45891  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 52-139 <CBO>  
A:Cross-references: GB:J00007; NID:9163053; PIDN:AAA30520.1; PID:9163054  
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J.  
Biochem. 104, 867-868, 1988  
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag  
A:Reference number: A44556; MUID:89213599; PMID:3148637  
A:Contents: annotation  
A>Note: structure and location of a carboxylate covalently bound to Ser  
C:Comment: Factor IX is activated by factor IXa, which excises the activation peptide pr

C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen  
A:Pathway: blood coagulation intrinsic pathway  
A:Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
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F:51-82/Domain: BGF homology <EG1>  
F:88-124/Domain: BGF homology <EG2>  
F:147-161/Domain: activation peptide #status experimental <AP>  
F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F:182-409/Domain: trypsin homology <TRY>  
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F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Diisulfi  
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F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
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RESULT 15  
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C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1993 #sequence revision 07-May-1993 #text\_change 03-May-2002  
C:Accession: S10511; A60576; B42696  
R:Dhanich, M.; Monard, D.  
Nucleic Acids Res. 18, 4251, 1990  
A:Title: cDNA sequence of rat prothrombin.  
A:Reference number: S10511; MUID:90332426; PMID:2377469  
A:Accession: S10511  
A:Molecule type: mRNA  
A:Residues: 1-617 <DHR>  
A:Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970  
R:Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.  
Endocrinology 126, 167-175, 1990  
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.  
A:Reference number: A60576; MUID:90091942; PMID:2293980  
A:Accession: A60576  
A:Molecule type: protein  
A:Residues: 44-58 <HEN>  
A>Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute  
R:Banfield, D.K.; MacCallilivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
A:Reference number: A42696; MUID:92212913; PMID:1557383  
A:Accession: B42696  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 383-617, 'E' <BAN>  
A:Cross-references: GB:M1397  
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydr  
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F:25-43/Domain: propeptide #status predicted <PP>  
F:28-88/Domain: Gla domain homology <Gla>  
F:44-617/Product: prothrombin #status experimental <PMAT>  
F:109-167/Domain: kringle homology <KR1>  
F:215-293/Domain: kringle homology <KR2>  
F:360-608/Domain: trypsin homology <TRY>  
F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:61-66,91-104,109-187,130-170,158-182,215-292,336-276,264-287,332-478,387-403,532-546,5  
F:402,458,564/Active site: His, Asp, Ser #status predicted

